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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"		
(57) Abstract <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>		

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule
15 (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

20 Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

25 In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

In a another aspect, the invention provides a method of determining the presence of or
30 predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF n according to the invention (wherein n is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2 n -1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2 n . For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu/>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

5 **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoetin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

25 **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia
5 areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes
10 may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the
15 proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by
20 interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and
25 dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_ma_bind	DNA/RNA binding protein/factor
	dna_ma_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
	reductase	reductase
10	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
	SIM	similar
15	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
	struct	structural associated protein
	sulfotransferase	sulfotransferase
20	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
	synthase	synthase
	tgf	transforming growth factor
25	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
	tm7	seven transmembrane domain G-protein coupled receptor
30	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
	tubulin	tubulin
	ubiquitin	ubiquitin
40	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2 n , wherein $n = 1$ to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2 n (wherein $n = 1$ to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), or a fragment thereof, any of whose bases may be changed from the disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), including fragments, derivatives,

analogues and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic
20 acid molecules include, but are not limited to, recombinant DNA molecules contained in a vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

- 5 As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.
- 10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

- Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
- 15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
- 20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
- 25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

- Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
- 30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2 n (wherein $n = 1$ to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and
5 Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A
10 non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at
15 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

20 In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions
25 leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present
30 invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2 n (wherein $n = 1$ to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2 n (wherein $n = 1$ to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2 n -1 for the corresponding n , such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (*v*), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (*v*), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch 1970 J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2n-1 (wherein n = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15 In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20 In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of ORFX with a ORFX ligand.

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A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477.

15 **Polypeptide libraries**

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)}_2$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by
15 techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*
30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the
5 nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as
10 described herein (e.g., ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY:
15 METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or
20 non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is
25 introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and
30 pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

 In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

 Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

 In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

5 **Transgenic animals**

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat.

5 Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed
10 additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene
15 (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous
20 ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous
25 ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the
30 endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also
5 referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs
and homologs thereof, can be incorporated into pharmaceutical compositions suitable for
administration. Such compositions typically comprise the nucleic acid molecule, protein, or
antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically
10 acceptable carrier" is intended to include any and all solvents, dispersion media, coatings,
antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like,
compatible with pharmaceutical administration. Suitable carriers are described in the most
recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field,
which is incorporated herein by reference. Preferred examples of such carriers or diluents
15 include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human
serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The
use of such media and agents for pharmaceutically active substances is well known in the art.
Except insofar as any conventional media or agent is incompatible with the active compound,
use thereof in the compositions is contemplated. Supplementary active compounds can also be
incorporated into the compositions.

20 A pharmaceutical composition of the invention is formulated to be compatible with its
intended route of administration. Examples of routes of administration include parenteral, *e.g.*,
intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical),
transmucosal, and rectal administration. Solutions or suspensions used for parenteral,
intradermal, or subcutaneous application can include the following components: a sterile diluent
25 such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene
glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl
parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as
ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for
the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with
30 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can
be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,
10 peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained
15 using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are
20 applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)
25 *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),
30 plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding
5 of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct
10 binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the
15 induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test
20 compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test
25 compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein
30 or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) *Cell* 72:223-232; Madura *et al.* (1993) *J Biol Chem* 268:12046-12054; Bartel *et al.* (1993) *Biotechniques* 14:920-924; Iwabuchi *et al.* (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (e.g., blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (e.g., drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (e.g., the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (e.g., drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (i.e. another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: __ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (i.e. screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the
10 individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

 An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of
20 a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to
25 stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be
30 administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX
5 nucleic acids of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological
10 sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid
15 probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

10 In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, e.g., U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of
15 collecting a sample of cells from a patient, isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an
20 amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli
25 *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such
30 molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a
10 sample and control nucleic acids, e.g., DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, e.g., PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that
5 cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest
10 mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

15 In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T
20 mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

25 In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments
30 of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, *e.g.*, Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, *e.g.*, Myers *et al* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, *e.g.*, Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, *e.g.*, Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, *e.g.*, Gasparini *et al* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (e.g., N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models,
5 in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or
15 suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number
20 in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the
25 epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include
5 *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

10 Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination);
15 benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate
20 (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of
25 apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
15 (Frostedgard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

 Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons, Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, *Leishmania* species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J*
30 *Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

 A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in
10 male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may
15 also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of
30 wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

- 20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell
interactions and their ligands (including without limitation, cellular adhesion molecules (such as
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,
10 antigen recognition and development of cellular and humoral immune responses). Receptors and
ligands are also useful for screening of potential peptide or small molecule inhibitors of the
relevant receptor/ligand interaction. A protein of the present invention (including, without
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*
Med. 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,
J Immunol Methods 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
of other factors which more directly inhibit or promote an inflammatory response. Proteins
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from
5 over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit
10 tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote
15 tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing
20 or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or
25 elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other
30 than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or
5 entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for
15 purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to
20 those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gj14691395[emb]CAB41562.1) - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gj2829508[sp]P71559[SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)]	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264567
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264905, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264780, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gj14415928[gb]AAD201571 - (AC06282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264683, 264768, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35699423, 55811578, 35695655, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gj1585562[sp]Q06456[NIRB_KLEPN - NITRITE REDUCTASE [NAD(PH)] LARGE SUBUNIT]		reductase	264807
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79558459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gj13878145[emb]CAA98871) - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264594
14	95105114 (27, 28)	Novel Protein sim. GBank gj12832781[emb]CAA128451 - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Anky repeat	potassium_channel	35698288, 35698052, 264510, 35695917, 264691, 264628, 35698423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gj1710781[sp]Q10234[RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5]	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20282744 (33, 34)	Novel Protein sim. GBank gij117484[sp]P4391[URE1_HAEN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)]	Contains protein domain (PF00449) - Urease	284600	
18	80246804 (35, 36)	Novel Protein sim. GBank gij2281102 (AC002333) - SF16 Isolog [Arabidopsis thaliana]		29331827, 284555, 284557, 284638, 284558	
19	80078624 (37, 38)	Novel Protein sim. GBank	UNCLASSIFIED	22278988, 284907, 284910, 284600, 284693	
20	20724558 (39, 40)	Novel Protein sim. GBank gij2506112[sp]P43672[UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP]	transport	284602	
21	80417554 (41, 42)	Novel Protein sim. GBank gij1730203[sp]P50442[GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE-GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)]	UNCLASSIFIED	22278985, 284906, 265008, 265010, 265011, 284602, 284605, 284768, 284688, 21908784, 284691, 18108376, 284638, 18108387, 284486	
22	11705858 (43, 44)	Novel Protein sim. GBank gij1877329[emb]CAB07077] - (292771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	284685	
23	80419176 (45, 46)			284488, 284907, 284909, 284600, 284602, 284603, 284605, 284682, 284768, 32833986, 284638, 284486	
24	20291697 (47, 48)			284600	
25	80253774 (49, 50)			284593	
26	80255394 (51, 52)		UNCLASSIFIED	22278996, 56182435, 265018, 264566	
27	80235785 (53, 54)	Novel Protein sim. GBank gij4808359[emb]CAB42783.1] - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - Ribosomal protein S14pS29e	18108370, 35898423, 284635, 284555	
28	79483581 (55, 56)		UNCLASSIFIED	284638	
29	82448765 (57, 58)	Novel Protein sim. GBank gij3122280[sp]O08333[KGPF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]	kinase	284601, 284762, 284768, 284769, 284638	
30	79199333 (59, 60)		UNCLASSIFIED	284908, 265019, 284687, 21906784, 21908768	
31	19848158 (61, 62)		UNCLASSIFIED	284534	
32	82449485 (63, 64)	Novel Protein sim. GBank gij3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	284905, 284805, 284762, 284768, 284687,	
33	79582628 (65, 66)	Novel Protein sim. GBank gij2129003[pir]G64507 - hypothetical protein MJ1685 - Methanococcus jannaschii	UNCLASSIFIED	284689 284687	
34	87467657 (67, 68)		UNCLASSIFIED	60432289, 284600, 284602, 284780, 18108357, 284768, 265020, 284691	
35	95005170 (69, 70)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	284600, 284687, 284558, 284639	
36	19642042 (71, 72)	Novel Protein sim. GBank gij3287739[sp]P73538[BIOB_SYNY3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)]	synthase	284566	
37	20369215 (73, 74)	Novel Protein sim. GBank gij2313134[sp]AAD07126.1] - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]	dehydrogenase	284603	

38	20466334 (75, 76)	Novel Protein sim. GBank gl 3805970 emb CAA06231 - (AJ004933) periplasmic nitrate reductase, large subunit [Rhodospirillum rubrum sp.]		reductase	284605
38	94300715 (77, 78)	Novel Protein sim. GBank gl 1929448 (L63543) - endodermis [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	284905, 284906, 284907, 66712502, 284908, 284909, 284511, 285009, 284910, 55812038, 284758, 265011, 284782, 284882, 284763, 284784, 284788, 285022, 284893, 284828, 284831, 284834, 284835, 284555, 284838, 18108381, 284556, 18108385, 284482
40	20635625 (78, 80)			UNCLASSIFIED	284592
41	80023287 (81, 82)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U89 [Human herpesvirus 6]			284591, 35695917
42	20724568 (83, 84)			UNCLASSIFIED	284602
43	20467089 (85, 86)	Novel Protein sim. GBank gl 3820594 (AF086781) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	284605
44	13085297 (87, 88)	Novel Protein sim. GBank gl 2494764 sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)	Contains protein domain (PF00858) - GMP synthase C terminal domain	synthase	284769, 284838
45	39384711 (89, 90)	Novel Protein sim. GBank gl 1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	284769, 284510, 284508
46	95003398 (91, 92)			ngf	284568
47	11696624 (93, 94)			UNCLASSIFIED	284889
48	79407218 (95, 96)				18108385, 284635, 284828
49	21659844 (97, 98)			UNCLASSIFIED	284603
50	80503998 (99, 100)				284508, 284603, 284769, 284889, 284636, 284558, 284488
51	80255569 (101, 102)	Novel Protein sim. GBank gl 3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	284593, 18108387
52	79208528 (103, 104)	Novel Protein sim. GBank gl 3914892 sp Q28264 SMA1 - HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)		struc	284634
53	36996970 (105, 106)	Novel Protein sim. GBank gl 3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	284762
54	79570897 (107, 108)			UNCLASSIFIED	284830, 284909, 284788
55	80202703 (109, 110)	Novel Protein sim. GBank gl 1633572 (U52064) - Herpesvirus thymus ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]		UNCLASSIFIED	29331824, 284102, 265018, 18108376
56	8758408 (111, 112)	Novel Protein sim. GBank gl 4321580 gb AAD15785 - (AF050114) alginatase [Pseudomonas sp. W7]			284604
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284557

58	91227508 (115, 116)	Novel Protein sim. GBank gij5616074jgb AAD45616.1 AF08194 - (AF081943) prolacte- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56192575, 264259, 60432049, 35896052, 66712502, 264908, 265008, 265010, 265011, 264881, 28148784, 35695917, 60170815, 264691, 264692, 264693, 18108374, 35896423, 58182323, 60432113
59	80077371 (117, 118)	Novel Protein sim. GBank gij1172920isp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00853) - Glycosyl transferase	transferase	264600, 264689, 264638
60	12958341 (119, 120)				
61	80426608 (121, 122)	Novel Protein sim. GBank gij1710216 (U79260) - unknown [Homo sapiens]		glycoprotein	264689 264766
62	13504968 (123, 124)				
63	16474553 (125, 126)				264630
64	20724578 (127, 128)	Novel Protein sim. GBank gij420945p j A47041 - transposase homolog (Insertion element [SAE1] - Alcaligenes eutrophus		UNCLASSIFIED	265019
65	79326308 (129, 130)	Novel Protein sim. GBank gij3122312isp O08134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gij3928723 emb CAA22218 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		transport	22278986, 264558
67	78852543 (133, 134)	Novel Protein sim. GBank gij231885isp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE [40 KD ANTIGEN]		dehydrogenase	265021
68	79817382 (135, 136)				
69	79841784 (137, 138)				264909
70	79871328 (139, 140)			UNCLASSIFIED	264908
71	85897458 (141, 142)				264908, 264908
72	87734977 (143, 144)	Novel Protein sim. GBank gij4415928 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264602, 265021
73	80025241 (145, 146)			UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87188474, 264682, 264766, 264688, 264689, 35895917, 265021, 60170815, 264691, 33657023, 264692, 264693, 264628, 264631, 264639, 22278000
74	20377410 (147, 148)			UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264887, 264689, 264692, 18108387
75	11618032 (149, 150)	Novel Protein sim. GBank gij2853098 emb CAA16914 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	264805
76	95105303 (151, 152)	Novel Protein sim. GBank gij4468811 emb CA838212 - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264889
77	10144718 (153, 154)	Novel Protein sim. GBank gij854085 emb CAA58337 - (X63413) U88 [Human herpesvirus 6]		UNCLASSIFIED	83373044, 264908, 264557
78	8758258 (155, 156)			UNCLASSIFIED	264563
				UNCLASSIFIED	264604

79	94140180 (157, 158)	Novel Protein sim. GBank gl 5689453 dbj BAA83010.1 - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		35686286, 22278988, 28331822, 28331824, 29331825, 28331827, 264905, 264906, 264907, 66712502, 264908, 264909, 265008, 265009, 264910, 60170831, 55812038, 33109954, 285017, 265018, 284288, 264768, 56181562, 21906765, 21906769, 29148764, 265020, 264690, 264691, 264692, 264693, 60431528, 35698423, 264631, 264632, 264634, 264636, 264638, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)			UNCLASSIFIED	264769, 264801, 265008, 264910, 264604, 264605, 264634, 264635, 264605, 264762, 264637, 264592, 264628, 264907, 264691, 264908, 264587, 264909, 264768, 264805
81	20467247 (161, 162)	Novel Protein sim. GBank gl 1723442 sp Q10258 YO2A_SCHPO - HYPOTHETICAL 89.0 KD PROTEIN C56F8.10 IN CHROMOSOME I		reductase	
82	16331388 (163, 164)	Novel Protein sim. GBank gl 2895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]		dehydrogenase	264567
83	94741180 (165, 166)	Novel Protein sim. GBank gl 3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264508, 264509, 264905, 264808, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264756, 264603, 264760, 264681, 18108351, 264762, 264682, 264764, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264566
84	80355375 (167, 168)	Novel Protein sim. GBank gl 173384 sp P45380 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTI-PORTER)		transport	264508, 264808, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264766, 264768, 264769, 35695655, 264638, 264637
85	80498600 (169, 170)	Novel Protein sim. GBank gl 2120998 p J S70882 - glycosyltransferase homolog - Bordetella pertussis		transferase	264605, 264762, 264687, 264769, 18108374, 264638, 264488
86	39559043 (171, 172)	Novel Protein sim. GBank gl 3256023 emb CAA17228.1 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			264810
87	13856808 (173, 174)			UNCLASSIFIED	264093

88	95344718 (175, 176)	Novel Protein sim. GBank gi 559703 dbj BAA07552 - (D38549) ha1025 is new [Homo sapiens]		5264507, 52646365, 18108398, 65274572, 58182575, 56994075, 35688286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264258, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432288, 29331827, 29331828, 35686052, 33656970, 264105, 264508, 264905, 264908, 264907, 264908, 29331830, 66712502, 52644045, 56182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 21908754, 52646317, 33109954, 52644298, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264389, 264288, 264766, 52644229, 21908768, 21908787, 21908788, 21908789, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35696423, 55811578, 65274791, 35695855, 60431850, 264636, 52644332, 58182323, 60170384, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264486, 264600
89	80077389 (177, 178)	Novel Protein sim. GBank gi 1710383 sp P48352 PXP_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		
90	82115998 (179, 180)	Novel Protein sim. GBank gi 2498891 sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION	UNCLASSIFIED protease	264760 285006
91	78908950 (181, 182)	Novel Protein sim. GBank gi 3367754 emb CAA20078 - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED	264691
92	79554871 (183, 184)	Novel Protein sim. GBank gi 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase_associated	264907, 264908, 264910, 265009, 264605, 264789
93	80496778 (185, 186)	Novel Protein sim. GBank gi 171919 sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - CBS domain	264908
94	78646649 (187, 188)			
95	11090238 (189, 190)			264594

96	94322125 (191, 192)	Novel Protein sim. GBank gl 4589560 dbj BAA76802.1 - (AB023175) KIAA0958 protein [Homo sapiens]	UNCLASSIFIED	22278995, 22278998, 264259, 26331822, 29331826, 35686052, 29146498, 264509, 264806, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21906765, 21908767, 21906769, 265020, 264692, 33857182, 35685763, 264628, 264629, 18108379, 264631, 264636, 18108381, 264559, 18108382, 83373044, 22278002, 264508
97	79605200 (193, 194)	Novel Protein sim. GBank gl 4583559 emb CAB40388.1 - (AJ005255) OxyR [Erwinia chrysanthemi]	UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gl 1001693 dbj BAA10430 - (D64002) hypothetical protein [Synechocystis sp.]	UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gl 1169479 sp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	264605
100	79840113 (199, 200)	Novel Protein sim. GBank gl 460887 pir J37485 - gene msg1 protein - mouse	UNCLASSIFIED	264693
101	80203298 (201, 202)	Novel Protein sim. GBank gl 2894166 emb CAA11773.1 - (AJ223998) PCZA361.18 [Ameycolatopsis orientalis]	UNCLASSIFIED	265020, 264102, 263972
102	20467258 (203, 204)	Novel Protein sim. GBank gl 1731040 sp P54509 YQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gl 1705505 sp P54729 BSA_MOUSE - BSA PROTEIN	UNCLASSIFIED	264591, 264595, 264602
105	79605206 (209, 210)	Novel Protein sim. GBank gl 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	complement	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gl 1705505 sp P54729 BSA_MOUSE - BSA PROTEIN	UNCLASSIFIED	264511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gl 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	ATPase-associated	26331824, 264591, 21606754, 265019
108	80237938 (215, 216)	Novel Protein sim. GBank gl 263377 emb CAB15264 - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	transport	18108374, 35685917, 22278996, 264113, 264600, 264602, 264603, 265017, 264910, 264908, 264636, 264766
109	95184148 (217, 218)	Novel Protein sim. GBank gl 2330781 emb CAB11265 - (Z98801) carboxypeptidase a precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	264758, 264603, 264630, 264638, 264637
110	79582823 (219, 220)			264987
111	39565458 (221, 222)			264564
112	79856038 (223, 224)		UNCLASSIFIED	264908
113	17959439 (225, 226)		UNCLASSIFIED	265007
114	80502101 (227, 228)		UNCLASSIFIED	264769

115	80251003 (228, 230)	Novel Protein sim. GBank gjl2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52845156, 52845080, 33656970, 284592, 21908754, 27486284, 18108379, 35898423, 284635, 52844332, 18108382
116	81298688 (231, 232)				284805, 284908, 284807, 284808, 284909, 284910, 284758, 285010, 284763, 284882, 284764, 284768, 284685, 284686, 284768, 284769, 33657023, 284689, 33657109, 284628, 18108374, 284631, 284632, 284634, 284636, 284637, 284638, 284639, 56528486, 284565, 284568
117	79636695 (233, 234)				284639, 284693
118	80222170 (235, 236)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	283974
119	91013071 (237, 238)	Novel Protein sim. GBank gjl732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 28331824, 60432288, 265007, 60433438, 284603, 284605, 18108351, 284769, 284689, 285020, 284534, 27486281, 284558, 83373044, 18108385, 284564
120	8756491 (239, 240)	Novel Protein sim. GBank gjl2131219 [pir] [S50157] - cyclin-dependent kinase chain SRB10 - yeast [Saccharomyces cerevisiae]		kinase	284603
121	80028153 (241, 242)				284595
122	20457620 (243, 244)	Novel Protein sim. GBank gjl2052147 [emb] [CAB08137] - (Z94752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	284605
123	8758278 (245, 246)				284604
124	79104017 (247, 248)	Novel Protein sim. GBank gjl2833385 [sp] [Q43134] [UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 285010, 285011, 18108355, 18108378, 18108380, 18108384
125	87797988 (249, 250)	Novel Protein sim. GBank gjl475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	284508, 284908, 285009, 284598, 22278002
126	56701283 (251, 252)	Novel Protein sim. GBank gjl5102785 [emb] [CAB45200.1] - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]			284511
127	20467267 (253, 254)				284605
128	80248473 (255, 256)	Novel Protein sim. GBank gjl130120 [sp] [P23620] [PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED - phosphatase	284807, 284909, 284910, 284600, 284601, 284803, 284805, 18108351, 284683, 284557
129	95280543 (257, 258)	Novel Protein sim. GBank gjl2508493 [sp] [P38036] [YGC8_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35698423, 35695855, 284600, 284602, 284603, 284604, 284605, 284508, 284808, 284564, 284628, 284682, 284585, 284683
130	80085583 (259, 260)	Novel Protein sim. GBank gjl854085 [emb] [CAA56337] - (X83413) U88 [Human herpesvirus 6]			284634
131	94995022 (261, 262)	Novel Protein sim. GBank gjl1076039 [pir] [S54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108378, 284769, 28331826, 284688, 22278998, 285021, 284600, 284511, 284601, 284602, 284605, 284905, 284638

132	10887692 (263, 284)	Novel Protein sim. GBank gj11877340[emb]CAB07068] - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264638 264905, 264688
133	94630883 (265, 286)				
134	79834880 (267, 288)	Novel Protein sim. GBank gj14585838[emb]CAB40932.1] - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	264905, 264605, 265021
135	19885057 (269, 270)	Novel Protein sim. GBank gj1460074[emb]CAB01049] - (Z77250) hypothetical protein Rv2586 [Mycobacterium tuberculosis]			264634
136	79846083 (271, 272)	Novel Protein sim. GBank gj12125896[emb]CAA73511] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	264508
137	79819770 (273, 274)				
138	79635971 (275, 276)	Novel Protein sim. GBank gj15420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264683, 264685, 264686, 264691, 264692, 264693
139	86880076 (277, 278)	Novel Protein sim. GBank gj15689912[emb]CAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265006, 265007, 265008, 265009, 264693
140	79825759 (279, 280)			UNCLASSIFIED	22278998, 265007, 264910, 60433358, 265010, 264602, 264605, 264768, 264688, 264769, 264693, 32833986, 18108374, 18108387
141	20700084 (281, 282)				264908
142	80028104 (283, 284)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	264600 264602, 265017
143	11072274 (285, 286)				
144	85009102 (287, 288)	Novel Protein sim. GBank gj13334127[sp]P87303[BAC2_MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)]		UNCLASSIFIED	264600
145	80027058 (289, 290)	Novel Protein sim. GBank gj13757569[emb]CAA21315] - (AL031863) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]			263878, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264628, 264638
146	13085682 (291, 292)	Novel Protein sim. GBank gj1140807[sp]P24536[Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN]	Contains protein domain (PF01675) - Transposase		22278998, 264602
147	94320366 (293, 294)	Novel Protein sim. GBank gj12827608[emb]CAA16663] - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	264905, 264906, 264908, 264510, 265009, 60433358, 264600, 264601, 264604, 264605, 264687, 264769, 18108385, 85274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gj12916947[emb]CAA17585] - (AL021999) hypothetical protein Rv0886 [Mycobacterium tuberculosis]		transport	265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (287, 298)	Novel Protein sim. GBank gjl1723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - transport ABC transporter	285010, 284600, 284601, 284603, 284604, 27486265, 284636
150	20284748 (289, 300)	Novel Protein sim. GBank gjl3724125 emb CAA11805 - (AJ224340) maltosephosphorylase [Lactobacillus sanfrancisco]		284600
151	20726398 (301, 302)	Novel Protein sim. GBank gjl729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - UNCLASSIFIED Metalloenzyme superfamily	284602
152	95002877 (303, 304)	Novel Protein sim. GBank gjl2497952 sp P55687 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM	peptidase	284602
153	80256865 (305, 306)	Novel Protein sim. GBank gjl3123021 sp Q80508 MT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))	UNCLASSIFIED	284593
154	82105968 (307, 308)	Novel Protein sim. GBank gjl19897 pir JN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	284810, 284762, 284691, 284634 284605
155	20428859 (308, 310)	Novel Protein sim. GBank gjl628710 pir S41739 - hypothetical protein - Escherichia coli	UNCLASSIFIED	284565
156	38564742 (311, 312)	Novel Protein sim. GBank gjl3895013 (AF032586) - CtrA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifHtrxC family	284691
157	10358687 (313, 314)	Novel Protein sim. GBank gjl1073072 pir C55543 - cnaU protein - Pseudomonas syringae pv. syringae	UNCLASSIFIED	284905
158	79761938 (315, 316)	Novel Protein sim. GBank gjl1073072 pir C55543 - cnaU protein - Pseudomonas syringae pv. syringae	UNCLASSIFIED	284905
159	78890378 (317, 318)	Novel Protein sim. GBank	UNCLASSIFIED	284905
160	11075119 (318, 320)	Novel Protein sim. GBank	UNCLASSIFIED	284905
161	80055007 (321, 322)	Novel Protein sim. GBank gjl1173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	284905
162	80016371 (323, 324)	Novel Protein sim. GBank gjl5304869 emb CAB48028.1 - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30pL7e	22278998, 284600, 284603, 35695917, 32833988, 35698423, 284638
163	11882308 (325, 326)	Novel Protein sim. GBank gjl2661691 emb CAA15795 - (AL009204) putative protease [Streptomyces coelicolor]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	284112, 284532, 22278002
164	80077802 (327, 328)	Novel Protein sim. GBank gjl4416478 sp AAD20378 - (AF125999) transposase [Mycobacterium avium]	UNCLASSIFIED	284639
165	10856067 (328, 330)	Novel Protein sim. GBank gjl76177 pir QQECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	284605, 284607, 284600 284691
166	88085003 (331, 332)	Novel Protein sim. GBank gjl2661691 emb CAA15795 - (AL009204) putative protease [Streptomyces coelicolor]	UNCLASSIFIED	284605, 284486
167	16395460 (333, 334)	Novel Protein sim. GBank gjl4416478 sp AAD20378 - (AF125999) transposase [Mycobacterium avium]	UNCLASSIFIED	285010
168	80079362 (335, 336)	Novel Protein sim. GBank gjl76177 pir QQECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli	UNCLASSIFIED	284600
169	80239581 (337, 338)	Novel Protein sim. GBank gjl76177 pir QQECFT - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		284558, 284557, 284558, 284559

170	79612364 (339, 340)	Novel Protein sim. GBank gil140888[sp]p27647[YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECO-PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator	284908 284595, 284604	
171	95283073 (341, 342)				
172	37797007 (343, 344)	Novel Protein sim. GBank gil4210905[sp]pAAD12048.1] - (AF045609) AgIG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	284789	transport
173	57529660 (345, 346)	Novel Protein sim. GBank gil132854[sp]p02387[RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	284769	ribosomalprot
174	95293078 (347, 348)	Novel Protein sim. GBank gil1881350[sp]pBAA18371] - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]	transport	284510, 284583, 284602, 284603, 284605, 284782, 284693	
175	79758270 (349, 350)	Novel Protein sim. GBank gil2072722[sp]pCAB08328] - (Z95121) manA [Mycobacterium tuberculosis]	isomerase	284565	
176	80068898 (351, 352)	Novel Protein sim. GBank gil1055198 (U40187) - similar to PIR:A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED	284907, 284910, 284881, 284558	
177	86684652 (353, 354)	Novel Protein sim. GBank gil232673[sp]pCAB10952] - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	284788, 80424179, 284687, 284688, 284769, 29331828, 80432289, 18108376, 284689, 18108387, 32833888, 22278998, 285020, 284600, 284801, 284802, 284603, 284604, 284605, 284635, 284782, 284638, 284808, 284584, 284637, 284638, 284486, 80433356, 284788	UNCLASSIFIED
178	78559526 (355, 356)	Novel Protein sim. GBank gil1906596 (U81788) - kinesin-73 [Drosophila melanogaster]	strud	284693, 33857109, 284635	
179	20263112 (357, 358)			284583	UNCLASSIFIED
180	80486958 (359, 360)	Novel Protein sim. GBank gil1169387[sp]p45256[DNAB_HAEIN - REPLICATIVE DNA HELICASE	helicase	284769	
181	78585369 (361, 362)	Novel Protein sim. GBank gil3170615 (AF059485) - DOCA [Mus musculus]	UNCLASSIFIED	21806767, 284635, 284638, 18108384	
182	80577899 (363, 364)				
183	11614017 (365, 366)	Novel Protein sim. GBank gil1076627[sp]pS54172 - Inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED	284259, 35896052, 56182435, 284511, 285018, 33857109, 284555, 284586	
184	10174167 (367, 368)	Novel Protein sim. GBank gil4371280[sp]pAAD18138] - (AC008280) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	284690	
				284510	UNCLASSIFIED

185	21860822 (368, 370)	Novel Protein sim. GBank gij3006178jemb[CAA18398.1] - (AL022304) putative mima transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	284604
186	80070329 (371, 372)	Novel Protein sim. GBank gij2829802sp[P94408]YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION	transport		284595
187	80186611 (373, 374)	Novel Protein sim. GBank gij3150260jemb[CAA18179] - (AL023834) Cydlin [Schizosaccharomyces pombe]	UNCLASSIFIED		284369
188	20464942 (375, 376)	Novel Protein sim. GBank gij2145853jir[S72938 - hix protein - Mycobacterium leprae]	kinase		284605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244jdb[BAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]	UNCLASSIFIED		35896052, 284602, 284605, 284782, 284689, 35895917, 18108370, 18108372, 284638, 284565
190	80086621 (379, 380)	Novel Protein sim. GBank gij120228sp[P28725]FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (ROTAMASE)	synthase		284563
191	88095012 (381, 382)	Novel Protein sim. GBank gij1705461sp[P53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	isomerase		284508, 284604, 284605, 284789, 284555
192	18333379 (383, 384)	Novel Protein sim. GBank gij4980892jgb[AAD35474.1]AE001171 - (AE001718) ABC transporter. ATP-binding protein [Thermotoga maritima]			284567
193	78910127 (385, 386)	Novel Protein sim. GBank gij1705461sp[P53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)			284608, 284693
194	20464949 (387, 388)	Novel Protein sim. GBank gij1705461sp[P53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)			284605
195	13518389 (389, 390)	Novel Protein sim. GBank gij1705461sp[P53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	transport		284636
196	95005568 (391, 392)	Novel Protein sim. GBank gij1705461sp[P53656]BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)			284600, 284689, 284638
197	80248665 (393, 394)	Novel Protein sim. GBank gij3122305sp[Q27778]KGF SCHMA - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE)	gaba		284602, 284682, 284692, 18108374
198	79163635 (395, 396)	Novel Protein sim. GBank gij1781203jemb[CAB08110] - (Z83859) gnd [Mycobacterium tuberculosis]	kinase		284602, 284682, 284692, 18108374
199	78890715 (397, 398)	Novel Protein sim. GBank gij1781203jemb[CAB08110] - (Z83859) gnd [Mycobacterium tuberculosis]			284638
200	79413849 (399, 400)	Novel Protein sim. GBank gij2842222 (AF030885) - telomere-associated recQ-like helicase [Lactago maydis]	6-phosphogluconate dehydrogenases		285008
201	86945924 (401, 402)	Novel Protein sim. GBank gij2804378jemb[CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]	UNCLASSIFIED		284595, 284588
			UNCLASSIFIED		29331828, 285007, 284512, 33657402, 284596, 285017, 18108351, 284682, 284683, 284787, 284629, 55810784, 284634, 284635, 58182323, 60432113, 22278000

202	79588046 (403, 404)	Novel Protein sim. GBank gi 231772 sp P30598 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - synthase Chitin synthase	284600
203	79843927 (405, 406)	Novel Protein sim. GBank gi 1504042 dbj BAA13220 - (D88984) similar to yeast adenylyate cyclase (S58776) [Homo sapiens]		22278995, 28331822, 28331825, 28331827, 284906, 21906754, 284683, 21906786, 21906789, 35698423, 284558
204	79855186 (407, 408)		UNCLASSIFIED	284909
205	10090583 (409, 410)	Novel Protein sim. GBank gi 2833808 emb CAB13310 - (Z89111) similar to hypothetical proteins [Bacillus subtilis]	transport	284909
206	8758473 (411, 412)		UNCLASSIFIED	284604
207	20754522 (413, 414)	Novel Protein sim. GBank gi 2134381 pir S60678 - polybromo 1 protein - chicken	UNCLASSIFIED	284558
208	20288281 (415, 416)			284605
209	80071088 (417, 418)	Novel Protein sim. GBank gi 2501040 sp O05814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)		284605, 284688
210	80168800 (419, 420)			284905, 284907, 284909, 284786, 284687, 284691, 284629, 18108374, 284638
211	80034539 (421, 422)			283978
212	82442474 (423, 424)	Novel Protein sim. GBank gi 5031809 ref NP_005536.1 pISLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	284508, 284805, 284906, 284907, 284908, 284600, 284782, 284534, 284632, 284634, 284635, 284839, 284488
213	80248562 (425, 426)	Novel Protein sim. GBank gi 3122359 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - isomerase Aconitase family (aconitate hydratase)	22278986, 284508, 284800, 284602, 284603, 284605, 33857023, 284565, 284486
214	80079381 (427, 428)	Novel Protein sim. GBank gi 116238 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - sph TCP-1/cpn60 chaperonin family	284600, 284693
215	14973283 (429, 430)			
216	80177716 (431, 432)	Novel Protein sim. GBank gi 3417287 (AC002310) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	284629
217	79603634 (433, 434)	Novel Protein sim. GBank gi 2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)	dna_ma_bind	284448
218	80258475 (435, 436)	Novel Protein sim. GBank gi 1173288 sp P38108 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN		284508
219	20438787 (437, 438)	Novel Protein sim. GBank gi 1781097 emb CAB06231 - (Z83884) gi B [Mycobacterium tuberculosis]	mapolymerase	284594
220	13499572 (439, 440)	Novel Protein sim. GBank gi 2984703 (AF052427) - unknown [Trypanosoma cruzi]	synthase	284604
221	11267498 (441, 442)	Novel Protein sim. GBank gi 4587313 dbj BAA78708.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	nucleaseinhib	284689
			UNCLASSIFIED	284555

222	79862802 (443, 444)	Novel Protein sim. GBank gj1877288[embjCAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	284605, 284769, 35698423
223	83053869 (445, 446)			UNCLASSIFIED	284906, 284907, 284603
224	79557820 (447, 448)			UNCLASSIFIED	284684, 284693
225	79559541 (449, 450)	Novel Protein sim. GBank gj2274851[dbjBAA21515] - (D84159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	284692
226	78172397 (451, 452)	Novel Protein sim. GBank gj1868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 284112, 33657023, 263981
227	81777186 (453, 454)			UNCLASSIFIED	35695917, 284636, 284907
228	79872285 (455, 456)				284768, 284807, 284908, 284692, 284593, 284639
229	79838288 (457, 458)				284908, 284910
230	11013209 (459, 460)				284631
231	20622207 (461, 462)	Novel Protein sim. GBank gj1835114[embjCAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]		UNCLASSIFIED	284908, 284600, 284603, 284692
232	80055035 (463, 464)				
233	80063054 (465, 466)	Novel Protein sim. GBank gj2842340 (AF032970) - Imidazole propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	284600, 284603, 284605, 284687, 284769
234	7523998 (467, 468)	Novel Protein sim. GBank gj3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	284604
235	80203671 (469, 470)				264369
236	78940001 (471, 472)	Novel Protein sim. GBank gj2104609[embjCAB08805] - (Z95398) PckA [Mycobacterium leprae]		UNCLASSIFIED	264106
237	11755273 (473, 474)				284805
238	79461401 (475, 476)				
239	82435180 (477, 478)	Novel Protein sim. GBank gj2495617[spjQ57252]YDLJ_HAEIN - HYPOTHETICAL PROTEIN H1163	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.	UNCLASSIFIED	264681
240	21635575 (479, 480)	Novel Protein sim. GBank gj3183458[spjP75786]YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA			284639
241	80377307 (481, 482)	Novel Protein sim. GBank gj3875920[embjCAB04111] - (Z81503) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D85450 comes from this gene; cDNA EST EMBL:D86888 comes from this gene [Caenorhabditis elegans]		transport	284908, 285010, 284603, 284762, 284682, 284638, 284638, 284486
242	82148454 (483, 484)				284259, 284769
243	79633207 (485, 486)			UNCLASSIFIED	284908, 284908, 284784, 284639
244	80248682 (487, 488)	Novel Protein sim. GBank gj2624302[embjCAA15575] - (AL008987) ald [Mycobacterium tuberculosis]		UNCLASSIFIED	284489, 284907, 284908, 284511, 284760, 284784, 284682, 284635, 284637
245	79883543 (489, 490)	Novel Protein sim. GBank gj2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	284906
246	79162828 (491, 492)	Novel Protein sim. GBank gj5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NRJ-like domain	UNCLASSIFIED	284600, 284602, 284605, 284769, 284689

247	79873185 (493, 494)	Novel Protein sim. GBank gl 1838006 emb CAB06848 - (Z85982) argB [Mycobacterium tuberculosis]		kinase	264809, 264681, 35696423, 18108387
248	80488983 (495, 498)	Novel Protein sim. GBank gl 1168574 sp P42464 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35698286, 264907, 264511, 264602, 264788, 264686, 265021, 35695855, 18108385
249	78764845 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264636
250	79819980 (499, 500)				21908768, 264682
251	84359489 (501, 502)			UNCLASSIFIED	52645156, 29331822, 29331824, 52644045, 265018, 21906785, 21906788, 265020, 27486261, 27486285, 35695763, 18108376, 264556, 264559, 264565
252	79737758 (503, 504)	Novel Protein sim. GBank gl 3327166 dbj BAA31651 - (AB014576) KIAA0676 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 508)	Novel Protein sim. GBank gl 3036880 emb CAA18513 - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gl 3915488 sp O34881 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION		UNCLASSIFIED	264508, 264908, 264602, 264687, 265021, 264486
255	11398315 (509, 510)	Novel Protein sim. GBank gl 1665720 dbj BAA04134 - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gl 465787 sp P34422 YL31_CAEEL - HYPOTHETICAL 88.0 KD PROTEIN F44B9.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank gl 1172039 sp P42315 SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459464 (515, 516)	Novel Protein sim. GBank gl 3127836 emb CAA18902 - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79910152 (517, 518)			collagen	264681, 264686, 264682
260	20378437 (519, 520)			UNCLASSIFIED	264692, 264556
261	20285863 (521, 522)	Novel Protein sim. GBank gl 123761 sp P24221 HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264389
263	88095045 (525, 528)	Novel Protein sim. GBank gl 3924709 emb CAA04648 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blast score 71). cDNA EST EMBL: T02069 comes from this gene; cDNA EST EMBL: D76135 comes from this gene; cDNA EST EMBL: D73147 comes from this gene; cDNA EST EMB...		UNCLASSIFIED	264488, 264905, 264906, 264807, 264908, 264909, 264512, 264910, 264758, 264598, 264604, 265019, 264805, 264780, 18108351, 264763, 264764, 264288, 264768, 264788, 264789, 264691, 264692, 264693, 264626, 264634, 264635, 264555, 264636, 264638, 264639
264	87370828 (527, 528)	Novel Protein sim. GBank gl 3043734 dbj BAA25531 - (AB011177) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264808, 21806754, 265018, 265019, 265020

265	95355846 (528, 530)	Novel Protein sim. GBank gij4588624[dij]BAA78834.1] - (AB023207) KIAA0980 protein [Homo sapiens]	kinase	264488, 35696286, 29331824, 56182181, 35696052, 284508, 284905, 284906, 284907, 66712502, 264908, 284909, 264511, 284512, 284910, 284982, 284595, 284758, 284596, 55811366, 284600, 285017, 264603, 284604, 284605, 284760, 18108351, 284762, 284881, 284764, 284288, 284766, 264768, 264769, 21808765, 21808767, 21808769, 285020, 284891, 33657023, 33657109, 33657182, 284828, 35696423, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284555, 284638, 83373044, 56528488, 87168518, 284584, 284566, 284488
266	7858075 (531, 532)		UNCLASSIFIED	264600
267	11382222 (533, 534)		UNCLASSIFIED	264828
268	78809568 (535, 536)		UNCLASSIFIED	264887, 264768, 264689
269	80025810 (537, 538)		UNCLASSIFIED	264802
270	84361144 (539, 540)	Novel Protein sim. GBank gij4507387[ref]NP_003182.1pTARS - Itheonyd-IRNA synthetase	UNCLASSIFIED	264693
271	78552301 (541, 542)		UNCLASSIFIED	264909, 284693
272	9874778 (543, 544)	Novel Protein sim. GBank gij4980738[g]AAD35331.1]AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]	synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gij1188224[sp]P44569[NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR	UNCLASSIFIED	264688
274	39524246 (547, 548)			264564
275	82787041 (549, 550)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryzopsis cuniculatus]	UNCLASSIFIED	284907, 284908, 284909, 284766, 284786, 284691, 284632, 284636
276	86871073 (551, 552)	Novel Protein sim. GBank gij134820[sp]P21897[SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		285008, 60432229
277	80078735 (553, 554)	Novel Protein sim. GBank gij129021[sp]P20984[OBG_BACSU - SPOB-ASSOCIATED GTP-BINDING PROTEIN	ribosomalprot	284600, 18108387
278	12868947 (555, 556)		UNCLASSIFIED	284689
278	95282719 (557, 558)	Novel Protein sim. GBank gij78839[p]rj[S03812 - uvrB protein - Micrococcus luteus	nuclease	284508, 284804, 21908764, 284638, 284557, 284404
280	5603817 (559, 560)			284259
281	80249599 (561, 562)	Novel Protein sim. GBank gij3123180[sp]Q18964[MYLN2 CAEEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II		18108392, 284634, 284555, 284556, 284557, 284558
282	18596682 (563, 564)		UNCLASSIFIED	285019
283	20614211 (565, 566)		UNCLASSIFIED	284555

284	91212160 (567, 568)	Novel Protein sim. GBank gl 2428094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 284508, 284905, 284600, 284602, 284605, 284682, 284784, 58181562, 21908784, 18108378, 284636, 284559, 18108387
285	8757940 (569, 570)	Novel Protein sim. GBank gl 2072674 (emb CAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	284603
286	80503235 (571, 572)	Novel Protein sim. GBank gl 765332 (bsj 57676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori=silkworms, Peptide Partial, 833 aa] [Bombyx mori]		UNCLASSIFIED	284689
287	12745521 (573, 574)	Novel Protein sim. GBank gl 1870009 (emb CAB06860) - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins, teIR family	UNCLASSIFIED	284557
288	20756502 (575, 576)	Novel Protein sim. GBank gl 2072674 (emb CAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]		UNCLASSIFIED	284593, 284800
289	80043804 (577, 578)	Novel Protein sim. GBank gl 2072674 (emb CAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]		UNCLASSIFIED	284788
290	80430175 (579, 580)	Novel Protein sim. GBank gl 2506684 (sp P40120) YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	284601
291	20747431 (581, 582)	Novel Protein sim. GBank gl 825182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	284605
292	80052555 (583, 584)	Novel Protein sim. GBank gl 1718065 (sp P53528) UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase	UNCLASSIFIED	284909, 284605, 284687, 284689, 284692
293	80062519 (585, 586)	Novel Protein sim. GBank gl 117422 (sp P10040) CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00808) - EGF-like domain	oncogene	35696052, 284906, 285011, 284628, 55811578
294	79830303 (587, 588)	Novel Protein sim. GBank gl 1181619 (dbj BAA11565) - (D82384) a variant of TSC-22 [Gallus gallus]			52844507, 29331822, 284592, 285020, 284639
295	78444180 (589, 590)	Novel Protein sim. GBank gl 3649789 (dbj BAA33403) - (AB012226) SecA [Vibrio alginolyticus]			284508
296	78607078 (591, 592)	Novel Protein sim. GBank gl 5689587 (emb CAB52004.1) - (AL109883) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284905, 284687, 284638
297	79631297 (593, 594)	Novel Protein sim. GBank gl 5689587 (emb CAB52004.1) - (AL109883) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284905, 284687, 284638
298	80418888 (595, 596)	Novel Protein sim. GBank gl 5689587 (emb CAB52004.1) - (AL109883) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284905, 284687, 284638, 284766

299	95293298 (597, 598)	Novel Protein sim. GBank gij220637[dbj BAA01477] - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		284488, 283994, 56994075, 22278987, 22278986, 22278998, 20281089, 28331824, 28331825, 28331826, 60432289, 28331827, 28331828, 284905, 284908, 284907, 284908, 52644045, 284909, 284511, 285008, 284910, 284595, 284598, 284758, 33657084, 87168559, 285018, 285019, 284764, 284288, 284766, 284687, 58181582, 284769, 21906765, 21906768, 21906769, 33657023, 284892, 33857108, 27486281, 18108370, 284628, 284629, 55811578, 35895855, 284631, 284634, 284635, 284638, 284639, 83373044, 18108387, 87168518, 22278000, 22279002, 284585, 284586, 284587
300	20711340 (598, 600)	Novel Protein sim. GBank gij145922 (M20881) - Iron diclrate transport protein precursor [Escherichia coli]	UNCLASSIFIED	transport	284602
301	13511332 (601, 602)	Novel Protein sim. GBank gij1174661[sp P44594 TGT_HAEIN - QUEUINE TRNA-RIBOSYL TRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]			284687
302	9875260 (603, 604)	Novel Protein sim. GBank gij1174661[sp P44594 TGT_HAEIN - QUEUINE TRNA-RIBOSYL TRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]			284808
303	79574895 (605, 608)	Novel Protein sim. GBank gij67985[pir J UNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase		284689
304	20711344 (607, 608)	Novel Protein sim. GBank gij67985[pir J UNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus			284602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728867[sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR			284763
306	8515876 (611, 612)	Novel Protein sim. GBank gij1657554[gb AAB18082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED		283978
307	80222801 (613, 614)	Novel Protein sim. GBank gij1170612[sp Q10793 RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNAASE HII)	UNCLASSIFIED		285010, 21906768, 285020, 18108374, 283977
308	80084305 (615, 616)	Novel Protein sim. GBank gij1170612[sp Q10793 RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNAASE HII)	Contains protein domain (PF01351) - Ribonuclease HII	nuclease	284910, 284600, 284605, 284687, 284689, 284638, 18108387
309	80504138 (617, 618)	Novel Protein sim. GBank gij5420387[emb CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]			284769
310	80053816 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminoimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]			284603
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminoimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]			284602
312	80054347 (623, 624)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminoimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	UNCLASSIFIED		284588
313	80048168 (625, 626)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminoimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]			284603, 284587

314	87645112 (627, 628)	Novel Protein sim. GBank gij3561583 (AF092175) - Ikaros (Dantio ratio)	Contains protein domain (PF00320) - GATA zinc finger	- dna_ma_bind	284259, 60432289, 28331828, 284905, 284908, 284908, 284908, 285008, 284910, 60432229, 33657402, 60433438, 33109854, 265011, 265017, 284603, 285018, 284288, 284786, 284692, 35695763, 284628, 284829, 284639, 60170394, 22279002, 284568
315	82356091 (629, 630)	Novel Protein sim. GBank gij1652820(bj)BAA175401 - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synchocystis sp.]			284508, 284600, 284762, 284687, 284768, 52644229, 284788, 284689, 284635, 284636, 284638, 284486
316	78911071 (631, 632)	Novel Protein sim. GBank		UNCLASSIFIED	284693
317	20466944 (633, 634)	Novel Protein sim. GBank gij118244[sp]P24178[DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (SDAP)]		UNCLASSIFIED	284605
318	94141836 (635, 636)	Novel Protein sim. GBank gij4680229[gb]AAD27563.1[AF11827 - (AF118274) DNB-5 (Homo sapiens)]	Contains protein domain (PF00528) Dictyostelium (slime mold) repeats	transport	284908, 284909, 284910, 284593, 284594, 284760, 284288, 284768, 284789, 21908769, 284691, 284693, 284628, 65274791, 284635, 284636, 284638, 83373044, 22279002, 284588
319	17289360 (637, 638)	Novel Protein sim. GBank gij1149693[emb]CAA60220 - (X86499) rbsC [Clostridium perfringens]		transport	285018
320	13527675 (639, 640)	Novel Protein sim. GBank gij2811033[sp]O05314[GLGC MYCTU - GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)]		synthase	284687
321	94134387 (641, 642)	Novel Protein sim. GBank gij1680718 (U66234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	284509, 284908, 284907, 284908, 285009, 284596, 284784, 284628, 284634, 284636, 284638, 284639, 83373044, 284587
322	68489053 (643, 644)	Novel Protein sim. GBank gij1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 284691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	284488, 285009, 284593, 284628, 284635
324	79174383 (647, 648)			UNCLASSIFIED	284687
325	79862891 (649, 650)			UNCLASSIFIED	284693
326	28774974 (651, 652)			UNCLASSIFIED	284288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gij451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			284488, 284803, 284509, 284910
328	80253202 (655, 656)			UNCLASSIFIED	284592
329	10173821 (657, 658)			UNCLASSIFIED	284510
330	66597767 (659, 660)	Novel Protein sim. GBank gij4191358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	284259, 284808
331	79754888 (661, 662)	Novel Protein sim. GBank gij80741[pr]IS20912 - regulatory protein whiB - Streptomyces coelicolor		transcriptfactor	284910, 284687, 284689, 284636, 284567
332	80071440 (663, 664)	Novel Protein sim. GBank gij114049[sp]P19480[AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F2A PROTEIN)]		reductase	35696423, 284636, 284638, 284565
333	13009553 (665, 666)				284687

334	80230771 (667, 668)	Novel Protein sim. GBank glj3222228[pilj]S32227 - glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - <i>Corynebacterium glutamicum</i>	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	dehydrogenase	264905, 264600, 264604, 264486
335	80057026 (668, 670)	Novel Protein sim. GBank glj2183938[embj]CAB06021 - (Z98800) glpQ2 [<i>Mycobacterium tuberculosis</i>]		esterase	264907, 264603, 264683, 18108374, 264636, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264688
337	11080829 (673, 674)				264602
338	95413134 (675, 676)	Novel Protein sim. GBank glj5454074[refj]NP_006303.1pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nuc_rept	264569, 18108397, 22276998, 29331822, 20281099, 29331824, 56182181, 68714117, 29331825, 35696052, 29331826, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168558, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264682, 264764, 264766, 264685, 264686, 264768, 52644229, 264689, 55811957, 35695917, 264692, 264693, 264626, 18108370, 18108374, 55811576, 35696423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18108380, 264636, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank glj4001713[dbj]BAA35087.1 - (AB015879) DnaK [<i>Porphyromonas gingivalis</i>]		eph	264593
340	80504149 (678, 680)	Novel Protein sim. GBank glj2842699[spj]Q92353JUBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C8G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264769, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank glj2888580 (AE001166) - conserved hypothetical protein [<i>Borrelia burgdorferi</i>]	Contains protein domain (PF00280) - Tryptophan synthase alpha chain	isomerase	264605
342	80054198 (683, 684)	Novel Protein sim. GBank glj1884739[embj]CAA70601.1 - (Y09452) Yed1 hypothetical protein [<i>Pseudomonas syringae</i>]			264603, 264604
343	20468782 (685, 686)				264605
344	80428870 (687, 688)	Novel Protein sim. GBank glj2117279[embj]CAB091041 - (Z95618) hypothetical protein Rv0807 [<i>Mycobacterium tuberculosis</i>]		UNCLASSIFIED	264600, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank glj3023317[spj]Q48935APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank glj4239787[embj]CAA754371 - (Y15166) NADP-glutamate dehydrogenase [<i>Pseudomonas aeruginosa</i>]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Valine dehydrogenase	dehydrogenase	264905

347	79156195 (693, 694)	Novel Protein sim. GBank gi 731675 sp P38795 YH4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION	UNCLASSIFIED	285006, 285008, 285010, 285018, 283987, 283981
348	80020208 (695, 696)	Novel Protein sim. GBank gi 1073610 pir J547672 - ugpb protein - Escherichia coli	transport	284602, 18108351, 18108387
349	17282112 (697, 698)			265007
350	80502370 (699, 700)	Novel Protein sim. GBank gi 3281599 emb CAB008171 - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]	nuclease	285008, 284769, 284889, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gi 2959367 emb CAA178211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]	glycoprotein	284769, 284905, 284908
352	11611585 (703, 704)	Novel Protein sim. GBank gi 4416302 gb AAD203071 - (AF105716) copia-type pol polyprotein [Zea mays]	protease	284595
353	80081653 (705, 706)	Novel Protein sim. GBank gi 1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	UNCLASSIFIED	284604
354	56626130 (707, 708)		UNCLASSIFIED	284628
355	80048344 (709, 710)		UNCLASSIFIED	284909, 284595, 284883, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	transcriptfactor	284909, 284591, 284592
357	80070568 (713, 714)	Novel Protein sim. GBank gi 497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]	oxidase	284605
358	37032756 (715, 716)	Novel Protein sim. GBank gi 2290990 (AF008000) - Btg1 [Bordetella pertussis]	UNCLASSIFIED	284768
359	80501488 (717, 718)		UNCLASSIFIED	284604, 284769
360	80026748 (719, 720)		UNCLASSIFIED	284594
361	80584075 (721, 722)	Novel Protein sim. GBank gi 3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylglucosaminyltransferase T5 [Rattus norvegicus]	transferase	22278986, 284259, 28331822, 28331824, 284605, 55811857, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank gi 113784 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)	amylase	284688
363	78750145 (725, 726)			
364	82443593 (727, 728)	Novel Protein sim. GBank gi 2828818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	dehydrogenase	284568 284769, 284602, 284604, 284508, 264762, 284638, 284486

365	88040288 (728, 730)	Novel Protein sim. GBank gij4928288[gb AAD33924.1] - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21908768, 21908767, 55811578, 21908769, 2914829, 22278995, 22278996, 265020, 265022, 264634, 264691, 264593, 33657023, 33657402, 264693, 264639, 264594, 26331824, 264758, 18108385, 29331827, 87168559, 265018, 22279000, 265019, 264482, 264781, 264681, 18108351, 265017, 264757
366	81821838 (731, 732)			
367	95357471 (733, 734)	Novel Protein sim. GBank gij4503843[ref NP_003908.1 pG2AD - UNKNOWN]	Contains protein domain (PF01802) - Adaptin N terminal region	60424178, 65274572, 56182575, 22278994, 56894075, 22278998, 264259, 26331822, 26331824, 56182181, 60424289, 86714117, 29331825, 60432289, 26331826, 29331827, 29331828, 264905, 264828, 56182435, 265006, 264512, 265008, 264591, 55812038, 55811386, 265010, 87168559, 265017, 265018, 264604, 265019, 55811150, 264448, 264369, 264288, 264686, 264768, 56181562, 21908768, 21908769, 55811857, 35895917, 265022, 60170815, 33657023, 65274620, 18108385, 263967, 33657109, 33657349, 35895783, 264628, 18108378, 55811578, 85274791, 35895855, 56182323, 63373044, 80432113, 264583, 264584, 264587, 264509
368	79607265 (735, 736)	Novel Protein sim. GBank gij3913028[sp P84967 ALR_MYCSM - ALANINE RACEMASE]	UNCLASSIFIED	264508, 264604, 264805, 264636
369	95292917 (737, 738)			
370	88080868 (739, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]		264805, 264592, 264605, 264766, 264681
371	95292599 (741, 742)	Novel Protein sim. GBank gij2995299[emb CAA18328] - (AL022268) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - IPP transferase	264805, 264808, 264510, 264600, 264601, 264802, 264603, 265018, 264604, 264605, 265021, 264692, 264636, 264584
372	80021107 (743, 744)	Novel Protein sim. GBank gij2508393[sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN]		264564
373	79863768 (745, 746)		UNCLASSIFIED	264809
374	78847568 (747, 748)	Novel Protein sim. GBank gij331840[emb CAA13184] - (AJ231122) z81f [Vibrio cholerae]	UNCLASSIFIED	264805, 264906
375	91230181 (749, 750)	Novel Protein sim. GBank gij5456834[gb AAD43716.1] - (AF152322) protocadherin gamma A2 [Homo sapiens]	cadherin	65274572, 264259, 26331828, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33657023, 264769
376	80505214 (751, 752)	Novel Protein sim. GBank gij1805408[dbj BAA08970] - (D50453) homologues to nitrite hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	UNCLASSIFIED	
377	10338083 (753, 754)			264806

378	80056153 (755, 758)	Novel Protein sim. GBank gii1076013 pir A49930 - carB (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gii1076013 pir A49930 - carB (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	264789
380	80060937 (759, 760)	Novel Protein sim. GBank gii216556 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	UNCLASSIFIED	264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)	Novel Protein sim. GBank gii3327136 dbj BAA31636 - (AB014561) KIAA0661 protein [Homo sapiens]			264592
383	83259025 (765, 766)				264595, 265017, 265021, 264638, 87188518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 26331822, 60432289, 26331827, 264288, 264786, 263987, 65274791, 35695855, 263981, 83373044, 264567
385	10237678 (769, 770)	Novel Protein sim. GBank gii1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases		264692
386	78633434 (771, 772)				264906
387	17860637 (773, 774)	Novel Protein sim. GBank gii1460074 emb CA801049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741378 (775, 776)	Novel Protein sim. GBank gii4240169 dbj BAA74863.1 - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.		35696286, 264805, 66712502, 60432228, 264593, 60433356, 264686, 264688, 21906765, 264691, 22279000, 264482
389	78316971 (777, 778)			UNCLASSIFIED	18108394, 22278988, 264630, 264556, 22279002
390	80078949 (779, 780)	Novel Protein sim. GBank gii854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264600
391	7657302 (781, 782)				264482
392	79786058 (783, 784)	Novel Protein sim. GBank gii3378523 emb CAA08671 - (AJ009832) cyclomaltodextrinase glucanotransferase [Thermotoga neopolitana]		UNCLASSIFIED	264908
393	33206031 (785, 786)				264802, 21806764
394	10104463 (787, 788)				
395	80229010 (789, 790)	Novel Protein sim. GBank gii2677780 (U70327) - unknown	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264693
396	20436224 (781, 792)	Novel Protein sim. GBank gii4507909 ref NP_000368.1 pWASJ - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			264508, 264563
397	80417014 (793, 794)	Novel Protein sim. GBank gii1518458 (U45988) - mitochondrial solute carrier [Onchocerca volvulus]			264556
398	91230517 (795, 796)		Contains protein domain (PF00153) - transport		265007, 265009, 264508, 264556, 264629, 264766
					18108398, 22278985, 22278996, 58994075, 22278998, 264259, 26331824, 26331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264786, 21906785, 21908786, 21908787, 265020, 265021, 33657023, 33657106, 264628, 35696423, 35695855, 264952, 18108380, 264567, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank glj3558091[dbj BAA31895] - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - kinase FGY family of carbohydrate kinases	kinase	284592, 284595
400	94117490 (799, 800)	Novel Protein sim. GBank glj72835[sp P39192 ALUS_HUMAN - III] ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00560) - cadherin Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278998, 284259, 28331824, 285008, 285007, 285009, 80432229, 33857402, 21806754, 285010, 285017, 285018, 285019, 18108351, 18108357, 21908785, 285021, 285022, 284691, 284692, 33857023, 18108370, 85274791, 284634, 284636, 80170394, 56182323, 284594
401	11397491 (801, 802)	Novel Protein sim. GBank glj49282[gb AAD3327.1 AF13211 - (AF132117) FruA [Staphylococcus aureus]		transport	
402	95420284 (803, 804)	Novel Protein sim. GBank glj5689487[dbj BAA3027.1] - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	phosphatase	85274572, 56182575, 35696288, 22278996, 22278998, 284083, 284259, 28331822, 29331824, 28331825, 28331826, 80432289, 29331827, 28331828, 284808, 284907, 284808, 285008, 284511, 285007, 285008, 284910, 284591, 33857402, 80433356, 80433438, 284596, 21908754, 52844288, 285010, 285011, 87168559, 285017, 285018, 285019, 284681, 18108351, 284682, 284448, 284288, 284684, 284766, 284767, 284686, 21908765, 21906766, 21908767, 21908768, 21908789, 55811957, 285020, 285021, 285022, 284690, 284693, 85274620, 35695783, 284628, 18108370, 284629, 18108379, 35698423, 55811576, 284635, 284638, 284557, 284639, 18108385, 22279002, 284563, 284564, 284585, 284586, 284768, 284632, 284639, 284563, 284682, 285009, 284682
403	80439913 (805, 806)			UNCLASSIFIED	
404	11808865 (807, 808)			polymerase	
405	78471280 (809, 810)	Novel Protein sim. GBank glj2661649[emb CAA15755] - (AL009198) dnaE2 [Mycobacterium tuberculosis]		UNCLASSIFIED	
406	78634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 284693
407	80478229 (813, 814)			UNCLASSIFIED	284769
408	80079958 (815, 816)			UNCLASSIFIED	284600
409	5640527 (817, 818)	Novel Protein sim. GBank glj3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		helicase	284259

410	95357406 (819, 820)	Novel Protein sim. GBank gi 475016 dbj BAA08184 - (D29801) Unknown [Mus musculus]		UNCLASSIFIED	284489, 52846365, 52846842, 58181686, 35898286, 52845080, 29331822, 29331824, 56182161, 29331825, 80424288, 358986052, 33656870, 264508, 264508, 264905, 264906, 264907, 264908, 52844045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52846317, 55811366, 265010, 265011, 265017, 264604, 265018, 55811150, 264762, 264764, 264766, 264867, 264768, 264769, 52844228, 21806766, 265020, 265021, 264534, 52844150, 264692, 33657023, 65274620, 33657109, 33657182, 27488261, 35898763, 264828, 264829, 60431528, 18108376, 263978, 35898423, 35898555, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 284486
411	80501670 (821, 822)			UNCLASSIFIED	284769
412	80241662 (823, 824)				284907, 264810, 263973, 22279002
413	11076446 (825, 826)	Novel Protein sim. GBank gi 3261784 emb CAB08987 - (Z95558) hlpX [Mycobacterium tuberculosis]		eph	284605
414	82050554 (827, 828)	Novel Protein sim. GBank gi 129038 sp P20707 OD01_AZ0V1 - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 264769, 264602, 284638, 284603, 264909, 264605
415	84453144 (829, 830)	Novel Protein sim. GBank gi 4868350 gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87186518
416	80402775 (831, 832)	Novel Protein sim. GBank gi 2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]		kinase	284488, 264800, 264602, 264764, 264636
417	20153787 (833, 834)	Novel Protein sim. GBank gi 170917 sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		284605
418	94125841 (835, 836)			UNCLASSIFIED	284889, 264693
419	95314273 (837, 838)			collagen	284908, 264910, 264764, 264639
420	37036349 (839, 840)	Novel Protein sim. GBank gi 3261659 emb CAB03751 - (Z81388) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	- phosphatase	284769
421	95292942 (841, 842)	Novel Protein sim. GBank gi 2916942 emb CAA17580 - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	- phosphatase	284906, 264800, 264601, 264603, 264604, 264760, 264769
422	79471293 (843, 844)	Novel Protein sim. GBank gi 231752 sp Q00767 CH61_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (GROEL PROTEIN 1) (HSP58)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	- eph	22278996, 264682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	284509

424	7898557 (847, 848)	Novel Protein sim. GBank gi 4826814 ref NP_004977.1 pKTN1 - kinesin receptor		strud	285019	
425	80431450 (848, 850)	Novel Protein sim. GBank gi 1703701 bbs 178482 - KRP5-kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	strud	284909, 265007, 55811388, 284788, 55810764	
426	80064522 (851, 852)				284605, 284559	
427	80057232 (853, 854)	Novel Protein sim. GBank gi 231829 sp P29929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	284603, 284636	
428	79487788 (855, 856)	Novel Protein sim. GBank gi 81286 p j S22697 - extensin - Volvox carterii (fragment)		UNCLASSIFIED	284683	
429	80081282 (857, 858)			UNCLASSIFIED	35698423, 35695763, 35695855, 265017, 284584, 284782	
430	80504192 (859, 860)	Novel Protein sim. GBank gi 1808154 emb CAB08451 - (284395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]	reductase		284508, 284805, 264509, 264808, 284809, 285008, 284600, 284687, 284769, 284689, 284636, 284638, 18108385, 264488	
431	20624249 (861, 862)				284586	
432	16525372 (863, 864)				265020	
433	81494303 (865, 866)	Novel Protein sim. GBank gi 3123552 emb CAA18608 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KUA0289 LIKE) [Homo sapiens]		UNCLASSIFIED	284907, 284808, 284909, 284910, 284582, 284595, 284758, 284604, 284760, 284782, 284783, 284636, 284637, 22279002	
434	94326323 (867, 868)	Novel Protein sim. GBank gi 2495272 sp Q99828 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 58182181, 58181562, 29331828, 35696052, 55810764, 55811576, 65274791, 35695855, 80432113, 55811150, 284636, 284786	
435	80502738 (869, 870)	Novel Protein sim. GBank gi 114105 sp P08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	284595, 264769	
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22278002	
437	11398291 (873, 874)			UNCLASSIFIED	264583	
438	11773835 (875, 876)			UNCLASSIFIED	284688	
439	80019495 (877, 878)	Novel Protein sim. GBank gi 3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			284905, 284600, 284602, 284604	
440	79841062 (879, 880)	Novel Protein sim. GBank gi 2291232 gb AA865351.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA). Score=288.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)	ATPase_associated	35698052, 284805, 284808, 264809, 265011, 35698423	
441	20386835 (881, 882)	Novel Protein sim. GBank gi 5039946 gb AA045904.1 AF16132 - (AF161328) histidine kinase CstS [Corynebacterium diptheriae]			284605	
442	85281058 (883, 884)	Novel Protein sim. GBank gi 1184780 (U46088) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	28331630, 284809	
443	82456427 (885, 886)	Novel Protein sim. GBank gi 5689893 emb CAB52058.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35698052, 284508, 284906, 264512, 284604, 284782, 284769, 284689, 284636	
444	11395897 (887, 888)	Novel Protein sim. GBank gi 1783249 dbj BAA11726 - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	284591	

445	78552708 (889, 890)	Novel Protein sim. GBank gij5531272[emb]CAB50897.1]- (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	264693
446	78810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264509
447	80438868 (893, 894)	Novel Protein sim. GBank gij1542914[emb]CAB02185]- (Z80108) fmi [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	dehydrogenase	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gij118794[sp]P10443[DP3A, ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264508, 264600, 264603, 264605, 264682, 264768, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gij4589508[dbj]BAA76775.1]- (AB023148) KIAA0831 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	264605, 264559
450	84631210 (899, 900)	Novel Protein sim. GBank gij2650814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	65274572, 22278988, 28331624, 28331826, 264906, 264910, 264592, 52648317, 265017, 21906767, 55811857, 56528488, 22279002
451	21433609 (901, 902)	Novel Protein sim. GBank gij2493000[sp]Q08450[SCOT, CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	264486
452	10267278 (903, 904)	Novel Protein sim. GBank gij4468689[emb]CAB38153.1]- (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264692
453	52560088 (905, 906)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]		UNCLASSIFIED	264907, 264600
454	38523922 (907, 908)	Novel Protein sim. GBank gij4506075[ref]NP_002733.1[pprkc - protein kinase C, mu]		transferase	264603
455	13088892 (909, 910)	Novel Protein sim. GBank gij113158[sp]P25516[ACO1, ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)]	Contains protein domain (PF00595) - kinase PDZ domain (Also known as DHR or GLGF).	kinase	264687
456	78563081 (911, 912)	Novel Protein sim. GBank gij4506075[ref]NP_002733.1[pprkc - protein kinase C, mu]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264691
457	78831273 (913, 914)	Novel Protein sim. GBank gij113158[sp]P25516[ACO1, ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)]		UNCLASSIFIED	264805
458	78581227 (915, 916)	Novel Protein sim. GBank gij1168574[sp]P42464[ATPB, CORGL - ATP SYNTHASE BETA CHAIN		UNCLASSIFIED	55812038, 285010, 285018, 284681
459	80567359 (917, 918)	Novel Protein sim. GBank gij1168574[sp]P42464[ATPB, CORGL - ATP SYNTHASE BETA CHAIN		kinase	22278997, 264259, 28331826, 285018, 264448, 284389, 21906765, 35698423
460	78245890 (919, 920)	Novel Protein sim. GBank gij1168574[sp]P42464[ATPB, CORGL - ATP SYNTHASE BETA CHAIN		UNCLASSIFIED	264908
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[sp]P42464[ATPB, CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33657023, 264559

462	79608589 (923, 924)	Novel Protein sim. GBank gil1348891 sp P45597 PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF003891) - PEP-utilizing enzymes	UNCLASSIFIED	284907
463	79786417 (925, 926)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	284905, 284906, 284908, 284909, 284910, 284991, 284995, 285011, 284632, 284635, 284636, 284637, 284638, 284639
464	82340151 (927, 928)			UNCLASSIFIED	284634
465	83005730 (928, 930)	Novel Protein sim. GBank gil5689776 emb CAB52137.1 - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00848) - Calpain family cysteine protease	calthypsin	285017, 21906784, 285020
466	20460845 (931, 932)	Novel Protein sim. GBank gil1808175 emb CAB06470 - (Z84395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	ribosomalprot	284605, 284559
467	80408035 (933, 934)	Novel Protein sim. GBank gil548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	284764
468	52562208 (935, 936)			UNCLASSIFIED	284692
469	19520527 (937, 938)	Novel Protein sim. GBank gil2114024 emb CAB08957 - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	284488
470	80502756 (939, 940)	Novel Protein sim. GBank gil2909459 emb CAA17347 - (AL021829) cobQ [Mycobacterium tuberculosis]		synthase	284602, 284769
471	17937351 (941, 942)	Novel Protein sim. GBank gil114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN		transport	285019
472	80047458 (943, 944)			UNCLASSIFIED	284596, 284685, 284557
473	20558783 (945, 946)	Novel Protein sim. GBank gil862343 (L10808) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	284369
474	80593365 (947, 948)			UNCLASSIFIED	22278997, 284692, 284288
475	82454665 (949, 950)			UNCLASSIFIED	284907, 284908, 284511, 285009, 284762, 284448, 284636, 284638
476	94143657 (951, 952)	Novel Protein sim. GBank gil5453858 ref NP_008328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	65274572, 80432048, 284259, 284508, 52844045, 55812038, 284758, 285011, 284288, 284686, 52844228, 85274791, 284638, 284566
477	79175833 (953, 954)			UNCLASSIFIED	284636
478	79633483 (955, 956)			UNCLASSIFIED	284690, 284693
479	80189746 (957, 958)			collagen	284686, 35895855, 285008, 284631, 284910, 284632, 284638, 285018, 284369, 284909
480	79390729 (959, 960)	Novel Protein sim. GBank gil1127551 (U18938) - orf2 [Batrachococcus balkensis]		mapolymerase	284369
481	79624578 (961, 962)			UNCLASSIFIED	284693
482	83050611 (963, 964)	Novel Protein sim. GBank gil4063042 (AF068085) - GP900; mucin-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	284909, 284686, 284768, 284693, 55811576, 58182323, 18108395

483	20283308 (985, 986)	Novel Protein sim. GBank gl 2104303 emb CAB08632 - (285387) hypothetical protein RV2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1	284600
484	11818048 (987, 988)	Novel Protein sim. GBank gl 3450883 (AF083334) - fibroin [Antheraea pernyi]	UNCLASSIFIED	284584
485	80181234 (989, 970)	Novel Protein sim. GBank gl 5042272 emb CAB44526.1 - (AL078818) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	UNCLASSIFIED	284369, 21808765, 22279000, 22279002
486	80058042 (971, 872)		dehydrogenase	284604
487	11813339 (973, 974)			284638
488	91222383 (975, 976)	Novel Protein sim. GBank gl 5724778 gb AAC3522.2 - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00820) - RhoGAP domain	284686, 66714117, 284768, 18108385, 55811578, 285006, 285008, 285009, 285019, 22279002, 284259, 18108370, 284907, 284764, 56182323, 284288, 284893
489	10867710 (977, 978)	Novel Protein sim. GBank gl 3882223 db BAA34471.1 - (AB018294) KIAA0751 protein [Homo sapiens]	kinase	284639
490	95381124 (979, 980)	Novel Protein sim. GBank gl 82091 pir A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)	collagen	22278998, 29331822, 29331828, 284107, 284909, 284110, 285009, 284592, 284593, 80433358, 284288, 284693, 283974, 283976, 20281071, 80432113
491	80498412 (981, 982)	Novel Protein sim. GBank gl 2894206 emb CAA17072 - (AL021840) hypothetical protein RV3258c [Mycobacterium tuberculosis]	UNCLASSIFIED	284769
492	87421284 (983, 984)			284600
493	11692942 (985, 986)			284638
494	87726604 (987, 988)	Novel Protein sim. GBank gl 5262605 emb CAB45743.1 - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284489, 35698286, 80432289, 29331828, 35886052, 284509, 284805, 284808, 284807, 284808, 284909, 284510, 284511, 285009, 284910, 33857402, 284762, 284764, 284768, 284769, 284888, 21808765, 21808769, 35889817, 285020, 284693, 33857109, 284629, 35698423, 35695855, 284634, 284638
495	80026599 (989, 990)	Novel Protein sim. GBank gl 2791517 emb CAA16054 - (AL021246) hypothetical protein RV2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	284602, 284682, 284638
496	78985824 (991, 992)	Novel Protein sim. GBank gl 230281 pdb 1R69 - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF01381) - Helix-turn-helix	284601, 285021
497	78949661 (993, 994)	Novel Protein sim. GBank gl 128736 sp P28225 PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)	oxidase	285006

488	88095488 (995, 998)	Novel Protein sim. GBank gi 1145789 (U41662) - neuruligin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	284259, 28331828, 35688052, 284508, 284509, 284905, 284808, 284907, 284908, 284909, 284510, 284511, 285009, 284910, 284591, 33857402, 284758, 265010, 265011, 284600, 284801, 284605, 284883, 284784, 284786, 284767, 284788, 284887, 284789, 21908767, 33857023, 284893, 284828, 284629, 35696423, 284630, 284632, 284634, 284635, 284637, 284638, 284558, 284639, 18108385, 284583, 284584, 284565, 284586, 284587
489	20438222 (987, 998)	Novel Protein sim. GBank gi 97480 pir J19739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	284605
500	11076810 (999, 1000)				284605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gi 5708250 emb CAB52363.1 - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gi 468678 emb CAB38132.1 - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278986, 265011, 264602, 284605, 284635
503	20264483 (1005, 1006)			UNCLASSIFIED	284584
504	10887321 (1007, 1008)			UNCLASSIFIED	284687
505	95003068 (1009, 1010)			UNCLASSIFIED	284389
506	18454292 (1011, 1012)	Novel Protein sim. GBank gi 4033509 sp P02598 CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struc	265010
507	20451588 (1013, 1014)	Novel Protein sim. GBank gi 2501069 sp Q48127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN-TRNA LIGASE) (TRPRS)		UNCLASSIFIED	284604
508	78841424 (1015, 1016)	Novel Protein sim. GBank gi 468088 sp P34618 YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	284808
509	11776398 (1017, 1018)				284638
510	83373465 (1019, 1020)			UNCLASSIFIED	284887, 284839
511	18525578 (1021, 1022)				285007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gi 2497419 sp P5635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	284585
513	78457404 (1025, 1026)	Novel Protein sim. GBank gi 1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	284683, 284888, 35698423, 284639
514	78813805 (1027, 1028)	Novel Protein sim. GBank gi 1184780 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 284909
515	78462591 (1029, 1030)				22278989, 284690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gi 2127400 pir J565770 - maltotigosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q38)		amylase	284910

517	95282894 (1033, 1034)	Novel Protein sim. GBank gij2883605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264585
518	8491831 (1035, 1036)	Novel Protein sim. GBank gij854063[embjCAA58337] - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264487
519	91677686 (1037, 1038)	Novel Protein sim. GBank gij5689365[dbj BAA83073.1] - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_ma_bind	52644507, 22278897, 22278998, 60432048, 264259, 52845080, 29331824, 68714117, 60424269, 29331826, 35696052, 264905, 29331830, 68712502, 264511, 265007, 264591, 60432228, 33857402, 60433438, 21908754, 33109854, 52844296, 87168474, 87168559, 265017, 265018, 264604, 265019, 21908765, 21908766, 21908767, 21908769, 264681, 264448, 264369, 264288, 264685, 265021, 60170815, 33857023, 264692, 52845129, 33857109, 27486262, 27486264, 35895763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 58526488, 60432113
520	79869188 (1039, 1040)				264789
521	11076821 (1041, 1042)	Novel Protein sim. GBank gij1169126[sp P48839 CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gij1172869[sp P4433 JRBKS HAEIN - RIBOKINASE	Contains protein domain (PF00284) - ptkB family carbohydrate kinase	kinase	264905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gij2132243[pir J561028 - hypothetical protein YPL238c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gij4033608[dbj BAA35136] - (AB012308) B2HC [Arthocladia crassispina]		ATPase_associated	264092, 264596, 265011
525	79810046 (1049, 1050)				264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gij4108610[embjCAA21365] - (AL031866) ORF42, len=388 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap, FastA scores: opt:468, E(): 8.5e-24, in Q84602 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504728 (1053, 1054)				
528	85484134 (1055, 1056)				
529	17936810 (1057, 1058)	Novel Protein sim. GBank gij731088[sp P24215 UXUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	264769
530	10887336 (1059, 1060)	Novel Protein sim. GBank gij42144[embjCAA25200] - (X00513) NusA protein (nusA) [Escherichia coli]		UNCLASSIFIED	56182575, 265017, 265018
531	80226578 (1061, 1062)			hydrolase	265019
532	90933444 (1063, 1064)	Novel Protein sim. GBank gij5282640[embj CAB45758.1] - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264687
				UNCLASSIFIED	264555, 264556, 264557, 264558, 18108365
				UNCLASSIFIED	264488, 264490, 264258, 264592, 264760, 265021, 264680, 263978, 264558

533	87761531 (1085, 1088)	Novel Protein sim. GBank gi14883836 gb AAD31593.1 AF11229 - (AF11229) Integral inner nuclear membrane protein MAN1 [Homo sapiens]				264907, 264908, 264768, 35685917, 264630, 264555
534	82368264 (1087, 1088)	Novel Protein sim. GBank gi12985352 emb CAA04606.1 - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED			264905, 265011, 264601, 264602, 264605, 264782, 264768, 265020, 264693, 264638 264906
535	79841850 (1089, 1070)	Novel Protein sim. GBank gi13878636 emb CAA88953 - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00089) - ATPase associated Eukaryotic protein kinase domain			
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi12495828 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5 REGION	reductase			18108376, 264805, 264906, 264807, 264909
537	84147448 (1073, 1074)	Novel Protein sim. GBank				265008, 264805, 85274791
538	87821863 (1075, 1076)	gi1134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen			26331822, 26331824, 26331825, 26331826, 26331827, 264908, 52844045, 33857402, 265017, 264782, 264683, 264288, 264685, 21908785, 35685763, 264558, 60170394, 264559, 22279002
539	28398268 (1077, 1078)	Novel Protein sim. GBank gi12498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone			264602, 265018
540	79637077 (1078, 1080)	Novel Protein sim. GBank gi13882241 dbj BAA34480.1 - (AB018303) KIAA0760 protein [Homo sapiens]	transcript factor			264693
541	87762268 (1081, 1082)		Contains protein domain (PF00086) - Zinc finger, C2H2 type			18108394, 22278957, 22278958, 264259, 264112, 265009, 33857402, 55812038, 52846317, 265017, 21908785, 264693, 55811576, 264835, 56528486, 264568 264910, 265018, 264689, 264638, 264486
542	95295838 (1083, 1084)	Novel Protein sim. GBank gi15042272 emb CAB44528.1 - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase			
543	79798280 (1085, 1086)	Novel Protein sim. GBank gi12781388 emb CAA15984 - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED			264602, 264908
544	20437191 (1087, 1088)		UNCLASSIFIED			264605
545	80434504 (1088, 1090)	Novel Protein sim. GBank gi14887211 gb AAD32237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]				264788, 264634, 264907, 264592, 264909 264600, 264602, 21908785
546	80248016 (1091, 1092)	Novel Protein sim. GBank gi11350855 sp P19178 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) [RNA POLYMERASE BETA' SUBUNIT]	mapolymerase			264604
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi12330021 (AF019250) - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]				
548	82114938 (1095, 1096)		UNCLASSIFIED			264488, 264805, 264910, 264780, 264693, 264639, 264583, 264584

548	95421904 (1097, 1098)	Novel Protein sim. GBank gll4337460(gb)AAD18133] - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108388, 22278895, 22278998, 22278997, 22278998, 22278998, 264259, 28331824, 68714117, 28331825, 28331826, 35896052, 265007, 265008, 284910, 284592, 33657402, 33109954, 285017, 285018, 265019, 18108351, 264448, 284784, 264369, 264288, 264788, 264688, 284688, 21908785, 21908788, 21908787, 21908788, 21908789, 265020, 284691, 33657023, 264692, 264693, 65274820, 52845128, 33657109, 27486281, 27486282, 27486284, 33657348, 55811576, 18108387, 60432113, 22279002
550	10886816 (1098, 1100)	Novel Protein sim. GBank gll312893(sp)P94985(SYFB MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	284688
551	80439980 (1101, 1102)	Novel Protein sim. GBank gll312893(sp)P94985(SYFB MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	284908, 264809, 264768
552	94672870 (1103, 1104)	Novel Protein sim. GBank gll312893(sp)P94985(SYFB MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)		UNCLASSIFIED	284688, 264639, 284563
553	80108002 (1105, 1106)	Novel Protein sim. GBank gll312893(sp)P94985(SYFB MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)	Contains protein domain (PF00008) - EGF-like domain	glycoprotein	55811957, 264828
554	78818378 (1107, 1108)	Novel Protein sim. GBank gll552087 (M33753) - crumbs protein [Drosophila melanogaster]		kinase	284908
555	7886347 (1109, 1110)	Novel Protein sim. GBank gll552087 (M33753) - crumbs protein [Drosophila melanogaster]			
556	20457127 (1111, 1112)	Novel Protein sim. GBank gll3914014(sp)P96380(MFD MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	284762
557	19523405 (1113, 1114)	Novel Protein sim. GBank gll5042273(emb)CAB44527.1] - (AL078818) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]		transcript factor	284508, 264805, 284559
558	20724428 (1115, 1116)	Novel Protein sim. GBank gll1170933(sp)P45331(METE_HAEIN - 5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)		dehydrogenase	284488
559	80084353 (1117, 1118)	Novel Protein sim. GBank gll4980587(gb)AAD35173.1(AE00169) - (AE001694) iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	284602
				UNCLASSIFIED	284634

560	80066533 (1119, 1120)	Novel Protein sim. GBank gi 2492595 sp Q53193 Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - transport ABC transporter	18108396, 264906, 264602, 264604, 18108374
561	20293187 (1121, 1122)		UNCLASSIFIED	264600
562	11698161 (1123, 1124)		UNCLASSIFIED	264689
563	79781420 (1125, 1126)	Novel Protein sim. GBank gi 4104925 (AF042276) - poly(hydroxycarboxylate) granule associated protein Ga2 [Pseudomonas putida]	UNCLASSIFIED	264910, 264691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gi 2792310 (AF040570) - unknown [Amycolatopsis mediterranei]	dehydrogenase	264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gi 3449294 dbj BAA32482 - (AB011532) MEGF8 [Rattus norvegicus]	Contains protein domain (PF00008) - synthase EGF-like domain	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi 4539568 emb CAB38487.1 - (AL035636) putative helicase [Streptomyces coelicolor]	helicase	264909, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264605, 264768, 264687, 264689, 35695917, 264693, 65274620, 264488
567	79560955 (1133, 1134)	Novel Protein sim. GBank gi 100506 pir S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flavaria trimeria (fragment)	UNCLASSIFIED	264681, 264691, 264593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gi 3915843 sp Q31212 IRS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00390) - Malic enzyme	264689
569	39506897 (1137, 1138)	Novel Protein sim. GBank gi 115122 sp P21627 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	Contains protein domain (PF00319) - Ribosomal protein S2	264565
570	78375927 (1139, 1140)		UNCLASSIFIED	18108376, 18108387, 264565
571	79793961 (1141, 1142)		transport	264907, 264909
572	36998838 (1143, 1144)		UNCLASSIFIED	264782
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi 4539223 emb CAB39881.1 - (AL049497) putative integral membrane protein [Streptomyces coelicolor]	UNCLASSIFIED	265007, 264601
574	13521592 (1147, 1148)			264636
575	13076416 (1149, 1150)	Novel Protein sim. GBank gi 118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN	polymerase	264687
576	20482248 (1151, 1152)	Novel Protein sim. GBank gi 5457825 emb CAB49116.1 - (AJ248283) PAB2227 [Pyrococcus abyssi]		264605
577	66727102 (1153, 1154)	Novel Protein sim. GBank gi 5042274 emb CAB44528.1 - (AL078818) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	35696052, 264636
578	11804477 (1155, 1156)			264638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi 1723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09	transport	264682, 264558

580	80059417 (1159, 1160)					22278998, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)				UNCLASSIFIED	265008, 264564
582	80049817 (1163, 1164)	Novel Protein sim. GBank gi 3243131 (AF045777) - titin	Contains protein domain (PF00047) - Immunoglobulin domain		struct	265021, 264555, 264557
583	79321392 (1165, 1166)	[Drosophila melanogaster] Novel Protein sim. GBank gi 2501162 sp P7728 YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION			transport	264594
584	79845024 (1167, 1168)				UNCLASSIFIED	264488, 264806, 264786, 264887, 35689423
585	79581454 (1169, 1170)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]			UNCLASSIFIED	265018, 264684, 21908769
586	38277466 (1171, 1172)				UNCLASSIFIED	264908, 265007
587	80497359 (1173, 1174)	Novel Protein sim. GBank gi 4467250 emb CAB37575 - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]			hydrolase	264800, 264602, 264605, 264769, 264690, 264557
588	79557239 (1175, 1176)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1 - (AB028014) KIAA1091 protein [Homo sapiens]			UNCLASSIFIED	265020, 264692
589	79805828 (1177, 1178)				UNCLASSIFIED	22278998, 264907, 264809, 264510, 265009, 265010, 264887, 264789, 356895917, 18108376, 264634, 264638, 264638
590	79815628 (1179, 1180)				UNCLASSIFIED	264906, 264809
591	10313540 (1181, 1182)	Novel Protein sim. GBank gi 2143293 emb CAB09390 - (Z95972) rpoB [Mycobacterium tuberculosis]			UNCLASSIFIED mapolymerase	264691
592	1388767 (1183, 1184)	Novel Protein sim. GBank gi 4511983 gb AAD21543.1 - (AF088896) electroltransfer ubi quinone oxidoreductase [Zymomonas mobilis]			MHC	263972
593	82348896 (1185, 1186)	Novel Protein sim. GBank gi 1272368 (U51896) - LfE			dehydrogenase	264511, 264762, 264769, 264488
594	20212392 (1187, 1188)	Novel Protein sim. GBank gi 1272368 (U51896) - LfE			UNCLASSIFIED	264605
595	10084084 (1189, 1190)	[Vibrio parahaemolyticus] Novel Protein sim. GBank gi 131490 sp P20966 PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EIL-FRU)				264769
596	13085170 (1191, 1192)				UNCLASSIFIED	264636
597	80259003 (1193, 1194)				UNCLASSIFIED	264592
598	94140216 (1195, 1196)				UNCLASSIFIED	264758, 55810764, 264555, 264556, 264637, 83373044
599	20385137 (1197, 1198)	Novel Protein sim. GBank gi 125328 sp P04951 KDSB_ECOLI - 3-DEOXY-MANNO- OCTULONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULONIC ACID SYNTHETASE) (CKS)			UNCLASSIFIED	264603
600	10357693 (1199, 1200)					
601	79810404 (1201, 1202)	Novel Protein sim. GBank gi 2127414 pir J560064 - hypothetical protein 2 - Corynebacterium glutamicum			UNCLASSIFIED	264806 264510

602	76250802 (1203, 1204)	Novel Protein sim. GBank gij3522861gbjAAC34243.1 - (AC0D411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	265007
603	11466067 (1205, 1206)			UNCLASSIFIED	264595
604	81675420 (1207, 1208)				264758
605	20436657 (1209, 1210)	Novel Protein sim. GBank gij1175322ispjP44917Y883_HAEIN - HYPOTHETICAL PROTEIN H10883		UNCLASSIFIED	264605
606	80334582 (1211, 1212)	Novel Protein sim. GBank gij5020284igbjAAD38043.1 AF15135 - (AF151383) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264784
607	95381506 (1213, 1214)	Novel Protein sim. GBank gij188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	264508, 264906, 85658542, 264682, 264687, 264688, 264534, 18108376, 35696423, 264638, 264555, 264638
608	11810888 (1215, 1216)			UNCLASSIFIED	264682
609	80084775 (1217, 1218)	Novel Protein sim. GBank gij2486701ispjP5552Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605
610	79829413 (1219, 1220)				264692
611	87586205 (1221, 1222)				264508, 264905, 264807, 264908, 264909, 264511, 264910, 264758, 264604, 264684, 264786, 264688, 264692, 264628, 264635, 264638, 264637, 264558
612	85287851 (1223, 1224)	Novel Protein sim. GBank gij1877388lembjCAB07118 - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264600, 264801, 264604, 264769, 264558, 264565
613	7523475 (1225, 1226)			UNCLASSIFIED	264389
614	79869348 (1227, 1228)	Novel Protein sim. GBank gij5114231igbjAAD0238.1 AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		kinase	18108372, 264563
615	39586698 (1229, 1230)	Novel Protein sim. GBank gij1339950dbjBAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		synthase	264600, 264602, 264629
616	20465331 (1231, 1232)	Novel Protein sim. GBank gij544387ispjP35873GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	264605
617	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498097ispjQ60769ITNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	inf	52845156, 21808785, 35696423, 21808788, 21808789, 22278994, 35696286, 22278998, 265020, 265021, 265007, 265008, 264636, 52844150, 33857023, 264692, 264693, 28331822, 28331824, 55812038, 83373044, 56182181, 80424269, 86714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35696052, 29331828, 27486282, 33657349, 56526498, 285018, 265018, 22278002, 264482, 264448, 29331830, 66712502, 264809

618	20632843 (1235, 1236)	Novel Protein sim. GBank gi 5459388[emb]CAB50746.1] - (AL098438) putative aminotransferase [Streptomyces coelicolor]		isomerase	284603	
619	91227224 (1237, 1238)					56994075, 29331826, 33856970, 285008, 33657402, 33109854, 87188559, 284448, 18108374, 83373044
620	81183143 (1239, 1240)	Novel Protein sim. GBank gi 464335[sp]Q05822[IDUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)]		phosphatase		28148488, 284758, 284369, 28148627
621	80239251 (1241, 1242)					
622	20456427 (1243, 1244)	Novel Protein sim. GBank gi 2633557[emb]CAB13080] - (Z89110) yJdF [Bacillus subtilis]		UNCLASSIFIED	284558, 284558, 284639	
623	10131798 (1245, 1246)	Novel Protein sim. GBank gi 1857710[sp]AAB48482] - (U87224) contactin associated protein [Rattus norvegicus]	Contains protein domain (PF00054) - Laminin G domain	UNCLASSIFIED	284603	
624	18534127 (1247, 1248)	Novel Protein sim. GBank gi 1705703[sp]P5225[CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK]		laminin	284906	
625	13084819 (1249, 1250)	Novel Protein sim. GBank gi 2894252[emb]CAA17114.1] - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		cytochrome	284596	
626	80082803 (1251, 1252)	Novel Protein sim. GBank gi 416592[sp]P32323JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	284688	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gi 3098418 (AF040844) - P140 [Mus musculus]		UNCLASSIFIED	284688	29331822, 284905, 284908, 33857023, 33657109, 284558
628	80077096 (1255, 1256)	Novel Protein sim. GBank gi 1711543[sp]P50528[SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284800	
629	79851602 (1257, 1258)	Novel Protein sim. GBank gi 1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	284806, 284807	
630	38565156 (1259, 1260)	Novel Protein sim. GBank gi 3236368 (AF064748) - S3-12 [Mus musculus]		UNCLASSIFIED	284490	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gi 140687[sp]P11868[YGGB_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)]			283978	
632	27843880 (1263, 1264)					
633	80477772 (1265, 1266)			UNCLASSIFIED	284908, 284600, 284605, 284769, 284689, 284488	
634	17938808 (1267, 1268)			UNCLASSIFIED	284769	
635	79574508 (1269, 1270)			UNCLASSIFIED	285018	
636	79910981 (1271, 1272)			UNCLASSIFIED	284689	
				UNCLASSIFIED	284596, 284762, 284683	

637	82455798 (1273, 1274)	Novel Protein sim. GBank gi 2326739 emb CAB10953 - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	284808, 284907, 284510, 284511, 284601, 284602, 284603, 284604, 284605, 18108351, 284762, 284768, 284687, 284769, 284689, 3585917, 284693, 284634, 284638, 284639, 284559, 18108385
638	14987457 (1275, 1276)	Novel Protein sim. GBank gi 4678682 emb CAB41074.1 - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			284638
639	80204210 (1277, 1278)	Novel Protein sim. GBank gi 458628 db BAA76838.1 - (AB023209) KIAA0892 protein [Homo sapiens]		struc	284112, 283974
640	17829579 (1279, 1280)	Novel Protein sim. GBank gi 1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	inapolymerase	285009, 285010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81518220 (1285, 1286)			UNCLASSIFIED	284806, 284808, 284758, 284288, 284632, 284635, 284639, 284584
644	11751367 (1287, 1288)			UNCLASSIFIED	284884
645	95010907 (1289, 1290)			UNCLASSIFIED	284806, 284762, 284693, 284639, 284559
646	80069083 (1291, 1292)			UNCLASSIFIED	284595, 284586
647	80257085 (1293, 1294)	Novel Protein sim. GBank gi 4507813 ref NP_003738.1 pTNKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	284809, 284591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gi 1044963 bbs 169846 - protamine [Monodonta turbinata, gonads, Peptide, 108 aa]		UNCLASSIFIED	284600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11786316 (1299, 1300)			UNCLASSIFIED	284888
651	11776932 (1301, 1302)	Novel Protein sim. GBank gi 1346916 sp P12283 PURA, ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)			284802, 284638
652	85516704 (1303, 1304)			UNCLASSIFIED	284805, 284907, 284909, 263978, 284637
653	82124947 (1305, 1306)	Novel Protein sim. GBank gi 1722977 sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278996, 284510, 284511, 284512, 284593, 21906754, 284603, 284760, 18108376, 284558
654	95010589 (1307, 1308)			UNCLASSIFIED	284808, 284595, 284632
655	79320692 (1309, 1310)	Novel Protein sim. GBank gi 130327 sp P26847 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - Acyltransferase	transferase	284592
656	80416739 (1311, 1312)			UNCLASSIFIED	284602, 284605, 284766, 284691
657	20811010 (1313, 1314)			UNCLASSIFIED	284557, 284558

658	87761815 (1315, 1316)	Novel Protein sim. GBank gl 5689493 dbj BAA83030.1 - (AB029001) KIAA1078 protein [Homo sapiens]		UNCLASSIFIED	22278998, 60432049, 29331822, 29331824, 29331828, 285007, 265008, 33857402, 33857084, 285017, 264448, 21906785, 21906786, 283987, 20281148, 18108370, 18108374, 284482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gl 2137872 pir l48724 - zinc finger protein PFZ - mouse	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcriptfactor	22278999, 60432049, 66714117, 29331827, 285007, 284786, 56181562, 18108359, 18108385, 18108370, 18108381
660	81897922 (1319, 1320)	Novel Protein sim. GBank		UNCLASSIFIED	284757
661	80028023 (1321, 1322)	gl 134180 sp P15401 SACY_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	284510, 265009, 284600, 284602, 284603, 284604, 284605, 32833986, 18108376, 284636, 18108387, 22278000
662	20483731 (1323, 1324)	Novel Protein sim. GBank gl 4545229 gb AAD2450.1 AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	284605
663	20628080 (1325, 1326)	Novel Protein sim. GBank gl 5689250 dbj BAA82881.1 - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	284605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gl 1652848 dbj BAA17766 - (D90909) DNA photolyase [Synecococcus sp.]		UNCLASSIFIED	284768
665	80079053 (1328, 1330)	Novel Protein sim. GBank gl 116841 sp P21640 COBJ_PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE) (PRECORRIN-3 METHYLASE)		isomerase	284600
666	78603142 (1331, 1332)	Novel Protein sim. GBank gl 3261829 emb CAB109271 - (Z98280) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	284907, 265007
667	94831802 (1333, 1334)	Novel Protein sim. GBank gl 5688851 dbj BAA82702.1 - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	284689, 284602, 284593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gl 3581853 emb CAA20809 - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomalprot	284905, 284906, 284908, 284600, 284601, 284603, 284605, 284760, 284689, 284636, 284638, 284639
669	12967154 (1337, 1338)	Novel Protein sim. GBank gl 2582531 (AF028444) - 2- isopropylmalate synthase [Streptomyces coelicolor]		UNCLASSIFIED	284637
670	80238549 (1339, 1340)			synthase	284905, 284906, 284908, 284601, 284762, 284766, 284689, 284638, 18108385, 284486
671	79601368 (1341, 1342)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	284690, 284692, 284693, 284636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gl 2114430 (U92703) - Orf-1/EBF-like-3 transcription factor [Mus musculus]		transcriptfactor	284910, 285017
673	82285788 (1345, 1346)	Novel Protein sim. GBank gl 4589285 gb AAD26430.1 AF13515 - (AF135154) ferric alkaligin siderophore receptor [Bordetella pertussis]			284759
674	79199258 (1347, 1348)			UNCLASSIFIED	284629

675	87895870 (1348, 1350)	Novel Protein sim. GBank gi 4980755 gb AAD35347.1 AE00170 - (AE001708) D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	284488, 22278989, 86714117, 284508, 284511, 285008, 80433438, 284600, 284601, 284602, 284603, 284604, 284605, 284782, 284687, 284789, 60431802, 18108374, 284638, 284639
676	78898607 (1351, 1352)	Novel Protein sim. GBank gi 1723568 sp Q10478 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07			285010
677	21844312 (1353, 1354)	Novel Protein sim. GBank gi 887208 (U03976) - dynein heavy chain isoform 5C [Tripleneustes gratilla]		ATPase-associated	284591, 284632
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 1586274 pf J2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF000053) - Laminin EGF-like (Domains III and V)	laminin	284758, 284682, 284557
679	78888855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278988, 284693
680	20726424 (1359, 1360)	Novel Protein sim. GBank			284600, 284602
681	94322017 (1361, 1382)	Novel Protein sim. GBank gi 5174483 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF000053) - Laminin EGF-like (Domains III and V)	laminin	284102, 284907, 284808, 285008, 284693, 283972, 83373044, 284568
682	11392478 (1363, 1384)	Novel Protein sim. GBank		UNCLASSIFIED	284595
683	80083680 (1365, 1366)	gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase Vh1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	284634
684	20465367 (1367, 1386)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			284605
685	80246735 (1369, 1370)				284909, 283987, 283981
686	79208606 (1371, 1372)				284631
687	80085829 (1373, 1374)				284693, 284635
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi 2688962 (AF027768) - LepA [Serratia marcescens]		peptidase	284807, 284638
689	88084256 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF000078) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284908, 284907, 285007, 285009, 60433438, 21908754, 284760, 18108358, 21908788, 21908789, 285021, 18108361, 283974, 18108379, 284557, 18108385, 22278002
690	80388750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A68)		UNCLASSIFIED	284510, 284511, 284764, 284769
691	81854392 (1381, 1382)			UNCLASSIFIED	284757
692	83608936 (1383, 1384)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55812038, 55811957, 285018, 55811150, 18108351, 284908, 60431528, 284594
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi 854063 emb CAA58337 - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	284635
694	82455883 (1387, 1388)	Novel Protein sim. GBank gi 287327 sp Q01033 VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278988, 284510, 284602, 284603, 284782, 284687, 284769, 284688

685	94147849 (1389, 1390)	Novel Protein sim. GBank gjl468339[embjCAB38059.1] - (AJ010901) MUC4 [Homo sapiens]	Contains protein domain (PF00094) - von Willebrand factor type D domain	UNCLASSIFIED	58182575, 264509, 264905, 264907, 29331830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274791, 264905, 264595
686	79830882 (1391, 1392)	Novel Protein sim. GBank gj2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	
687	11767889 (1393, 1394)	Novel Protein sim. GBank gjl1731343[spQ10894]YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
688	86895862 (1385, 1386)			UNCLASSIFIED	264688, 35695917
689	79582558 (1387, 1388)			UNCLASSIFIED	264682
700	79839098 (1389, 1400)			UNCLASSIFIED	264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gjl1001238[dbjBAA10477] - (D64003) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	264486, 264510, 264511, 264602, 264605, 264689
702	79814789 (1403, 1404)	Novel Protein sim. GBank gjl2498935[spQ46338]SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		UNCLASSIFIED	264809
703	20446820 (1405, 1406)			oxidase	264604
704	94312224 (1407, 1408)	Novel Protein sim. GBank gjl3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenomonaditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 58181562, 33657109, 264629, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gjl421091[pirjS30730] - hypothetical protein o208 - Escherichia coli		UNCLASSIFIED	265008
706	20288062 (1411, 1412)	Novel Protein sim. GBank gjl3024872[spQ55780]Y074_SYN3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gjl3420608[gbjAAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		264603
708	20708292 (1415, 1416)	Novel Protein sim. GBank gjl3649741[embjCAA03985] - (AJ000281) mucin [Homo sapiens]			264801, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gjl3080425[embjCAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]		strucd	18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)				264389
711	17931418 (1421, 1422)	Novel Protein sim. GBank gjl4758886[refjNP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B		265019
712	80258164 (1423, 1424)			apolipoprotein	264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gjl1703288[spQ11056]AM12_MYCTU - PUTATIVE AMIDASE CY50.19C		hydrolase	264906, 264807
714	27847651 (1427, 1428)	Novel Protein sim. GBank gjl4502351[refjNP_001692.1]pBAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyltransferase			264508, 264555

715	78639423 (1429, 1430)	Novel Protein sim. GBank gi 1789035 (AE000352) - ori. hypothetical protein [Escherichia coli]		UNCLASSIFIED	284907
716	79559072 (1431, 1432)				284692
717	79491842 (1433, 1434)	Novel Protein sim. GBank gi 2494074 sp P55653 GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)		dehydrogenase	284636
718	94319658 (1435, 1436)	Novel Protein sim. GBank gi 3873679 emb CAA94886 - (Z71178) similar to pro-collagen domains; cDNA EST EMBL:D27978 comes from this gene; cDNA EST EMBL:D27977 comes from this gene; cDNA EST EMBL:D34199 comes from this gene; cDNA EST EMBL:D84392 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 284681, 18108354, 284684, 284685, 284686, 284687, 284689, 21906789, 18108361, 284681, 284692, 55810764, 284635, 18108381, 18108382, 83373044, 18108388
719	17679564 (1437, 1438)	Novel Protein sim. GBank gi 2104302 emb CAB08631 - (Z85387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011
720	79841684 (1439, 1440)				284908
721	15020180 (1441, 1442)	Novel Protein sim. GBank gi 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	284629
722	9862603 (1443, 1444)	Novel Protein sim. GBank gi 498253 (U02372) - integrase [Vibrio cholerae]			284910
723	19755599 (1445, 1446)	Novel Protein sim. GBank gi 2253054 emb CAB10705 - (Z87559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	284691
724	10128494 (1447, 1448)	Novel Protein sim. GBank gi 4063015 (AF083081) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	284809
725	76678678 (1449, 1450)			UNCLASSIFIED	284905, 284907
726	13088282 (1451, 1452)			UNCLASSIFIED	284636
727	13522872 (1453, 1454)				284634
728	20268471 (1455, 1456)	Novel Protein sim. GBank gi 2633810 emb CAB13411 - (Z88112) similar to hypothetical proteins [Bacillus subtilis]			284567
729	11293753 (1457, 1458)			UNCLASSIFIED	284490
730	18900373 (1459, 1460)	Novel Protein sim. GBank gi 2494660 sp Q45291 GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	284584
731	80058750 (1461, 1462)	Novel Protein sim. GBank gi 1148192 (L47838) - putative [Bacillus subtilis]		UNCLASSIFIED	284605
732	80258175 (1463, 1464)	Novel Protein sim. GBank gi 1168396 sp P46881 AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	284591, 284594, 284595
733	20446838 (1465, 1466)				284604
734	20435987 (1467, 1468)	Novel Protein sim. GBank gi 3184080 emb CAA19338 - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284604
				ubiquitin	284604

735	11607959 (1469, 1470)	Novel Protein sim. GBank gi 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELG INTERGENIC REGION			264594
736	10878734 (1471, 1472)	Novel Protein sim. GBank gi 400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	264636
737	78945340 (1473, 1474)		Contains protein domain (PF00815) - Regulator of G protein signaling domain	UNCLASSIFIED	265020
738	17895353 (1475, 1476)	Novel Protein sim. GBank			265008
739	79833670 (1477, 1478)	Novel Protein sim. GBank gi 2508887 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)		oxidase	264910
740	19881557 (1479, 1480)	Novel Protein sim. GBank gi 3261828 emb CAB10925 - (Z98260) mrp [Mycobacterium tuberculosis]			264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi 3877494 emb CAA88472.1 - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED	264689, 35896286, 264510, 264808, 18108382
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)		UNCLASSIFIED	29331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED	264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264829, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264584, 264567
744	80230421 (1487, 1488)				18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264766
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi 78921 pir IS04846 - UDP-N- acetylmutamoylalanine-D-glutamate-2, 6-diaminopimelate-D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein	264806
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi 3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase	264800
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi 2887411 dbj BA24848 - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase	56714117, 264905, 264509, 264906, 264807, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21908768, 35895917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)				264690

749	20469118 (1487, 1498)	Novel Protein sim. GBank		UNCLASSIFIED	284604
750	20296427 (1498, 1500)	gi 1169727 sp P44948 FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE)			284600
751	21636169 (1501, 1502)	Novel Protein sim. GBank	Contains protein domain (PF00068) - Eukaryotic protein kinase domain	kinase	284605, 284559
752	82450366 (1503, 1504)	gi 5380068 gb AAD2851.1 AF159689 serine/threonine kinase PKN3 [Mycococcus xanthus]			
753	80508718 (1505, 1508)	Novel Protein sim. GBank	Contains protein domain (PF00202) - Amino transferases class-III pyridoxal phosphate	UNCLASSIFIED	284508, 284907, 284510, 285011, 284762, 284688, 35695855, 284636, 18108387
754	95083741 (1507, 1508)	gi 2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORF8)		UNCLASSIFIED	284808, 284600, 284602, 284604, 284760, 284769, 284634
755	80185449 (1509, 1510)			UNCLASSIFIED	284508, 284906, 284907, 284908, 284909, 284758, 284802, 284764, 284769, 284628, 284629, 284630, 284632, 284634, 284635, 284637, 284638, 83373044, 18108385
756	94631686 (1511, 1512)	Novel Protein sim. GBank		UNCLASSIFIED	284448, 284690
757	79468533 (1513, 1514)	(AL031317) putative dehydrogenase [Streptomyces coelicolor]			284769, 284688, 284638, 284639
758	78983178 (1515, 1516)	Novel Protein sim. GBank		UNCLASSIFIED	284682, 284685
759	78475667 (1517, 1518)	(AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		amylase	285007, 18108387, 265007, 18108387
760	87628888 (1519, 1520)	Novel Protein sim. GBank		UNCLASSIFIED	284694, 284686
761	79877968 (1521, 1522)	definition line found [Caenorhabditis elegans]			
762	80023563 (1523, 1524)	Novel Protein sim. GBank	Contains protein domain (PF00122) - transport E1-E2 ATPase		29331822, 284908, 52844045, 56182435, 60170831, 21908754, 285017, 285018, 284681, 284687, 284688, 21908786, 21908788, 285020, 265021, 265022, 284635, 22278000
763	20294813 (1525, 1526)	Novel Protein sim. GBank		UNCLASSIFIED	284766
764	39515024 (1527, 1528)	gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdtB [Thermotoga maritima]		UNCLASSIFIED	284907, 284593, 285020
					284600
					284603

765	80025347 (1529, 1530)	Novel Protein sim. GBank gij3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	284805, 284806, 284594, 284686, 33657023
766	82417404 (1531, 1532)				
767	10296742 (1533, 1534)	Novel Protein sim. GBank gij541121 [pir]S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	264605, 264762, 18108374
768	78416080 (1535, 1536)				284807
769	80086554 (1537, 1538)	Novel Protein sim. GBank gij2982501 [emb]CAA06184 - (AJ004932) neuropathy target esterase [Homo sapiens]		UNCLASSIFIED esterase	264592, 264595 55810764, 264559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gij283437 [pir]S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	264805, 284907, 264828, 284909, 265010, 264786, 264628, 264629, 264634, 264638, 264555
771	95329509 (1541, 1542)	Novel Protein sim. GBank gij4769004 [gb]AAD29715.1 [AF14059] - (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35566286, 264259, 66714117, 264107, 68712502, 58182435, 264112, 55812038, 87168559, 264288, 21906786, 33657023, 65274820, 65274791, 18108381
772	78971362 (1543, 1544)			UNCLASSIFIED	264810
773	78945363 (1545, 1546)			UNCLASSIFIED	265020
774	79856129 (1547, 1548)	Novel Protein sim. GBank gij5531324 [emb]CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264909
775	20820141 (1548, 1550)			UNCLASSIFIED	264555
776	78942693 (1551, 1552)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a		265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank gij4505461 [ref]NP_003624.1 [p]NRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01344) - Kelch motif	protease	21806754, 265020, 60170815, 264691
778	20691310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264803
780	95288987 (1559, 1560)	Novel Protein sim. GBank gij1144520 [U34956] - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264807, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)				264905, 264807, 265010, 264600, 264601, 18108382, 18108374, 264556
782	8758528 (1563, 1564)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	264805
783	18410781 (1565, 1566)				265020
784	80051197 (1567, 1568)			UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 264588
785	56073541 (1569, 1570)	Novel Protein sim. GBank gij3451335 (AC005525) - F22162.1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696032, 264804
786	20438842 (1571, 1572)	Novel Protein sim. GBank gij138748 [p]P10805 [UGPA ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA]	transport		264603
787	80258364 (1573, 1574)			UNCLASSIFIED	264593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746078 (AF015310) - BTH1 [Brassica napus]		synthase	264809, 264802, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	265007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gij5706378 [dbj]BAA83099.1 - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87168559, 265018, 21908765, 21908767, 21908789, 21908769, 265020, 264692, 22279000, 264563
791	94651627 (1581, 1582)	Novel Protein sim. GBank gij5689948 [emb]CA851985.1 - (AL109863) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264638
792	80058786 (1583, 1584)	Novel Protein sim. GBank gij393194 (L02375) - S-antigen [Plasmodium falciparum]		struc	265021, 264631, 264635, 264558
793	79638730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046 - (D28046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81639294 (1587, 1588)	Novel Protein sim. GBank gij105884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264908, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb]CAB07082 - (Z92771) birA [Mycobacterium tuberculosis]		carboxylase	264488, 35696052, 264905, 264907, 265010, 35698423, 264638
796	86669451 (1591, 1592)				50432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gij2995447 [emb]CAA71519 - (Y10495) CDV-1R protein [Mus musculus]		struc	22278998, 264093, 264094, 66714117, 21908767, 21908789, 265020, 265022
798	79665209 (1595, 1596)			transcript factor	264687, 264768, 264693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gij4467250 [emb]CAB37575 - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264909, 264910, 264638, 264638
800	79970189 (1599, 1600)			UNCLASSIFIED	264488
801	80499399 (1601, 1602)	Novel Protein sim. GBank gij2781517 [emb]CAA16054 - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		transport	264508, 264511, 265008, 265009, 264769, 264567, 264486
802	79834588 (1603, 1604)	Novel Protein sim. GBank gij4887211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264905, 264693
803	20467520 (1605, 1606)			struc	264605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]		kinase	264510
805	79599993 (1609, 1610)				264508
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb]CAA04683 - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp]Q21828 [YNFDC_AEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264764

808	35108817 (1615, 1616)	Novel Protein sim. GBank gi3913092[sp]Q46170[ARCD_CLOPE - ARGININE/ORNITHINE ANTIPORTER		transport	284909, 284602, 21908784, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi3913016[sp]P74309[ALF1_SYNV3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)]	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	284508, 284806, 264909, 265007, 264910, 264758, 284600, 284602, 284603, 284605, 284687, 264769, 284689, 284636, 264488
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi401472[sp]P30863[YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MILTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	284389
811	80078280 (1621, 1622)			UNCLASSIFIED	284558
812	10297654 (1623, 1624)			UNCLASSIFIED	284692
813	79612280 (1625, 1626)			UNCLASSIFIED	284906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi146168 (J01617) - glutaminyl- tRNA synthetase [Escherichia coli]		synthase	284805, 284602, 284605, 284682, 264687, 284769, 284636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi14589632[dbj]BAA76848.11 - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	284488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 284905, 284908, 285007, 33657402, 60433356, 60433438, 284758, 285011, 285017, 285018, 285019, 284389, 284288, 284885, 21906765, 21906767, 265020, 265021, 284692, 65274620, 33657109, 284628, 18108376, 284635, 284638, 60170394, 56182323, 284584, 284600
816	19881910 (1631, 1632)	Novel Protein sim. GBank gi1781144[emb]CAB06254] - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	284595
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi1477468 (U35244) - vacuolar protein sorting homolog v-ps33a [Rattus norvegicus]			65274572, 22278999, 60424269, 35896052, 55812038, 21908768, 55811957, 35895917, 33657023, 18108370, 18108374, 55810784, 35896423, 55811576, 284636
818	80938190 (1635, 1636)			transport	284585
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi1001352[dbj]BAA10839] - (D64006) ABC transporter [Synecocystis sp.]		UNCLASSIFIED	284600, 284602, 264604
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi1588814[sp]P37484[YVBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION			
821	79762590 (1641, 1642)			UNCLASSIFIED	284910
822	80215310 (1643, 1644)			UNCLASSIFIED	284510, 284594, 284637
823	94892299 (1645, 1646)	Novel Protein sim. GBank gi13878400[emb]CAA95828] - (Z71284) predicted using GeneFinder. Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841): cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST...		strut	284509, 284687, 284691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi1370076[emb]CAA66887] - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		284910, 284763, 264769, 284693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp P77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16669 - (AL021846) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312 - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336892 gb AAD17897 - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264508, 264508, 264509, 264606, 264907, 264908, 264909, 264512, 264910, 264591, 264758, 264800, 264766, 264768, 21908768, 35685917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 83373044, 18108385, 264563, 264566, 264486
829	81742215 (1657, 1658)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetyl(muramyl) tripeptide synthetase MurC [Heliobacillus mobilis]		UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)			UNCLASSIFIED	264603
831	87112435 (1661, 1662)	Novel Protein sim. GBank gi 1870004 emb CAB06855 - (Z82539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	56714117, 264910, 264639
832	19536322 (1663, 1664)			UNCLASSIFIED	264908
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase		264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)				264768, 263984, 21908767, 264910, 264632, 264635, 264258, 264639, 264693, 83373044, 264758, 35685052, 22279002, 264508, 264905, 264906, 264448, 263972, 264808, 264909
836	68126552 (1671, 1672)	Novel Protein sim. GBank gi 698315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]	transport		35685917, 264557
837	78450450 (1673, 1674)			UNCLASSIFIED	264595
838	78184203 (1675, 1676)	Novel Protein sim. GBank gi 728667 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264687
839	78641125 (1677, 1678)	Novel Protein sim. GBank gi 2496533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264908
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein (finger)	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)		264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gjl138805 sp P08045 XFIN_XENLA - XFIN PROTEIN	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank gjl211432 dbj BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00369) - Zinc finger present in dystrophin, C8P/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 58182323, 264558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gjl3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gjl222472 dbj BAA20844 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcript factor	265011
845	18346844 (1689, 1690)	Novel Protein sim. GBank gjl625679 pir A36829 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	264829 264907
846	78693448 (1693, 1694)				264908
847	78469365 (1695, 1696)			UNCLASSIFIED	265020
848	79756367 (1697, 1698)			UNCLASSIFIED	264568
849	78817849 (1699, 1700)	Novel Protein sim. GBank gjl3183245 sp P78061 YCJ_K_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gjl5454130 ref NP_008280.1 pTLN - talin	Contains protein domain (PF01608) - ILWEG domain		264468, 52644507, 264469, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52845080, 29331822, 29331824, 68714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 28146488, 28146498, 264107, 264905, 264908, 264907, 264908, 52844045, 56182435, 285008, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644288, 265010, 265011, 87188559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264368, 264685, 264768, 264687, 264768, 264769, 21908765, 21908766, 21908767, 21908768, 28148827, 21908769, 29148629, 55811857, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264891, 264692, 33857023, 264693, 263966, 33857108, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281088, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)	Novel Protein sim. GBank gi 3402836 emb CAA76082 - (Y16138) 2-enoate reductase [Mooresella thermoacetica]		reductase	284638 284566
854	80052438 (1707, 1708)				
855	79641130 (1709, 1710)				284692
856	11594238 (1711, 1712)			UNCLASSIFIED	284591
857	79210165 (1713, 1714)			UNCLASSIFIED	284630, 284634
858	80248910 (1715, 1716)				285008, 285009, 284601, 284602, 284603, 18108351
859	20296634 (1717, 1718)				284559
860	80041748 (1719, 1720)			UNCLASSIFIED	284489
861	65857045 (1721, 1722)			UNCLASSIFIED	33657023, 284630
862	80079467 (1723, 1724)				284600
863	80578931 (1725, 1726)	Novel Protein sim. GBank gi 2246532 (U83872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	284488, 18108398, 35658286, 284259, 18108351, 284288, 285021
864	94939904 (1727, 1728)				
865	80045310 (1729, 1730)	Novel Protein sim. GBank gi 5689884 emb CAB52047.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01478) - S4 domain	UNCLASSIFIED	284259, 284112, 263974 284635, 284600, 284636, 284581, 284602, 284693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gi 4557876 ref NP_000341.1 pABCR - ATP binding cassette transporter		transport	284288, 284557, 264558
867	80062402 (1733, 1734)				
868	10075384 (1735, 1736)			UNCLASSIFIED	284605
869	80062406 (1737, 1738)				284909
870	80248651 (1739, 1740)	Novel Protein sim. GBank gi 628660 pir S37755 - Adenyl- transferase - Escherichia coli		transferase	284605, 284687, 18108374 284601, 284636
871	20378285 (1741, 1742)	Novel Protein sim. GBank gi 1708180 sp Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG		UNCLASSIFIED	284603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gi 1545959 emb CAA67763 - (X99384) paladin [Mus musculus]		UNCLASSIFIED	35698286, 22278998, 284259, 29331822, 29331824, 29331825, 60432288, 29331826, 29331827, 29331828, 35696052, 284509, 284905, 284908, 284907, 284908, 284909, 284510, 285006, 284511, 284512, 285007, 285008, 285009, 284810, 284591, 60433356, 284596, 52846317, 67168474, 285010, 284602, 284603, 285017, 285018, 284605, 18108351, 284764, 284766, 284768, 52844229, 284769, 21906765, 265021, 284534, 284691, 52845129, 284628, 284629, 35698423, 65274791, 284631, 284632, 284635, 284636, 284556, 284637, 284638, 284639, 60432113, 22279000, 22279002, 284584
873	20189728 (1745, 1746)	Novel Protein sim. GBank gi 4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	284585

874	80077682 (1747, 1748)	Novel Protein sim. GBank gij134319sp P07819 SCR8_BACSU - SUCROSE-8- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			UNCLASSIFIED	264600
875	86608446 (1749, 1750)	Novel Protein sim. GBank gj1481000 p S37594 - much - human (fragment)				264259, 264448, 264288, 264557, 87168518
876	86465157 (1751, 1752)	Novel Protein sim. GBank gj1328283 (AF010496) - Iron(iii) dictrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF000005) - ABC transporter	transport		264907, 264601, 264602, 264605, 265020, 80431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gij1731074 sp P40349 URB1_ USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF003320) - GATA zinc finger	transcript factor		22278998, 264909, 264369
878	80187289 (1755, 1756)	Novel Protein sim. GBank gij1351614 sp Q09853 YAE0_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase-associated		264369, 264555
879	94328862 (1757, 1758)	Novel Protein sim. GBank gj13875304 emb CAA98434 - (Z74030) predicted using GeneFinder; cDNA EST EMBL: C07809 comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e8.3 comes from this gene; cDNA EST yk488h9.3 comes from this gene; cDNA EST yk488h9.5 com...				56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264883, 21908768, 21908768, 80170615, 33857023, 65274820, 33857109, 18108374, 35895855, 264563
880	8491135 (1759, 1760)	Novel Protein sim. GBank gij137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF000051) - Kringle domain	calthepsin		264508
881	11290122 (1761, 1762)			UNCLASSIFIED		264508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gj12632098 emb CAA75667 - (Y15513) Proctos protein [Drosophila melanogaster]		UNCLASSIFIED		264558
883	79582989 (1765, 1766)			UNCLASSIFIED		264688
884	13517921 (1767, 1768)	Novel Protein sim. GBank gj1155068 emb CAA84425 - (X94978) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED		264638
885	80052457 (1769, 1770)	Novel Protein sim. GBank gj12078027 emb CAB03467 - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]		UNCLASSIFIED		264605, 18108362
886	11685138 (1771, 1772)					264680
887	94315307 (1773, 1774)	Novel Protein sim. GBank gj12695834 emb CAA15904 - (AL021006) sucA [Mycobacterium tuberculosis]		dehydrogenase		35696052, 264808, 264600, 264603, 35695917, 35695855, 264638
888	10083399 (1775, 1776)	Novel Protein sim. GBank gj15689395 dbj BAA82981.1 - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED		264908
889	20385917 (1777, 1778)	Novel Protein sim. GBank gj11881338 dbj BAA19365 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis]				264603
890	18904337 (1779, 1780)	Novel Protein sim. GBank gj1854085 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]				264629

891	13516878 (1781, 1782)	Novel Protein sim. GBank gi 4959398 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	284636	
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 545526 bb 143833 - LBP- 1b-transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namaiwa cells, Peptide, 541 aa]		transcript factor	22278986, 22278988, 28331828, 35686052, 284808, 284809, 285009, 285011, 284802, 285019, 284768, 21908785, 21908788, 21908769, 285020, 285021, 58528488, 284689, 283987	
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi 2829888 sp P80608 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		synthase		
894	11102240 (1787, 1788)				263978	
895	80239868 (1789, 1790)			UNCLASSIFIED	284508, 284600, 284555, 284559	
896	79747803 (1791, 1792)				284632	
897	94991823 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284688, 28331828, 284511	
898	87895108 (1795, 1796)				56182575, 60432288, 56182435, 60432229, 55811957, 22278000, 284488	
899	11100483 (1797, 1798)				284601	
900	80499788 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U68480) - YncC [Bacillus subtilis]		transport	284789, 284691, 284563	
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	284907, 284802, 284605, 284769, 35695917, 18108378, 284563	
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 335570 emb CAA20001 - (AL031124) 3-Isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - Aconitase family (aconitase hydratase)	isomerase	284908, 285008, 284602, 284604, 284769, 284688, 284693	
903	82080206 (1805, 1806)	Novel Protein sim. GBank gi 2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35686052, 284805, 284510, 284511, 284512, 284805, 284760, 18108351, 284762, 284687, 284768, 284769, 284688, 21908784, 35695917, 27486282, 35695955, 284634, 284636, 284488	
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 726887 sp P40908 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	284604	
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23816.1 AC00718 - (AC007188) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	284909	
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			284595, 284605	
907	87913201 (1813, 1814)					
908	11754482 (1815, 1816)					
909	20727807 (1817, 1818)	Novel Protein sim. GBank gi 3868940 db BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	60432289, 284601, 284690	
910	16776208 (1819, 1820)	Novel Protein sim. GBank gi 4589726 db BAA76883.1 - (AB003137) DnaJ homolog protein [Salix glauca]	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	UNCLASSIFIED	284638	
				UNCLASSIFIED	284602	
				epb	265009	

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35885 RL7A_ORYSA - 80S RIBOSOMAL PROTEIN L7A		ribosomal prot	265010, 264604, 60432113
912	20448663 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07921.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 268895]		hydrolase	264559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 5689571 dbj BAA83069.1 - (AB028040) KIAA1117 protein [Homo sapiens]			18108398, 22278988, 66714117, 264806, 264591, 21908788, 265020, 55811576, 264638
916	79444091 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20185985 (1833, 1834)				
918	91226795 (1835, 1836)	Novel Protein sim. GBank gi 1655699 emb CAA89032 - (Y07752) pterophorin-S [Volvox carter]		UNCLASSIFIED synthase	264605 264258, 29331826, 264808, 265018, 264448, 265020, 264635, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 5689988 emb CAB52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265008, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79808095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I) Novel Protein sim. GBank gi 3850084 emb CAA21811.1 - (AL033388) alcohol dehydrogenase [Schizosaccharomyces pombe]		peptidase	264508
921	19858634 (1841, 1842)			UNCLASSIFIED	264600
922	78982605 (1843, 1844)				
923	86895830 (1845, 1846)	Novel Protein sim. GBank gi 287078 sp P28514 TBB6_ARATH - TUBULIN BETA-6 CHAIN		tubulin	265019, 22279002 264907, 285008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)				264510
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497688 sp Q0883 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811857, 263972, 264639
927	37038201 (1853, 1854)			UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Caliphora vicina]			dehydrogenase	264605
929	20630338 (1857, 1858)	Novel Protein sim. GBank gij4115935jbjAA03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]			UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gij4490609jembjCA838642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]				264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij545939jembjCAB50754.1] - (AL086839) putative integral membrane transport protein [Streptomyces coelicolor]		Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gij568952jbjBAA83045.1] - (AB029016) KIAA1093 protein [Homo sapiens]			transport	264508, 264905, 264906, 264909, 264600, 264602, 264603, 264605, 264768, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij222624jembjCAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		Contains protein domain (PF00827) - UBA domain	UNCLASSIFIED	264508, 264688, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gij119111jbp12879jEBN2_EBV - EBNA-2 NUCLEAR PROTEIN				264389, 22279002
935	80063162 (1869, 1870)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]			UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij1360659jirjCGHUV - collagen alpha 1(V) chain precursor - human			UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij222624jembjCAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]			synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij3560168jembjCAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]			UNCLASSIFIED	264602
939	11071694 (1877, 1878)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]				264600
940	94144252 (1878, 1880)	Novel Protein sim. GBank gij2494784jspjQ50728jGJAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264905, 264908, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264766, 264768, 264769, 33657023, 33657109, 264628, 264829, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11398414 (1881, 1882)	Novel Protein sim. GBank gij2494784jspjQ50728jGJAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)				264593
942	19484122 (1883, 1884)	Novel Protein sim. GBank gij732353jspjP39806jYWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION			UNCLASSIFIED	264760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gij732353jspjP39806jYWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION			UNCLASSIFIED	264600, 264687, 264689, 264563
944	80218096 (1887, 1888)	Novel Protein sim. GBank gij732353jspjP39806jYWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION			synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353jspjP39806jYWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION		Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	70248402 (1891, 1892)	Novel Protein sim. GBank gij732353jspjP39806jYWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION				265017

947	81802898 (1893, 1894)	Novel Protein sim. GBank gl 2896770 emb CAA17247 - (AL021898) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278896, 264907, 264909, 285008, 285009, 284910, 284758, 284600, 284802, 285018, 284805, 284789, 284689, 284693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gl 2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		fgf	18108398, 58182575, 22278997, 22278999, 80432049, 28331822, 29331828, 284907, 58182435, 58111388, 265011, 284600, 285017, 285018, 285019, 18108351, 285020, 285021, 285022, 27486285, 263972, 55811576, 284638, 80170394, 284568
949	88081788 (1897, 1898)	Novel Protein sim. GBank gl 4507985 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	28331825, 21806764, 27486281, 21808786, 52844298, 33657348, 87168518, 56994075, 285020, 285021, 87168559, 52844150, 284637
950	79485872 (1899, 1900)	Novel Protein sim. GBank gl 1079461 p S43865 - cytochrome b, type II - potoroo (fragment)	Contains protein domain (PF00038) - Intermediate filament proteins	struct	284683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gl 5420387 emb CAB46879.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gl 5305702 gb A041779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		calhespin	284910, 284691
953	10186003 (1905, 1906)	Novel Protein sim. GBank gl 2495642 sp O47142 YFHS_ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	284510
954	8893326 (1907, 1908)	Novel Protein sim. GBank gl 2360965 (AF018253) - D- amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	284508
955	95313410 (1908, 1910)	Novel Protein sim. GBank gl 5454084 ref NP_008319.1 pSIP1 - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 284509, 284805, 284906, 284907, 284908, 284909, 284510, 284910, 284758, 284759, 285010, 284801, 284780, 18108351, 284782, 284763, 284764, 284768, 284688, 284787, 284687, 284768, 284769, 284689, 284628, 284629, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 58182323, 284639, 18108388, 284563, 284584
956	80064224 (1911, 1912)	Novel Protein sim. GBank gl 2052129 emb CAB08155 - (Z94752) rlmJ [Mycobacterium tuberculosis]			284605
957	80056208 (1913, 1914)			UNCLASSIFIED	284603, 18108362
958	80038446 (1915, 1916)	Novel Protein sim. GBank gl 1709787 sp Q00451 PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	284908, 284910, 284762, 263978, 284637
959	80026847 (1917, 1918)	Novel Protein sim. GBank gl 2131050 emb CAB09260 - (Z95844) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	284602, 284692
960	37815408 (1918, 1920)	Novel Protein sim. GBank gl 2129478 p S51839 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	284259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				284593

963	80590374 (1925, 1926)				UNCLASSIFIED	284510, 284288, 284555, 284556, 284558, 284559, 284488
964	79832019 (1927, 1928)	Novel Protein sim. GBank glj4589822[dbj]BAA76833.1] - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	284112, 284910, 284689
965	81228485 (1929, 1930)	Novel Protein sim. GBank glj5420387[emb]CAB6679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264488, 265017, 264448, 284634, 284558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	264908, 284592, 284598, 284604, 284788, 21808784, 284892, 284693, 284829, 284638, 284638
967	79255708 (1933, 1934)	Novel Protein sim. GBank glj1731207[sp]Q11156jRGX3 MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	284780
968	79560288 (1935, 1936)	Novel Protein sim. GBank glj2661838[emb]CAA75187] - (Y14984) putative transport protein [Methylophilus methylotrophus]			transport	284693
969	79818470 (1937, 1938)	Novel Protein sim. GBank glj5418878[emb]CAB6422.1] - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		cna_ma_bind	35698288, 284885, 284688, 35695917, 284892, 18108374, 284635
970	95085947 (1939, 1940)				UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147620, 284828, 285008, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 284288, 21908787, 21908788, 18108370, 18108374, 18108377, 284630, 284635, 18108380, 83373044, 18108387, 18108388
971	78918770 (1941, 1942)				UNCLASSIFIED	285007, 285020, 22279002
972	20710704 (1943, 1944)					284557
973	20370183 (1945, 1946)	Novel Protein sim. GBank glj1723118[sp]P53990Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				284804
974	80057103 (1947, 1948)				UNCLASSIFIED	284565
975	10198018 (1949, 1950)				UNCLASSIFIED	284510
976	80205742 (1951, 1952)	Novel Protein sim. GBank glj3881459[emb]CAA92988.1] - (Z88753) predicted using GeneFinder; Similarly to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL: D27680 comes from this gene; cDNA EST EMBL: D27679 comes from this gene; cDNA EST EMBL: D84477 comes from this ge....			UNCLASSIFIED	284508, 284908, 284758, 284632, 284639, 284563
977	10355349 (1953, 1954)	Novel Protein sim. GBank glj549458[sp]Q05335jXYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	284906
978	80025927 (1955, 1956)				UNCLASSIFIED	284600, 284802, 284603, 284604
979	80447820 (1957, 1958)	Novel Protein sim. GBank glj3171904[emb]CAA75868] - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	284787, 284788, 285008, 265007, 284908
980	80025928 (1959, 1960)				UNCLASSIFIED	284600, 284802, 284605
981	80098550 (1961, 1962)	Novel Protein sim. GBank glj3599940 (AF017388) - facogential dysplasia protein 2 [Mus musculus]			UNCLASSIFIED	284692, 284555, 284556, 284557, 284558

982	80195670 (1963, 1964)	Novel Protein sim. GBank gij2850220[embjCAA71575] - (Y10545) fused-ccdB [Escherichia coli]		UNCLASSIFIED	264404
983	80985041 (1965, 1966)	Novel Protein sim. GBank gij476388[prjJB43402 - myosin heavy chain-B, neuronal - chicken]		struct	65274572, 58182575, 264808, 264808, 265007, 265008, 264758, 265010, 55811150, 33857023, 264634, 264557, 264558
984	20466876 (1967, 1968)	Novel Protein sim. GBank gij3451504[embjCAA07660.1] - (AJ007747) hypothetical protein BblPS1.21 [Bordetella bronchiseptica]		UNCLASSIFIED	264605
985	85481368 (1969, 1970)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z95436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1	transferase	56182435, 264600
986	87102868 (1971, 1972)			UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)				264909
988	19858881 (1975, 1976)			UNCLASSIFIED	264600
989	88095328 (1977, 1978)			UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057748 (1979, 1980)	Novel Protein sim. GBank gij5725506[gbjAAD48080.1]AF06015 - (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Repolysin (M12B) family zinc metalloprotease	oxidase	264259, 264808, 265009, 264810, 264598, 264369, 264288, 264766, 264628, 264635, 264568
991	10106140 (1981, 1982)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z95436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylylase and Guanylate cyclase catalytic domain	UNCLASSIFIED	264909
992	79845694 (1983, 1984)			UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)	Novel Protein sim. GBank gij3329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	264807
994	11090590 (1987, 1988)				264602
995	84321811 (1989, 1990)	Novel Protein sim. GBank gij5106572[gbjAAD39760.1]AF14394 - (AF143946) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264808, 56182435, 265008, 264591, 264592, 60432228, 60431735, 33857402, 264595, 264758, 21808754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21808765, 21908768, 21906789, 55811957, 264692, 264893, 264629, 35898423, 55811576, 35895855, 264836, 264555, 264556, 264558, 83373044, 22278002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2811719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 29331824, 263978, 55811957, 56526486, 87168518, 264910, 264906, 264565, 264586, 264683, 264768
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35696286, 22278997, 22278998, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264686, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530[spjP04929jHRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR]			264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2508897 sp P46480 YFCA_HAEIN - HYPOTHETICAL PROTEIN H0198		UNCLASSIFIED	264682	
1000	20727944 (1998, 2000)			UNCLASSIFIED	264602	
1001	66673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 gb BAA20833 - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ark repeat	kinase	60432049, 264807, 264809, 264511, 264603, 264693, 264684, 264687, 264689, 29148627, 21905769, 264692, 18108385, 22279000 265008, 264369, 265020	
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 588121 sp P37709 TRHY_RABIT - TRICHOHYALIN		shud		
1003	17833491 (2005, 2006)				265019	
1004	16314967 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264635	
1005	79617144 (2008, 2010)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508	
1006	37815429 (2011, 2012)	Novel Protein sim. GBank gi 4062879 db BAA36210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	264259	
1007	79820871 (2013, 2014)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1 - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	264905	
1008	68094444 (2015, 2016)			synthase	265007, 264802, 264805, 264760, 264636	
1009	57451269 (2017, 2018)	Novel Protein sim. GBank gi 3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264102, 264288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592	
1011	65546816 (2021, 2022)	Novel Protein sim. GBank gi 2342847 gb AA88591.1 - (U90853) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35696052, 264805, 264764, 264768, 35695917, 264629	
1012	95294456 (2023, 2024)	Novel Protein sim. GBank gi 3413411 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35696052, 264805, 264600, 264601, 264602, 264605, 264762, 264768, 264768, 264689	
1013	86095772 (2025, 2026)			UNCLASSIFIED	264591, 21908768	
1014	86088828 (2027, 2028)			UNCLASSIFIED	29331824, 265019, 265020	

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gij4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	strud	22278994, 22278995, 56994075, 22278996, 22278999, 284259, 28331825, 29331828, 284807, 56182435, 284510, 264591, 264593, 80433356, 284594, 55812038, 284758, 21906754, 33657084, 265010, 284600, 265017, 265018, 285019, 18108351, 21906765, 21906768, 21906767, 21908768, 55811957, 265022, 33657023, 65274820, 33657182, 32833986, 18108370, 18108377, 55811576, 35688423, 284630, 22279000, 284565
1016	79556694 (2031, 2032)	Novel Protein sim. GBank gij2506989 [P41407] IACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	264686, 264693
1017	11068213 (2033, 2034)	Novel Protein sim. GBank gij5103943 [b] BAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00488) - Bacterial extracellular solute-binding proteins, family 5	transport	284600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gij4493973 [emb] CAB39032.1 - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 29148627, 264563
1019	11703607 (2037, 2038)			UNCLASSIFIED	264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 284600, 284762, 264769, 264689, 18108370, 284636, 284638, 264488
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gij4633807 [gb] AAD28859.1 [AF127795] trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gij11781230 [emb] CAB06277 - (Z83887) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35689052, 264508, 285008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gij3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase, associated	264593
1024	80057128 (2047, 2048)			UNCLASSIFIED	52846842, 33657402, 33657023, 18108379, 55811576, 284631, 284556, 284557, 264559, 18108388, 284568
1025	79644200 (2049, 2050)	Novel Protein sim. GBank gij3483045 [emb] CA20556 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	264693
1026	80025948 (2051, 2052)	Novel Protein sim. GBank gij1174922 [sp] Q02322 [UVRD_HAEIN - DNA HELICASE II]		helicase	264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gij4757728 [ref] NP_004886.1 [PAGTA - angiotensin/vasopressin receptor AIIVAVP-like]		UNCLASSIFIED	265017

1026	20297928 (2055, 2056)	Novel Protein sim. GBank gi 2791409 emb CAA16003 - (AL021184) acc [Mycobacterium tuberculosis]	Contains protein domain (PF000330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	284600	
1028	94665090 (2057, 2058)			UNCLASSIFIED	284595	
1030	80095343 (2059, 2060)			UNCLASSIFIED	284907, 284908, 284510, 284512, 285009, 285010, 285011, 284600, 284602, 284603, 284605, 284769, 18108372, 18108374	
1031	95289117 (2061, 2062)			UNCLASSIFIED	284805, 284808, 284909, 284595, 284692, 284630, 284834, 284838	
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gi 4503895 ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	284689	
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gi 2982990 AE000882 - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35866052, 284908, 284510, 18108354, 284687, 284769, 284688, 60431802, 18108385, 284485	
1034	78245837 (2067, 2068)	Novel Protein sim. GBank gi 405895 U00007 - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	284906	
1035	78956355 (2069, 2070)			UNCLASSIFIED	284692	
1036	85804998 (2071, 2072)			UNCLASSIFIED	284905, 66712502, 284908, 284768	
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 284909, 60433438, 285019	
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gi 790819 L39881 - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		284604, 284634	
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gi 2805967 AF030027 - 24 [Equine herpesvirus 4]		UNCLASSIFIED	284092, 284093, 284094, 284683, 284689, 283987	
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gi 2352095 U97022 - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	284595	
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gi 3256635 dbj BA029218.1 - (AP0000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	284807	
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gi 2058299 emb CAA66953 - (X88309) ARI protein [Drosophila melanogaster]			284605	
1043	80037138 (2085, 2086)	Novel Protein sim. GBank gi 1870167 emb CAA70125 - (Y08921) msfK [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	284565, 284587	
1044	80025952 (2087, 2088)			UNCLASSIFIED	285006, 284602, 265017	
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gi 5689890 emb CAB52053.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]			29331825, 284637	
1046	11754882 (2091, 2092)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	helicase		284686	
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gi 421047 dbj BA074555.1 - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	284769	
1048	78186400 (2095, 2096)	Novel Protein sim. GBank gi 3413419 emb CAA20278 - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophysial hormones, N-terminal Domain	UNCLASSIFIED	284687	
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gi 5051636 gb AAD38328.1 AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	284905, 284634	
1050	79471521 (2099, 2100)			UNCLASSIFIED	284686	

1051	80475471 (2101, 2102)				UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442982 (2103, 2104)	Novel Protein sim. GBank gij1312375[sp]P35138[SERB_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)] (AL034386) dJ1156812.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases		dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gij1544131[emb]CAB46717.1 - (AL034386) dJ1156812.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]				264688, 18108374, 29331824, 83373044, 21908754, 52645156, 56182435, 264689, 29331827, 27486281, 35898052, 21908765, 35898423, 21908768, 56182575, 21908769, 55811957, 87168518, 358986286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52844150, 264908, 264288, 29331822, 52645080, 264766
1054	79580225 (2107, 2108)				UNCLASSIFIED	264688
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gij15052508[gb]A038584.1[AF145609] BCDNA GH02833 [Drosophila melanogaster] Novel Protein sim. GBank gij13021676[db]BAA25358] - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase		helicase	264907, 264602, 264681, 264288, 21908768, 33857109, 55810784, 35898555, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank gij13021676[db]BAA25358] - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]			mapolymerase	264806
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gij1226281 (U50308) - No definition line found [Caenorhabditis elegans]			UNCLASSIFIED	264682
1058	80376576 (2115, 2116)					264764
1059	94662754 (2117, 2118)	Novel Protein sim. GBank gij1170018[sp]P48808[GREY_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREY (TRANSCRIPT CLEAVAGE FACTOR GREY)]			transcriptfactor	35898052, 35898555, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gij12489087[sp]Q08332[UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)]			glycoprotein	29146489, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gij190254[pir]A28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse			phosphatase	264634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gij1334200[sp]O49854[GCSP_SOLITU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)]			dehydrogenase	264503
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gij12489986[sp]Q41228[IPSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)]				264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gij182654[pir]JA0086 - 10K zein precursor - maize				265007, 265008, 18108351, 18108385

1065	80021208 (2129, 2130)	Novel Protein sim. GBank gij212098[pir][S70682 - glycosyltransferase homolog - Bordetella pertussis]		transferase	284600, 284602, 284689
1066	17899878 (2131, 2132)	Novel Protein sim. GBank gij2508382[sp]P15042[DNLI_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))]		synthase	285009
1067	10132178 (2133, 2134)	Novel Protein sim. GBank gij4007869[emb]CAA22355] - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldol/keto reductase family	reductase	284809 284688, 18103362, 284558, 284600, 284760
1068	82082057 (2135, 2136)	Novel Protein sim. GBank gij4589484[dbj]BAA76770.1] - (AB023143) KIAA0928 protein [Homo sapiens]		UNCLASSIFIED	284604
1069	83002854 (2137, 2138)	Novel Protein sim. GBank gij120304[sp]P15932[FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)]		UNCLASSIFIED	284604, 284780
1070	82101892 (2139, 2140)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	284602
1071	20710588 (2141, 2142)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	284602
1072	82356540 (2143, 2144)	Novel Protein sim. GBank gij477532[pir][A48175 - Motch B protein - mouse (fragment)]	Contains protein domain (PF00008) - EGF-like domain	synthase	284606
1073	79814400 (2145, 2146)	Novel Protein sim. GBank gij3893109[emb]CAA76840] - (Y17820) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	284687, 284688, 21908784, 35696052, 35895917, 35895855, 284600, 284601, 284602, 285009, 284605, 284508, 284905, 284690, 284906, 284762, 284628, 284788
1074	80105982 (2147, 2148)	Novel Protein sim. GBank gij1176203[sp]P46442[HYCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		synthase	284606
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gij4033487[sp]Q44472[TUD4_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		UNCLASSIFIED	56994075, 22278988, 284594, 284757, 284596, 265018, 265019, 284681, 284389, 284688, 285020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij4033487[sp]Q44472[TUD4_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		ATPase-associated	284789
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487[sp]Q44472[TUD4_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		kinase	284805
1078	20288874 (2155, 2156)	Novel Protein sim. GBank gij3413828[emb]CAA20286] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284600
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij3413828[emb]CAA20286] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	18108394, 284789, 284634, 284636
1080	11787188 (2159, 2160)	Novel Protein sim. GBank gij3413828[emb]CAA20286] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284684
1081	94747080 (2161, 2162)	Novel Protein sim. GBank gij3413828[emb]CAA20286] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	83373044, 285019, 22278002, 284482, 18108351, 284882, 284908, 284693, 284487
1082	81490656 (2163, 2164)	Novel Protein sim. GBank gij3413828[emb]CAA20286] - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284758, 284768, 284789, 21908787, 284511, 284910, 284634, 284635, 284905, 284636, 284906, 284637, 284907, 284908, 284784, 284636, 20281089, 284766, 284595

1083	8746717 (2165, 2166)	Novel Protein sim. GBank gi1722945 sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427.23		UNCLASSIFIED	60424179, 284905, 284908, 284510, 60432229, 284759, 87188474, 284805, 284788, 284889, 18108384, 18108376, 35895855, 284638 284789
1084	37799308 (2167, 2168)	Novel Protein sim. GBank gi418384 sp P32057 WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475388 (2169, 2170)	Novel Protein sim. GBank gi1899190 (U90204) - heal shock protein 80 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - eph		60432229, 284687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gi1172956 sp P46176 RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	TCP-1qpn60 chaperonin family Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	284488
1087	79603978 (2173, 2174)	Novel Protein sim. GBank gi4160198 emb CAA15431 - (AL008583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHROMatin Organization Modifier) domain	helicase	29331827, 284693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gi2983155 (AE000893) - phosphoglucomutase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	284905, 284801, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gi4981768 gb AAD36290.1 AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	284488, 284511, 265011, 284682, 284788, 284689, 21808764, 35895917, 285020, 32833986, 18108370, 35895855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gi4007880 emb CAA22366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			284604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gi2495562 sp P77239 YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	284637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gi2880098 emb CAA17986.1 - (AL022121) ntl [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	264586 284789, 35895917, 35895855, 284600, 284602, 284803, 284605, 18108351
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gi1001642 db BAA10373 - (D84002) dGTP triphosphohydrolase [Synecocystis sp.]		UNCLASSIFIED	284686
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gi4565587 emb CAB40855.1 - (AL049828) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	284906, 285007, 284595, 284600, 284602, 284603, 284604, 284805, 284782, 284788, 284789, 284636, 284558, 18108387, 80432113, 284482, 284488
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gi115001 sp P19206 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		synthase	284600, 284602, 284603, 284604, 284805, 35895917, 284692, 284631
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gi115001 sp P19206 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)			
1097	79239560 (2193, 2194)	Novel Protein sim. GBank gi114135 sp P08205 ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		UNCLASSIFIED	285019
1098	79186424 (2195, 2196)	Novel Protein sim. GBank gi114135 sp P08205 ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	284687

1099	39523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- NT)-METHYLTRANSFERASE (MIG- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	284603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp Q84420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	284259, 284638
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01398) - Topoisomerase DNA binding C4 zinc finger	isomerase	284769
1102	79777814 (2203, 2204)			UNCLASSIFIED	284910, 284809
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 1906598 U81788 - kinesin-73 [Drosophila melanogaster]		struct	284757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2935448 AF048976 - synaptic ras GTPase-activating protein p135 Syngap [Rattus norvegicus]		UNCLASSIFIED	28331822, 21906754, 284555, 284558, 284558, 22278002
1105	80255121 (2209, 2210)				284566
1106	79314110 (2211, 2212)			UNCLASSIFIED	284555, 284389
1107	80470019 (2213, 2214)				284908, 284789
1108	80440818 (2215, 2216)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		transport	284907, 284510, 284511, 284600, 284602, 284605, 284768, 284769
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 2995310 emb CAA18338 - (AL022286) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	284602, 284605, 284638
1110	80503554 (2219, 2220)				
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 AE000868 - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			284908, 284593, 285010, 284601, 284603, 284604, 284605, 284682, 284768, 284693, 284638
1112	95010088 (2223, 2224)				18108370, 284557
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA18628 - (AL023862) putative oxidoreductase (Streptomyces coelicolor)		UNCLASSIFIED	284908
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir J554876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	284602, 284604, 284605, 284762, 284769, 284585
1115	11765583 (2229, 2230)				284636
1116	79841152 (2231, 2232)			UNCLASSIFIED	284688
					284908

1117	95305485 (2233, 2234)	Novel Protein sim. GBank gll3255965[emb]CAA94089] - (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	18108392, 284488, 283994, 284489, 18108398, 58182575, 22278995, 22278998, 35898288, 58994075, 22278997, 22278998, 22278999, 284259, 29331822, 58182181, 29331824, 86714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35898052, 33658970, 28146488, 284508, 284905, 284509, 284908, 284907, 284908, 68712502, 284909, 52844045, 58182435, 284510, 284511, 285008, 285007, 284512, 285008, 285009, 284910, 60170831, 284591, 284592, 284593, 60433356, 284594, 60433438, 284595, 5812038, 284596, 284758, 284759, 21908754, 33109954, 33857084, 285011, 87168559, 284600, 284601, 284602, 284603, 285017, 284604, 285018, 284605, 285019, 284760, 5811150, 284681, 284762, 18108351, 284448, 284682, 284784, 284683, 284288, 284389, 284684, 284685, 284788, 284787, 284688, 284687, 284788, 284789, 284688, 18108359, 284688, 21908765, 21908766, 21908767, 21908768, 21908769, 5811957, 29148784, 35895917, 285020, 285021, 285022, 60170815, 284680, 284681, 33857023, 284682, 284693, 65274820, 33857109, 33857182, 27486281, 27486282, 27486284, 33857349, 27486285, 35895783, 284691
1118	78583328 (2235, 2236)			UNCLASSIFIED	284691
1119	79642463 (2237, 2238)			UNCLASSIFIED	284807
1120	78480483 (2239, 2240)	Novel Protein sim. GBank gll5420387[emb]CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 285018, 285019, 284681, 285021, 60170815, 18108367
1121	78471716 (2241, 2242)	Novel Protein sim. GBank gll1644450 (U87864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	284683, 284632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	284639, 284563
1123	78637119 (2245, 2246)	Novel Protein sim. GBank gll98800[pir]S17768 - 3-dehydroquinase synthase (EC 4.8.1.3) - Mycobacterium tuberculosis		synthase	284693, 27486285
1124	79811596 (2247, 2248)			UNCLASSIFIED	284909
1125	78757861 (2249, 2250)			UNCLASSIFIED	284910
1126	78758914 (2251, 2252)	Novel Protein sim. GBank gll138154[sp]P03643[VG]G_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	284905, 284909, 284910
1127	11800930 (2253, 2254)			UNCLASSIFIED	284682
1128	8384885 (2255, 2256)	Novel Protein sim. GBank gll5002704[emb]CAB44358.1] - (AJ242630) DNA polymerase I [Methylobacterium sp. DMA]	Contains protein domain (PF00478) - DNA polymerase family A	UNCLASSIFIED	284511

1129	80422480 (2257, 2258)	Novel Protein sim. GBank gij5689485jdbj[BAA83026.1] - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank		UNCLASSIFIED	264595
1131	80055381 (2261, 2262)	gij4981328jgbjAAD35881.1(AE001174 - (AE001174) bioY protein [Thermotoga maritima]		UNCLASSIFIED	35686286, 22278998, 28331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gij1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278998, 264806, 265009, 264600, 264602, 264604, 264605, 264760, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235378 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gij4539171jembj[CAB39700.1] - (AL048485) conserved hypothetical protein [Streptomyces coelicolor]			264508, 264600, 264602, 264603, 18108376
1136	78842052 (2271, 2272)	Novel Protein sim. GBank		UNCLASSIFIED	264806, 264808
		gij4982454jgbjAAD36931.1(AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]			
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gij4972746jgbjAAD34768.1] - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - TPR Domain	collagen	22278998, 22278999, 35686052, 264907, 265009, 80433358, 264598, 265010, 264448, 264682, 264767, 264688, 265020, 264692, 55811578, 35685855, 264631, 264632, 22279002
1138	78841163 (2275, 2276)	Novel Protein sim. GBank gij731607jspjP36739jYHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR		struc	264808
1139	78633561 (2277, 2278)	Novel Protein sim. GBank gij3850031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264883
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	78638019 (2281, 2282)			UNCLASSIFIED	265019, 264693
1142	19635848 (2283, 2284)			UNCLASSIFIED	264631
1143	87762159 (2285, 2286)	Novel Protein sim. GBank gij3928000jembj[CAA05880] - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 264908, 264600, 264632, 87168518
1144	80089988 (2287, 2288)			UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264568, 264909
1145	14610262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062092 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35686286, 264760, 264805, 264488, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gij2499003jspjP78422jTHID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gij2886734jembj[CAA17213.1] - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2289, 2300)	Novel Protein sim. GBank gi 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]			ATPase associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264596, 264758, 264764, 264766, 264788, 264693, 264628, 60431850, 264564, 264588, 264587
1151	60070874 (2301, 2302)	Novel Protein sim. GBank gi 4324655 gb AAD16878 - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]			polymerase	264595
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gi 3874275 emb CAB07311.1 - (Z92825) predicted using GeneFinder. Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL.C12555 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from lhi....			glycoprotein	264488, 22278988, 264805, 264629, 264486
1153	60027783 (2305, 2306)	Novel Protein sim. GBank gi 4240315 dbj BAA74938.1 - (AB020720) KIAA0913 protein [Homo sapiens]			UNCLASSIFIED	264910, 264555, 264557
1154	83002895 (2307, 2308)	Novel Protein sim. GBank gi 4240315 dbj BAA74938.1 - (AB020720) KIAA0913 protein [Homo sapiens]			UNCLASSIFIED	265008
1155	79411088 (2309, 2310)	Novel Protein sim. GBank gi 586855 sp P37617 ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZNF11)-TRANSLLOCATING P-TYPE ATPASE		Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	264690, 264636
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gi 18480 sp P32139 YIHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION			transport	264603
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gi 2486481 sp Q50724 Y08S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C			UNCLASSIFIED	264908, 264907, 264758, 264766, 264769, 264689, 264636, 264566
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gi 2486481 sp Q50724 Y08S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C			UNCLASSIFIED	264908, 264762, 264687, 264769, 264689, 18108374, 35695855
1159	79186451 (2317, 2318)	Novel Protein sim. GBank gi 1138406 dbj BAA11490 - (D76995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]				264687
1160	91229893 (2319, 2320)	Novel Protein sim. GBank gi 1138406 dbj BAA11490 - (D76995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]				29331822, 29331824, 66714117, 29331826, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gi 2443342 dbj BAA22380 - (D88784) alpha 2 type I collagen [Rana catesbeiana]			UNCLASSIFIED	264369
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gi 2443342 dbj BAA22380 - (D88784) alpha 2 type I collagen [Rana catesbeiana]			UNCLASSIFIED	264693
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gi 4503375 ref NP_001376.1 pDPYS - dihydropyrimidinase			UNCLASSIFIED	29331827, 264808
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gi 5052594 gb AAD38607.1 AF145632 - (AF145632) BcDNA.GH06032 [Drosophila melanogaster]			transport	18108398, 29331827, 29331828, 26146498, 28146499, 18108354, 21908788, 29148627, 21908789, 264693, 18108382, 18108385
1165	80491888 (2329, 2330)	Novel Protein sim. GBank gi 4589476 dbj BAA76766.1 - (AB023139) KIAA0922 protein [Homo sapiens]			UNCLASSIFIED	264802, 264603, 264769, 18108370, 18108374, 264565
1166	88098456 (2331, 2332)	Novel Protein sim. GBank gi 4589476 dbj BAA76766.1 - (AB023139) KIAA0922 protein [Homo sapiens]				264488, 35696286, 22278989, 264259, 66714117, 60432289, 35696052, 264805, 58182435, 265008, 60433438, 264759, 21808754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113

1167	78963862 (2333, 2334)	Novel Protein sim. GBank gij2580433[dbj BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	284488
1168	88094678 (2335, 2336)			UNCLASSIFIED	284259, 28331827, 56182435, 60433438, 285019, 33857023, 35695855, 284566
1169	11805403 (2337, 2338)			UNCLASSIFIED	284681
1170	21832244 (2339, 2340)			UNCLASSIFIED	284602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gij2772814 (AF028248) - procollagen D [Mytilus edulis]		UNCLASSIFIED	284556
1172	78610113 (2343, 2344)	Novel Protein sim. GBank gij4757848[ref NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810764, 35896052, 284634, 284488
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gij2564053[dbj BAA22946] - (AB007632) Bm trachealless [Bombix mori]			284508, 284908, 284907, 284908, 284591, 284632, 284638, 284639
1174	20293077 (2347, 2348)	Novel Protein sim. GBank gij2911027[emb CAA17520] - (AL021858) mmsA [Mycobacterium tuberculosis]		dehydrogenase	284600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gij118333[sp P23234 DCIP_ENTCL - INDOL-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	284601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	284508, 284805, 284593, 284602, 284605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gij118791[sp P28643 FABG_CUPLA - 3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00108) - short chain dehydrogenase	reductase	284605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gij5031697[ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated	65274572, 18108398, 22278998, 22278999, 28331826, 284508, 284908, 284828, 33857402, 33109954, 284769, 21808765, 21808768, 21808768, 55811957, 33857023, 284629, 55811576, 35696423, 284638, 284556, 58182323, 60432113, 22278000, 22278002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gij2980090[emb CAA17888.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	284603
1180	11794448 (2359, 2360)	Novel Protein sim. GBank gij2558814[emb CAA04787] - (AJ001493) dehydroquininate dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	284638
1181	17846362 (2361, 2362)			UNCLASSIFIED	265017
1182	81494284 (2363, 2364)	Novel Protein sim. GBank gij5420387[emb CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]			265007, 265008, 284584, 284908, 284893
1183	79574044 (2365, 2366)	Novel Protein sim. GBank gij4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]			284689, 35696423, 284638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gij2129478[ref S51839 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	284602
1185	79491185 (2369, 2370)			glycoprotein	263867

1186	20224012 (2371, 2372)				UNCLASSIFIED	264559
1187	79248834 (2373, 2374)				UNCLASSIFIED	29331825, 265017, 18108351
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gij2966039 (AF054525) - hypothetical protein [Synecococcus PCC7002]			UNCLASSIFIED	264905, 264908
1189	79609387 (2377, 2378)					
1190	79830589 (2379, 2380)					264692
1191	80310105 (2381, 2382)				UNCLASSIFIED	265018
1192	13521641 (2383, 2384)				UNCLASSIFIED	264468
1193	11103584 (2385, 2386)					264638
1194	79893947 (2387, 2388)	Novel Protein sim. GBank gij654085[emb]CAA58337] - (X83413) U88 [human herpesvirus 6]			UNCLASSIFIED	263978
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gij1790277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	265007, 265008
1196	13000888 (2391, 2392)	Novel Protein sim. GBank gij2497360[sp]Q50715[IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)]			UNCLASSIFIED	264605
1197	11392317 (2393, 2394)					
1198	85280101 (2395, 2396)	Novel Protein sim. GBank gij1709525[sp]P54673[P3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)]				264803
1199	81862011 (2397, 2398)					264259, 264757, 33109954, 21908768
1200	9848880 (2399, 2400)	Novel Protein sim. GBank gij2499877[sp]P70645[BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)]			UNCLASSIFIED	264910
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gij606342 (U18997) - ORF_o622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			cathepsin	264765, 264769
1202	80082633 (2403, 2404)				ribosomalprot	264600, 264558
1203	82125373 (2405, 2406)				UNCLASSIFIED	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gij2500728[sp]Q59912[SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT]				264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264828, 264908, 264908, 264768
1205	80053981 (2409, 2410)					264905, 264769, 264638
1206	80241985 (2411, 2412)				UNCLASSIFIED	264556
1207	79841192 (2413, 2414)				UNCLASSIFIED	264556, 264557, 264558
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gij2645560 (AF027954) - Bd-2-related ovarian killer protein [Rattus norvegicus]			apoptosis	29331824, 264908, 285021, 18108370
						264764, 264683, 264769, 264688, 264689

1208	78185742 (2417, 2418)	Novel Protein sim. GBank gi1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	284687, 284688
1210	56426884 (2419, 2420)			UNCLASSIFIED	284807, 284693
1211	94656555 (2421, 2422)	Novel Protein sim. GBank gi1421095 pir S30688 - hypothetical protein o248 - Escherichia coli		transferase	284591, 284592, 284595
1212	78167928 (2423, 2424)	Novel Protein sim. GBank gi1380625 emb CAB07858 - (Z93785) predicted using GeneFinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01882 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		284689, 283987
1213	78859633 (2425, 2426)	Novel Protein sim. GBank gi1226282 pir I1505375A - vir gene [Bordetella pertussis]		kinase	284909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gi15728285 gb AA048398.1 AF12816 - (AF128162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	284808
1215	80050108 (2428, 2430)	Novel Protein sim. GBank gi12326739 emb CAB10853 - (Z98288) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	285009, 284601, 284602, 284603, 33857109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi1417328 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYL TRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOYL-PYRUVYL TRANSFERASE) (EPT)		transferase	284604
1217	95011344 (2433, 2434)				
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gi1805460 db BAA09022 - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		UNCLASSIFIED	284905, 284807, 284908, 284591, 284766, 284681, 284693, 284628, 284630, 284636, 284584
1219	91216252 (2437, 2438)			dehydrogenase	284601
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi14240315 db BAA74938.1 - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	58181686, 28331822, 60432289, 284601, 284692, 284628
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi12143886 pir I152523 - nucleoporin p82 homolog - rat (fragment)			52844507, 284905, 284908, 285008, 285018, 285020, 52844150, 33657023, 284693, 33657182, 35895783, 284634, 22279000, 22279002, 284482
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi1730805 sp P39683 SPHR_SYNIP7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	284768, 285020, 284906
1223	11615847 (2445, 2446)				284601
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gi1172627 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	284593 284593, 284600, 284601, 284603, 284605, 284768, 18108376, 284635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb]CAB08836] - (Z95436) hypothetical protein RV384c [Mycobacterium tuberculosis]			polymerase	264768
1226	80237518 (2451, 2452)					264805, 264512, 264689
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gij1706788[sp]P8133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]			UNCLASSIFIED	264908, 264637, 264639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gij1653901[dbj]BAA18811] - (D90817) acriflavine resistance protein [Synecocystis sp.]	Contains protein domain (PF00873) - AcrB/AcrD/AcrF family			264605, 264634
1229	94328135 (2457, 2458)				UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374, 264909, 264605, 18108388
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family		eph	
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gij1215733 [U48718] - OphC [Agrobacterium tumefaciens]			UNCLASSIFIED	264808
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij118298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]			transport	264909
1233	80255179 (2465, 2466)				UNCLASSIFIED	265017, 264564
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gij729871[sp]P40280[H2A_MAIZE - HISTONE H2A]	Contains protein domain (PF00125) - Core histone H2A/H2B/H3/H4		histone	265008, 265010, 18108381
1235	79914423 (2469, 2470)					264634, 264782
1236	81827147 (2471, 2472)	Novel Protein sim. GBank gij3875133[emb]CAA94750] - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL... protein-coupled receptor LGR4 [Rattus norvegicus]			UNCLASSIFIED	265018, 5581150, 264585, 264757
1237	83371782 (2473, 2474)					264758, 264601, 264768, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)					
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij4007890[gb]AAC95339] - (AF084383) DOK protein [Mus musculus]	Contains protein domain (PF00560) - Leudra Rich Repeat		glycoprotein	264259, 28331822, 28331824, 35698052, 264508, 264908, 52844045, 52848317, 264288, 264788, 264693, 264632, 264634, 264558, 87168518, 264563
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1176192[sp]P45420[YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLT-NANT INTERGENIC REGION PRECURSOR]			oncogene	264509, 264511, 264759, 264760, 264784, 264557
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383[sp]P19904[GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)]	Contains protein domain (PF00120) - Glutamine synthetase			264769
1242	79775890 (2483, 2484)				UNCLASSIFIED	264601, 264604, 264638
						264908, 264807, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gij3355671[emb]CAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264809
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2970846 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338[db]BAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849[emb]CAA20805] - (AL031541) putative phenylalanyl-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264836, 264557, 264584
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gij1352403[sp]P094871F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 26331826, 264108, 264508, 264907, 264828, 265009, 80433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2791407[emb]CAA16001] - (AL021184) hypothetical protein RV1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694365 (2499, 2500)	Novel Protein sim. GBank gij112785[sp]P051003MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	78850448 (2501, 2502)				264809
1252	78458087 (2503, 2504)			UNCLASSIFIED	264883, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij5670178[gb]AAM46616.1[AF161317] NRAMP manganese transport protein MntA [Salmonella typhimurium]		glycoprotein	264800, 264803, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160[pir]S22128 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21806787, 55811957, 264692, 264556, 264639
1255	78169728 (2509, 2510)				264638
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2995353[emb]CAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	80432288, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3183308 (AF089300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)				264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264908, 264448, 264908
1260	80084608 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gi 568951 dbj BAA83038.1 - (AB028010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01689) - cadherin	28331824, 264906, 284908, 264768, 284769, 284689, 284693, 284639, 18108384, 284583
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gi 95100 pir J521334 - hypothetical protein 4 - Agrobacterium tumefaciens	UNCLASSIFIED	284634
1263	20710997 (2525, 2526)	Novel Protein sim. GBank gi 3550958 (AF004840) - CDO [Rattus norvegicus]	struct	284602
1264	80083396 (2527, 2528)			284634
1265	80253578 (2529, 2530)		UNCLASSIFIED	284563
1266	79914804 (2531, 2532)		UNCLASSIFIED	284768, 284636, 284638, 284567
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gi 1085002 pir J55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	transport	284259, 21906754, 284389
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gi 4886445 emb CAB43370.1 - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	18108398, 22278995, 56994075, 60424269, 28331827, 264109, 284512, 285007, 285008, 285009, 284595, 33109954, 33657084, 87188559, 284600, 285018, 285019, 284389, 284688, 21906767, 285020, 52844150, 284691, 33657023, 33657349, 18108374, 284556, 18108385, 60432113, 22279002, 284488
1269	79821946 (2537, 2538)	Novel Protein sim. GBank gi 3334791 emb CAA1893g - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]	UNCLASSIFIED	284508, 284805, 284906, 284687, 284693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gi 2851834 sp O50581 Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	285010, 284601
1271	79840499 (2541, 2542)		ATPase associated	35896052, 284908
1272	79462878 (2543, 2544)			284686, 284689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gi 1655665 emb CAB03731 - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]	UNCLASSIFIED	284508, 284639
1274	96010802 (2547, 2548)			
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gi 123726 sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C82.5)	Contains protein domain (PF00183) - Hsp90 protein	284905, 284908, 284909, 284769
1276	21148844 (2551, 2552)	Novel Protein sim. GBank gi 2129478 pir J551939 - chitinase (EC 3.2.1.14) precursor - beet	- eph	284602
1277	20438195 (2553, 2554)			
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gi 1175473 sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN H40183	UNCLASSIFIED	284389
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gi 1929513 (U64318) - ATP synthase subunit beta [Moorelia thermococcalis]	UNCLASSIFIED	284556
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gi 4938504 emb CAB43882.1 - (AL076465) putative protein [Arabidopsis thaliana]	synthase	284603
			struct	284605
				283976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gij1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	28331825, 28331828, 284768, 83373044
1282	87537895 (2563, 2564)	Novel Protein sim. GBank gij3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	285008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gij3281721[emb]CAB070571 - (292770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gij3928022 (AF057696) - LspB [Haemophilus ducreyi]			284604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gij417154[sp]P33126[HS82_ORYSA - HEAT SHOCK PROTEIN 82]	Contains protein domain (PF00183) - eph		284766, 284889, 283987
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gij2078004[emb]CAB084511 - (295207) gorA [Mycobacterium tuberculosis]	reductase		264605, 264639
1287	80417530 (2573, 2574)				
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gij5353510[gb]AAD42161.1[AF08891 - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen	UNCLASSIFIED	265011, 284802, 284788, 284887, 284769, 284889, 18108370, 284638, 18108385, 284583
1289	11813647 (2577, 2578)				
1290	19528027 (2578, 2580)	Novel Protein sim. GBank gij1169995[sp]P46023[GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR]	Contains protein domain (PF00001) - tm7	UNCLASSIFIED	284563
1291	80470268 (2581, 2582)	Novel Protein sim. GBank gij2072674[emb]CAB083051 - (295120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - helicase		265007, 265008, 264789
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gij1835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - transcript factor		284092, 284259, 28331822, 28331824, 284508, 284806, 284808, 284512, 285008, 285009, 284591, 285019, 284389, 284288, 284886, 284788, 284893, 18108374, 284632, 58182323, 284639, 83373044, 22279002, 284482, 284563
1293	80067338 (2585, 2586)				
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gij2129173[pir]F64453 - oxalacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii	UNCLASSIFIED		265008, 55812038, 284389, 284558
1295	11688851 (2589, 2590)	Novel Protein sim. GBank gij5441779[emb]CAB46803.11 - (AL098811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	biolindap		284602, 284605, 284760, 18108351, 284889, 33657023, 284559
			dehydrogenase		284689

1298	11687804 (2591, 2592)	Novel Protein sim. GBank gi 4982191 gb AAD36886.1 AE00180 - (AE001805) DNA- directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease	UNCLASSIFIED	284591, 284639
1297	78639300 (2593, 2594)	Novel Protein sim. GBank gi 4982191 gb AAD36886.1 AE00180 - (AE001805) DNA- directed DNA polymerase I [Thermotoga maritima]	5'-3' exonuclease	UNCLASSIFIED	284693
1296	84239508 (2595, 2596)	Novel Protein sim. GBank gi 1943770 (U87181) - F53F10.1 gene product [Caenorhabditis elegans]		struct	18108348, 285017
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gi 3445181 (AC005498) - R31665.2 [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	284488, 284908, 284808, 22278002, 284586
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi 4082973 dbj BAAC36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	284605
1301	17839814 (2601, 2602)	Novel Protein sim. GBank gi 3445181 (AC005498) - R31665.2 [Homo sapiens]		UNCLASSIFIED	284908
1302	85416198 (2603, 2604)				85658542, 265020
1303	8684121 (2605, 2606)				284908
1304	78377198 (2607, 2608)			UNCLASSIFIED	284508
1305	19805898 (2609, 2610)			UNCLASSIFIED	284586
1306	13068230 (2611, 2612)	Novel Protein sim. GBank gi 3242273 emb CAB07017 - (Z82689) hypothetical protein Rv0238c [Mycobacterium tuberculosis]		UNCLASSIFIED	284636
1307	82201028 (2613, 2614)	Novel Protein sim. GBank gi 1502421 (U59433) - 3-ketacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	284907, 284592, 284764
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gi 95819 pir S16288 - ferric enterobactin transport protein fepC - Escherichia coli		reductase	284555
1309	78263011 (2617, 2618)	Novel Protein sim. GBank gi 5458220 emb CAB48893.1 - (AL098837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		transport	284906, 18108354
1310	20466318 (2619, 2620)	Novel Protein sim. GBank gi 455118 gb AAD21084 - (AF123158) zinc finger DNA binding protein 99 [Homo sapiens]		UNCLASSIFIED	284605
1311	67613142 (2621, 2622)				
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi 455118 gb AAD21084 - (AF123158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00088) - Zinc finger, C2H2 type	dna_ma_bind	35688286, 28331827, 284908, 285008, 284764, 284786, 284688, 21908787, 21908769, 35689517, 284691, 284693
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi 4929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00888) - Ribosomal protein S16	ribosomalprot	22278998, 22278999, 284259, 20281099, 29146498, 284508, 284908, 66712502, 60433358, 60433438, 265011, 265017, 284683, 284288, 21906785, 21908787, 29146827, 21908788, 35689517, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22278000, 284563, 18108390
1314	56928053 (2627, 2628)				22279002, 284564
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi 2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	284693
					284681

1316	95381608 (2631, 2632)	Novel Protein sim. GBank gi 5589407 dbj BAA82987.1 - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181686, 20281171, 29331822, 29331824, 80424289, 29331825, 35988052, 52644045, 264591, 80432229, 265018, 265018, 55811150, 56181562, 21906785, 21906787, 21906788, 35695917, 60170815, 33657023, 65274820, 33857108, 35695783, 35695855, 18108387, 87168518, 60432113, 22278002, 264564
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gi 4836757 gb AAD30541.1 AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264083, 264806, 264908, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gi 4860204 gb AAD27567.1 AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264808, 264908, 265008, 265008, 264592, 265018, 264786, 56181562, 18108368, 264628, 264628, 18108377, 264638
1320	86603567 (2639, 2640)	Novel Protein sim. GBank gi 4240183 dbj BAA74870.1 - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812036, 265018, 21906788, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gi 4868505 emb CAB43377.1 - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcript factor	60432049, 29331828, 264807, 264908, 264909, 264910, 55812038, 264601, 264762, 264784, 264786, 264788, 264789, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gi 5262591 emb CAB45738.1 - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_mg_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gi 5459516 dbj BAA02407.1 - (AB028921) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21908788, 21906787, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278986, 22278988, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264788, 264789, 21906788, 265022, 18108378, 264631, 264632, 264634, 264636, 264638, 264563, 264564, 264565, 264568
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gi 3294501 U64857 - similar to the DPT/Kunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264908, 264907, 264908, 264908, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264768, 264691, 35699423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gi 1397275 U61947 - C06G3.8 (gene product) [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	Contains protein domain (PF00278) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278986, 22278987, 22278989, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 58182435, 264112, 265008, 265009, 21908754, 285010, 285011, 285017, 265018, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21908767, 21908769, 29148829, 265020, 264690, 264691, 264692, 264693, 263987, 33857109, 33857182, 27488262, 33857349, 18108370, 18108374, 55810764, 35895855, 264634, 58182323, 83373044, 87188518, 80432113, 22279000, 22279002, 264583, 264587 264488, 22278987, 29331828, 264595, 18108351, 264766, 22279002, 264482, 264587
1328	87753493 (2655, 2656)			UNCLASSIFIED	
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56528486
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 dbj BAA76815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264688, 21906765, 55811957, 265020, 33857023, 33657109, 263973, 55811576, 35898423, 35695855, 58182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	85274572, 22278996, 56894075, 22278999, 60432048, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52844045, 58182435, 284510, 21906754, 87168559, 265018, 265019, 264448, 264288, 264389, 264686, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52844150, 33857023, 56182323, 18108387, 60432113, 22279002
1333	88098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 dbj BAA83047.1 - (AB028018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 68712502, 264591, 60433356, 60433438, 55812038, 265010, 284639, 55526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2682535 (AF-036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi 4240285 dbj BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 284288, 21906765, 21906767, 21906768, 21906769, 265020, 33857109, 27488264, 18108374, 264558, 264638, 264557, 60170394, 264559, 18108385, 264583

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi485445 sp P33485 NUA_PRYKA - PROBABLE NUCLEAR ANTIGEN				264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi568947 dbj BAA83018.1 - (AB028980) KIAA1067 protein [Homo sapiens]		UNCLASSIFIED		56182575, 56994075, 22278998, 22278999, 264092, 264259, 60432259, 26331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264882, 264448, 264883, 264369, 264688, 264689, 21908766, 21908769, 265020, 264691, 27488281, 20281069, 18108379, 55811578, 35695855, 56182323, 60432113, 22279002, 264597
1338	80366114 (2675, 2676)			UNCLASSIFIED		26331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED		35698032, 264909, 264688, 264556, 264558
1340	88316311 (2679, 2680)					264905, 264907, 87168559, 264764
1341	86101485 (2681, 2682)					264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi5019584 emb CAB44507.1 - (AL035542) dJ994E9.5 (ns6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7		264628
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - Leucine Rich Repeat	strud		264910, 264686, 264534
1344	20562559 (2687, 2688)					263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi214410 pir j55210 - tricarboxylate carrier - rat (fragment)		glycoprotein		264909, 60170394
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi33881052 emb CAA19523 - (AL023843) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22278000, 22278002, 264566
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504379 ref NP_003858.1 pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein		264906, 264908, 264909, 265008, 264910, 265011, 265017, 264784, 264786, 264787, 264769, 264631, 264634, 264638, 264567, 264488
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi3398720 dbj BAA32100 - (AB010998) peptidylarginine deiminase type IV [Rattus norvegicus]		UNCLASSIFIED		264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22278002, 264488

1349	81225548 (2687, 2688)	Novel Protein sim. GBank gi 2144101 pir 55210 - Irtcarboxylate carrier - rat (fragment)		UNCLASSIFIED	52846842, 35698288, 22278986, 22278988, 22278990, 264259, 29331822, 29331824, 35698052, 264509, 284905, 264907, 284908, 264909, 264511, 265008, 264512, 284910, 60170831, 264591, 60433438, 284757, 21908754, 285017, 265018, 284605, 284780, 264782, 264288, 264786, 264889, 21908785, 21908786, 21908787, 21908788, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33857349, 18108374, 18108376, 35696423, 60170384, 22278000, 22278002, 264563, 284584
1350	87083136 (2689, 2700)			UNCLASSIFIED	52846842, 264259, 29331825, 264908, 264511, 264604, 264288, 21908789, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22278002, 284488
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gi 4867239 gb AAD32246.1 - (AF084584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264908, 264907, 264638
1352	80076366 (2703, 2704)			UNCLASSIFIED	284693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gi 2144101 pir 55210 - Irtcarboxylate carrier - rat (fragment)		UNCLASSIFIED	35698288, 60424289, 264805, 264509, 264908, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264782, 264784, 264786, 52844229, 58181562, 35695917, 265022, 33657023, 264693, 35695783, 60431528, 264629, 263978, 35696423, 35695655, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 284584, 284588
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gi 4889108 gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331828, 264908, 265008, 33657402, 21908754, 265011, 87188559, 264684, 264368, 264769, 264689, 21908785, 21908788, 52844150, 33657023, 264692, 264693, 18108374, 83373044, 87188518, 22278000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gi 1469199 db BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00078) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	- dna_ma_bind	22278986, 22278997, 264259, 66714117, 264511, 21908754, 265010, 264769, 264689, 21908785, 21908788, 21908789, 264532, 27488282, 264629, 264638, 264556, 264638, 264639, 264482, 264484

1356	95313961 (2711, 2712)	Novel Protein sim. GBank gij1113865 (U40342) - ninein [Mus musculus]		stud	18100397, 22278995, 22278998, 22278998, 22278998, 284094, 29331828, 284905, 285006, 285007, 285008, 285010, 285017, 285018, 285019, 284784, 18108354, 284889, 21906785, 285022, 18108384, 35698423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gij897693[emb]CAA90330] - (Z50028) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		284259, 29331822, 29331825, 284510, 87188559, 285018, 284448, 284288, 21906785, 21908788, 21908788, 285021, 284893, 18108378
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gij556219 (L36831) - transcription regulator [Mus musculus]			284757
1359	67711643 (2717, 2718)			UNCLASSIFIED	284907, 284909, 284510, 284511, 284512, 18108351, 284784, 284534, 33857023, 18108374, 284634, 284635, 284638, 284639, 18108385, 284488, 284567
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gij2588282[emb]CAA75612] - (Y15417) acetate-CoA ligase [Coprinus cinereus]		synthase	80432288, 284605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gij5689443[dbj]BAA83005.1] - (AB028876) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00538) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35698288, 22278997, 22278999, 284259, 29331828, 284508, 284509, 284905, 284907, 284908, 285007, 285009, 33109854, 21906754, 87188474, 285011, 284781, 284883, 284288, 284788, 284789, 284689, 21906788, 285020, 285021, 33657023, 55811578, 35698423, 284634, 80432113, 22278902, 284482, 284488
1362	95287961 (2723, 2724)	Novel Protein sim. GBank gij5689411[dbj]BAA82889.1] - (AB028860) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	58182575, 58181888, 80432049, 284259, 29331822, 58182181, 29331827, 35698052, 28331828, 284905, 284908, 284908, 284595, 55812038, 85859542, 55811150, 284681, 284288, 284368, 58181582, 80431528, 55810784, 35698423, 80431850, 284558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gij1130484 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	284488, 29331826, 284807, 284687, 284689, 284693
1364	88179488 (2727, 2728)				60432289, 60433358, 60433438, 87188559, 284603, 18108351, 21906788, 35698423, 60432113
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gij458562[dbj]BAA76803.1] - (AB023176) KIAA0859 protein [Homo sapiens]		oncogene	284786
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gij1084944[pir]S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	285007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank g 4884088 emb CAB43240.1 - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52648842, 52646365, 22278985, 50994075, 35898286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35898052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21908754, 265011, 87188559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264389, 264686, 264787, 264689, 21908785, 21908786, 21908788, 21908789, 55811957, 265020, 265021, 265022, 264534, 60170815, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35898423, 35895855, 264635, 264555, 264637, 264558, 52844332, 60170394, 264558, 18108381, 18108385, 58526486, 22279000, 264563, 264587
1388	94320078 (2735, 2736)	Novel Protein sim. GBank g 464561 sp P35289 RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35898052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87188559, 264600, 264801, 264760, 264764, 264765, 264768, 52644229, 264689, 35895917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264566, 264488, 264587, 265008, 60432228, 60433356, 33657084, 21908784, 21908788, 264555, 264638, 264559, 264567
1389	86634033 (2737, 2738)	Novel Protein sim. GBank g 2082702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95316910 (2739, 2740)	Novel Protein sim. GBank g 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278998, 264259, 29331822, 29331824, 29331826, 29331827, 35898052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21908787, 35895917, 18108362, 35898423, 264632, 264635, 264636, 264555, 264638, 264558, 264638, 18108385, 65274727, 264404, 264563, 264568, 264486
1371	95336512 (2741, 2742)	Novel Protein sim. GBank g 5032203 ref NP_005714.1 pTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265016, 265018, 264762, 264448, 35895917, 33657109, 33657182, 33657349, 35895855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank glij840708[jbjiBAA09334] - (D50685) trans-aldolase [Trypanosoma cruzi]		collagen	263978	264769, 21806765, 21806767, 22278999, 264691, 264910, 55812038, 265010, 264681, 264684
1373	80489421 (2745, 2746)			UNCLASSIFIED		264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274791, 264555, 264556, 264557, 83373044, 60432113
1374	95087038 (2747, 2748)	Novel Protein sim. GBank glij11876[piriJC1241 - beta-Interferon-Induced protein - rat]		Interferon		52844507, 52845156, 52846842, 52846365, 56182575, 56181896, 22278986, 56994075, 35698286, 22278987, 22278988, 22278989, 264259, 29331822, 52845080, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 35698052, 33856970, 264905, 264508, 264908, 264907, 264908, 29331830, 264909, 265008, 264511, 265007, 265008, 265009, 33857402, 60433358, 52646317, 33109954, 33657084, 52844296, 87168474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108331, 264448, 264764, 264288, 264369, 264768, 52644229, 21806785, 21806786, 21806767, 21806788, 21806769, 55811957, 35695917, 265020, 265021, 52844150, 33857023, 264693, 65274620, 52845128, 33857109, 27488261, 33857348, 27488265, 35695763, 18108376, 55810784, 35696423, 35695955, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 60432113, 22278000, 22278002, 264583, 264584, 264586, 264587, 264768, 264769, 35695917, 22278997, 264691, 264259, 26331822, 264693, 35698052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264808, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264536, 264639, 33857402, 264595, 18108385, 56526488, 265010, 265011, 264800, 264583, 264762, 264584, 264565, 264764, 264486, 264768
1375	94236942 (2748, 2750)	Novel Protein sim. GBank glij5848176[jbjiAAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		
1376	87389050 (2751, 2752)	Novel Protein sim. GBank glij138350[spjP28989]VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		
1377	86884242 (2753, 2754)	Novel Protein sim. GBank glij1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase, associated		29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22278002

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gjl4107015[dbj BAA36283] - (AB001772) PEM-5 [Clona savigny]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264389, 264288, 29148627, 55811957, 264691, 18108368, 33657109, 18108368, 264635, 263981, 18108385
1379	85879344 (2757, 2758)	Novel Protein sim. GBank gjl3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627062 (2759, 2760)	Novel Protein sim. GBank gjl4037737[gb AAD30662.1] - (AF088834) germ cell specific Y-box binding protein [Homo sapiens]	nuc_rept		264510, 264512, 265009, 264288, 264564
1381	88179856 (2761, 2762)	Novel Protein sim. GBank gjl4731580[gb AAD28508.1] (AF125384) L82A [Drosophila melanogaster]	UNCLASSIFIED		87188538, 265017, 264628, 22279002
1382	94847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	22278994, 22278997, 22278999, 29331822, 29331824, 29331828, 265007, 60432228, 60433358, 85658542, 265017, 265018, 264685, 264788, 21908768, 35695917, 33657023, 27486281, 27486262, 35695763, 35695855, 87188518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED	18108398, 264692
1384	88915895 (2767, 2768)			UNCLASSIFIED	264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264810, 264760, 18108351, 264766, 264768, 35695855, 264630, 264638, 264555, 264638, 264483, 264584, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gjl2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]	UNCLASSIFIED		35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gjl2384910 (AF022882) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]	Inf		60432288, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264586
1387	87787958 (2773, 2774)	Novel Protein sim. GBank gjl4180304[emb CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]	UNCLASSIFIED		264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gjl4895184[gb AAD32753.1] (AC007231) putative disease resistance protein [Arabidopsis thaliana]	glycoprotein		65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264809, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87188598, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21908767, 21908768, 21908769, 265021, 264682, 33657023, 33657109, 35695855, 264598, 60170384, 83373044, 22279000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gij5689387dbj BAA82977.1 - (ABD28948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 284259, 29331822, 29331824, 29331825, 60432289, 29331828, 29148499, 284908, 68712502, 55812038, 285017, 285018, 285019, 18108351, 284369, 21906785, 21906786, 21908767, 21908788, 265020, 285021, 284692, 33657023, 33657349, 18108370, 18108374, 55811576, 284555, 284556, 284557, 60170394, 83373044, 22278000, 284563, 284584
1390	94111916 (2779, 2780)	Novel Protein sim. GBank gij3702295 (AC005783) - R33083_1 [Homo sapiens]	peptidase	peptidase	52645156, 52646355, 264259, 52645080, 29331825, 29331826, 284908, 52644045, 285009, 33657084, 52644296, 87168474, 87168559, 285017, 285018, 284780, 284682, 284288, 284686, 284687, 56181582, 52844229, 21906785, 21908769, 35695917, 265020, 285021, 60170615, 52644150, 33657023, 27486281, 27486284, 65274791, 264631, 264555, 52844332, 87168518, 22279000, 264567
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gij1346910j P28650 PUA1_MOUSE - ADENYLOSUCCLINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase	UNCLASSIFIED	29331826, 29331828, 29331830, 284448, 284288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gij726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35696286, 58994075, 22278997, 22278998, 22278999, 60432049, 284259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35686052, 29331828, 33656970, 284907, 52644045, 265008, 265007, 285008, 60431735, 60433358, 52646317, 55811386, 52644286, 265010, 87168559, 265017, 284604, 265018, 265019, 264448, 284288, 284369, 284786, 21908784, 21908787, 35695917, 265020, 265021, 33657109, 52845129, 27486281, 27486282, 27486285, 33657349, 35685783, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52844332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264568, 18108391
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	284763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	284829
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gij2274845j BAA21534 - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	285009, 18108381

1396	95363253 (2791, 2792)	Novel Protein sim. GBank gi 2135904 pir j54810 - pHLEIF1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331826, 29148498, 29148499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264602, 265017, 265018, 265019, 18108354, 52844229, 18108356, 21908767, 29148827, 21908768, 21908769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567, 35696286, 264907, 66712502, 264510, 35695917, 264892, 264693, 35696423, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264788, 21908767, 265020, 33857023, 27486281, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]			
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gi 246887 sp Q09232 YQ22 CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	
1400	95418064 (2799, 2800)	Novel Protein sim. GBank gi 283920 pir j527939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264768, 21908768, 21908767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264909, 264758, 264788, 21908769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nel homolog [Homo sapiens]	Contains protein domain (PF00008) - EGF-like domain	- tgf	264905, 264907, 264908, 264909, 264112, 264693, 33857109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21908765, 21908768, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	83274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433436, 265017, 264683, 18108385

1405	95085068 (2808, 2810)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 (Human herpesvirus 6)			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264583, 264482, 264488, 264587, 264907, 264605
1406	57612369 (2811, 2812)	Novel Protein sim. GBank gi 624076 gb AAC96425.1 - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Pro Accession Number P13993 [Paramedium bursaria Chlorella virus 1]	collagen		
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gi 2827886 (AF015037) - endooligopeptidase A related protein: EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 68714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265006, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264686, 21908765, 21908768, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95381477 (2815, 2816)	Novel Protein sim. GBank gi 2584953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264498, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21908767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264583, 264564, 264585, 264586, 264587, 264693
1409	86644385 (2817, 2818)	Novel Protein sim. GBank gi 2662165 db BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gi 2493780 sp Q60994 ACR3_MOUSE - 30 KO ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	Contains protein domain (PF00386) - complement C1q domain		29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21908767, 263974, 264631, 264586

1411	87818641 (2821, 2822)	Novel Protein sim. GBank g13123155 sp P91343 YM3M_CAEEL - HYPOTHETICAL 48.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278998, 29331822, 60432289, 29331828, 284907, 265017, 265019, 284682, 21906767, 21906768, 21906769, 285020, 284890, 284891, 33657023, 33657109, 27486284, 264628, 263972, 284634, 284559, 18108385 264757
1412	84390919 (2823, 2824)			UNCLASSIFIED	
1413	95416559 (2825, 2826)	Novel Protein sim. GBank g1387912 emb CAA94370 - (Z70310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S37771). cDNA EST EMBL:U01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	58994075, 29331822, 35696052, 29331828, 29331830, 284809, 52844045, 284510, 52844296, 85858542, 87168474, 265017, 265018, 284681, 284687, 21906768, 35695917, 285020, 52844150, 284692, 263987, 27486284, 35695763, 284639, 18108387, 264566 264682, 284683, 265022, 264636
1414	94675860 (2827, 2828)	Novel Protein sim. GBank g13252981 (AF088921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	
1415	94326948 (2829, 2830)	Novel Protein sim. GBank g11871187 (U90439) - unknown protein [Arabidopsis thaliana]			52846385, 56182575, 22278894, 22278895, 56894075, 22278998, 22278997, 22278998, 22278998, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52844045, 264113, 264511, 33857402, 264757, 21906754, 55811388, 265017, 265018, 265019, 284761, 284683, 284369, 284288, 284688, 284689, 21906766, 21906767, 29146627, 21906769, 55811957, 265020, 265021, 284690, 33657023, 63274620, 52845128, 27486282, 27486284, 60431528, 284629, 35695855, 56182323, 264559, 60432113, 264404, 22278002, 284482

1416	94325977 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39748.1 AF123052 - (AF123052) MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108382, 18108394, 18108397, 18108398, 22278995, 22278998, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29148498, 284905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87189559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52844229, 264688, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 55811957, 29148629, 265020, 52844150, 18108361, 33657023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108378, 55811576, 65274791, 264634, 264636, 58182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22278900
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi 4956935 dbj BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)		UNCLASSIFIED	264259, 264908, 265010, 52844229, 21906764, 21906768, 264680, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072284 (U95097) - milotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432288, 265006, 87168474, 264288
1420	87298828 (2839, 2840)	Novel Protein sim. GBank gi 5174421 ref NP_008023.1 pCPNE - copine VI (neuronal)	ATPase_associated	28331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi 3876090 emb CAA03459.1 - (Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gene...	kinase	18108358, 18108398, 18108397, 21906766, 18108398, 21906767, 58182575, 21906768, 21906769, 58181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 80170815, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35698423, 35695855, 264512, 265007, 60431850, 60432228, 60431735, 56182323, 264558, 60170394, 83373044, 55612036, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22278902, 55811150, 264563, 264682, 264763, 264448, 264586, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gij4503939[ref]NP_000928.1pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)			mapolymerase	56994075, 35686286, 87168559, 55811857, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)				UNCLASSIFIED	264686, 264489, 264682, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gij437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]		Contains protein domain (PF00620) - RhoGAP domain	strud	29331822, 29331825, 29331827, 29146498, 264905, 264906, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264788, 264687, 21906765, 21906768, 21906767, 21906768, 29148627, 55811857, 29148629, 265021, 264691, 264692, 56528486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gij100798[pri]S14959 - proline- rich protein - wheat			UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gij2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]			UNCLASSIFIED	264488, 60424179, 35698286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108365, 56528486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gij5816074[gbl]AAD45616.1JAF08194 - (AF061943) protate- derived STE20-like kinase PSK [Homo sapiens]		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 56984075, 22278997, 29331828, 29331830, 264628, 265006, 265007, 265008, 265009, 264683, 264286, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264584
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gij138350[sp]P28968[VGLX_HSVB - GLYCOPROTEIN X PRECURSOR			glycoprotein	56181666, 264258, 264907, 265007, 265009, 264595, 265010, 264686, 65274620, 264629, 65274791, 22279002, 264586
1429	87888889 (2857, 2858)				UNCLASSIFIED	264112, 264595, 265017, 265018, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gij1181619[blj]BAA11565] - (D82384) a variant of TSC-22 [Gallus gallus]				264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264768, 265020, 264691, 264683, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gij414797 (L18968) - pyruvate dehydrogenase phosphatase [Bos taurus]			phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148829, 263988
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gij2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]		Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)				UNCLASSIFIED	264682, 264691

1435	94708213 (2869, 2870)	Novel Protein sim. GBank gi 3970850 dbj BAA34789.1 - (AB015330) HRIHFB2007 [Homo sapiens]			22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 68714117, 29331826, 33858970, 284508, 284805, 68712502, 29331830, 264909, 265007, 265008, 264810, 265009, 60433356, 60433438, 284596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264782, 264448, 264288, 264789, 21906787, 21906768, 21906789, 265020, 285021, 265022, 284890, 284891, 33857108, 284628, 18108374, 18108376, 55811576, 284638, 60170394, 56182323, 284559, 83373044, 87168518, 60432113, 22279000, 22279002, 284563, 284482, 284585, 263978, 284557, 284559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi 3183977 emb CAA39515 - (X58044) protein HIRG [Mus musculus]		UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 68714117, 29331826, 284807, 56182435, 285009, 18108351, 284692, 284693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi 1905908 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF). Contains protein domain (PF00450) - Serine carboxypeptidase	kinase	284488, 284508, 264908, 264809, 264757, 284600, 284601, 284605, 284768, 284769, 284690, 35898423, 264558, 264583, 284568
1439	91231864 (2877, 2878)	Novel Protein sim. GBank gi 3876289 emb CAA94892 - (Z71180) similar to BPTKUNITZ inhibitor domain; cDNA EST EMBL:D88293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]		cathepsin	22278994, 22278996, 35698288, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35898052, 33858970, 284107, 284508, 284509, 284807, 68712502, 29331830, 56182435, 264511, 265008, 285007, 285009, 60432229, 60433438, 264595, 55812038, 55811388, 265011, 265017, 285018, 285019, 18108351, 284448, 18108354, 264288, 18108355, 264767, 21906785, 21906786, 21906767, 21906768, 21906769, 55811857, 35895917, 285020, 265021, 285022, 33657109, 18108370, 18108374, 55810784, 35895855, 284634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 284486
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gi 2662165 dbj BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	284808, 284909, 285008, 285010, 285017, 265018, 265019, 18108351, 284389, 265020, 33657023, 33657109, 60431528, 55811576, 284635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gij493956jemb CAB11123.2 - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:...	Contains protein domain (PF00846) - F-box domain.	18108392, 264488, 263994, 264488, 58182575, 22278994, 22278995, 56994075, 35698286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 86714117, 29331826, 29331827, 29331828, 35698052, 28146488, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21908754, 85658542, 87188474, 265010, 87188559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264781, 264782, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52844229, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35895917, 265020, 265021, 80170815, 52844150, 264691, 264692, 33657023, 85274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35698423, 85274781, 35695955, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22278000, 22279002, 264563, 264483, 264564, 264566, 264567, 264488	
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gij5103027 dbj BAA78765.1 - (AB023419) mSox7 [Mus musculus]		transcript factor	264806, 285007, 264693, 264558
1443	87108935 (2885, 2886)	Novel Protein sim. GBank gij4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	52845080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gij3874447 emb CAB02772 - (Z81039) predicted using Genefinder; cDNA EST EMBL:Y01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 comes from this gene; cDNA EST yk308			

1449	87860859 (2897, 2898)				UNCLASSIFIED	56714117, 284908, 284908, 284591, 284601, 284784, 284632
1450	87458696 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35686286, 35696052, 265008, 265009, 60170631, 33109954, 264683, 264689, 35696423, 35695855, 56526486
1451	87787970 (2801, 2802)	Novel Protein sim. GBank gij4160304[emb]CAA106001 - (AJ132182) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264683, 264683, 263978, 264630
1452	85692896 (2803, 2804)	Novel Protein sim. GBank gij2832908[db]BAA24608.11 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2805, 2806)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]			kinase	264510, 264768
1454	11204898 (2907, 2908)					264556
1455	87797896 (2809, 2910)				UNCLASSIFIED	29331822, 66714117, 29331825, 264805, 29331830, 265008, 285008, 265009, 265011, 265018, 18108351, 21908768, 33657109, 18108376, 264632, 56182323, 87188518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21908765, 21908766, 21908767, 21908769, 29148629, 18108370, 22278000
1457	80076800 (2913, 2914)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)				transport	56182575, 22278999, 80432048, 264259, 29331826, 29331827, 28331828, 284102, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1459	95380820 (2917, 2918)	Novel Protein sim. GBank gij5524667[sp]AAD4333.1[AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]		Contains protein domain (PF00188) - C2 domain	kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 285017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 284566
1460	95354602 (2919, 2920)				UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274820
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]		Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate		22278997, 29331822, 35696052, 265009, 264758, 265017, 265018, 265019, 264760, 264389, 264687, 21908765, 21908768, 265022, 33657109, 27488261, 264555, 83373044
1462	87732018 (2923, 2924)				UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)	Novel Protein sim. GBank gij1770465[emb]CAA689121 - (X98259) M-phase phosphoprotein 8 [Homo sapiens]		Contains protein domain (PF00385) - 'chromo' (Chromatin Organization Modifier) domain	struct	60432049, 264259, 28148499, 284906, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264636, 18108385, 18108388

1464	87620482 (2927, 2928)	Novel Protein sim. GBank gij3874447[embj CAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL:TO1209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278998, 22278997, 22278998, 29331822, 29331824, 29331825, 35896052, 20281100, 264905, 29331830, 264809, 265007, 33657402, 21908754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21908765, 21908766, 21908767, 21908769, 35895917, 264691, 33657023, 264692, 35896423, 35895855, 264630, 264631, 264639, 264565
1465	87425182 (2928, 2930)	Novel Protein sim. GBank gij4599598[idb BAA76821.1] - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56994075, 60432049, 264259, 58182181, 60432269, 29331827, 52644045, 264511, 265007, 265008, 284596, 55812038, 55811386, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 58181562, 21908768, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87606227 (2931, 2932)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gij4507241[ref NP_003137.1 pSSRP - structure specific recognition protein 1		struc	264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gij4507241[ref NP_003137.1 pSSRP - structure specific recognition protein 1			
1469	78236174 (2937, 2938)	Novel Protein sim. GBank gij1908596 (U81788) - kinesin-73 [Drosophila melanogaster]		struc	22278998, 264758, 265018, 265019, 21906769, 265020, 33657109, 22279002
1470	94980482 (2939, 2940)	Novel Protein sim. GBank gij5649170[idb AAD43131.2 AF159092] syd709613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108397, 18108398, 35896052, 29148499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108368, 18108374, 18108381, 18108382, 18108384, 18108388
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gij3876146[idb CAB01750] - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL:TO1851 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins		18108394, 18108398, 56182575, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432228, 60433356, 264595, 60433438, 264758, 33108954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264369, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87168518, 80432113, 264404, 22279002, 264482, 264567, 264487

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF13298 - (AF132988) CGI-34 protein [Homo sapiens]			UNCLASSIFIED	284905, 18108351, 21906765, 284486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis- specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)		MHC	18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 86714117, 29331825, 29331826, 35696052, 284908, 284907, 56182435, 285007, 284756, 285018, 285019, 284780, 284784, 284288, 284685, 284686, 284786, 21906788, 55811957, 285021, 284691, 284693, 284629, 55811578, 284634, 284638, 56182323, 22279002, 284566, 284486
1474	85600989 (2947, 2948)	Novel Protein sim. GBank gi 2484880 sp Q82176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat		struct	284488, 35695917, 35698286, 284682, 33657023, 284693, 33657109, 35696052, 284508, 284905, 284908, 284907, 284629, 284908, 284909, 35698423, 35695855, 284511, 284910, 284632, 284634, 284635, 284636, 284637, 284536, 284557, 284638, 284758, 60432113, 284604, 284605, 284585, 284586, 284764, 284486, 284685, 284768
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain		UNCLASSIFIED	284681, 284682, 284288, 284568
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004664.1 PANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain		glycoprotein	60424179, 56181688, 29331824, 60424269, 29331826, 35696052, 284508, 284905, 284908, 284907, 284908, 284909, 284512, 285007, 285008, 285009, 284910, 33657402, 284595, 284596, 55812038, 285011, 284601, 284782, 18108351, 284288, 284369, 284685, 284786, 284689, 55811857, 284691, 284692, 284693, 18108370, 60431528, 18108374, 35698423, 284634, 284635, 284636, 60431850, 284555, 284638, 284557, 284639, 18108382, 18108388, 60432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2488308 sp Q80870 DP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)			UNCLASSIFIED	284259, 284107, 284905, 285008, 285010, 285011, 284682, 284288, 265020, 265021, 263974
1478	11754412 (2955, 2956)					284686

1479	91640140 (2857, 2858)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15298 - (AF15298) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	58182575, 22278985, 22278986, 22278989, 22278999, 29331822, 29331824, 68714117, 264908, 264907, 56182435, 265008, 60170831, 33657402, 264758, 33109954, 21806754, 265017, 265019, 264448, 264288, 264767, 264687, 52644228, 21906764, 264689, 21908765, 21908788, 21908769, 265020, 265021, 60170815, 264691, 27486282, 33857349, 18108370, 60431528, 263978, 55811578, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1 - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 58182575, 22278995, 35696286, 58994075, 22278986, 22278987, 22278998, 22278999, 264081, 264259, 35696052, 29148498, 264103, 264105, 264108, 264907, 52844045, 264112, 265007, 265008, 265009, 60433358, 60433438, 264598, 33109954, 33657084, 52844286, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264789, 21908765, 21908766, 21908787, 21908788, 21908769, 265020, 265021, 60170815, 52844150, 33857109, 33857182, 263972, 35695655, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	67021442 (2861, 2862)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF14679) PFT27 [Mus musculus]		MHC	285008, 285007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF12292) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	284908, 264910, 264758
1483	94115503 (2865, 2866)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33856970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21908768, 21908769, 264638, 18108380, 87168518, 22279000
1484	94131544 (2867, 2868)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35898288, 264259, 264107, 264909, 265008, 60433358, 33657402, 60433438, 264288, 21908765, 21908766, 29148627, 33857023, 27486262, 18108374, 35698423, 83373044, 60432113
1485	80194441 (2869, 2870)	Novel Protein sim. GBank gi 5360129 gb AAD42883.1 AF15511 - (AF15511) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gij4589516jdbj[BAA76780.1] - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF000069) - kinase Eukaryotic protein kinase domain	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566 21906754, 264486
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gij5018275jembj[CAB4443.1] - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]	synthase	
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gij5712131jbbjAAD47379.1jAF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - fgl Viral (Superfamily 1) RNA helicase	264666, 264769, 264889, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264909, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264584, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gij2487303jspjQ82786jFRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - immunoglobulin domain prostaglandin	21806787, 22278999, 265022, 284259, 264893, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 86712502, 35698423, 35698555, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264568, 264369, 264288
1490	87390127 (2979, 2980)		UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170815, 33657109, 35698555, 264635, 60170394, 56526486, 22279002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gij295671 (L11275) - selected as a weak suppressor of a mutant of the subunit ACA40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]	UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85605363 (2983, 2984)	Novel Protein sim. GBank gij1656005 (U71205) - rtt [Mus musculus]	Contains protein domain (PF00071) - oncogene Ras family	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2885, 2886)	Novel Protein sim. GBank gij5689515[dij]BAA83041.1] - (AB029012) KIAA1089 protein [Homo sapiens]	UNCLASSIFIED	264488, 52846365, 65274572, 56182575, 22278984, 35698286, 56994075, 22278989, 60432048, 29331824, 29331828, 35698052, 264508, 264905, 264906, 52844045, 264909, 56182435, 285008, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264882, 264685, 264686, 52644229, 21908765, 21908768, 21908768, 21908769, 265020, 265021, 60170815, 52644150, 33657023, 18108364, 18108365, 33657109, 33657182, 27488261, 27488262, 27488264, 33657349, 27488265, 35695763, 18108370, 264629, 18108374, 52844332, 56182323, 87168518, 22279002, 264564, 264586, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gij728832[sp]P39189[ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY IIII	kinase	264907, 265008, 264769, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gij458958[dij]BAA76816.1] - (AB023189) KIAA0872 protein [Homo sapiens]	transcript factor	22278987, 264259, 264906, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264585, 264568, 264488, 264587
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gij5420387[emb]CAB46876.1] - (A243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	35698288, 264906, 265019, 264693
1497	81895428 (2993, 2994)	Novel Protein sim. GBank gij3874925[emb]CAA92581] - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene...	kinase	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	80834938 (2995, 2996)	Novel Protein sim. GBank gij728836[sp]P39183[ALU6_HUMAN - III] ALU SUBFAMILY SP WARNING ENTRY IIII	oncogene	264488, 65274572, 28331822, 265017, 265018, 21908765, 29148627, 29148629, 18108374, 264637, 264638, 264587
1499	88451589 (2997, 2998)	Novel Protein sim. GBank gij2570188 (U54556) - microfilament sheath protein SHP3 [Litomosoides sigmodontis]	glucosylase	263978, 264586
1500	80499388 (2999, 3000)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	22278989, 264769, 18108379
1501	85785287 (3001, 3002)	Novel Protein sim. GBank gij2078483 (U43200) - antifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	264559
1502	80206141 (3003, 3004)			264508, 264112, 264604, 264604, 52844150, 55811576, 264632, 264556, 264638, 56182323, 264583, 264488
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gij3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:g1171989) [Homo sapiens]	transferase	29331822, 265007, 264389

1504	79840051 (3007, 3008)			Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	284893
1505	86102872 (3009, 3010)	Novel Protein sim. GBank gi 4753775 emb CAB41870.1 - (AJ132545) protein kinase [Homo sapiens]		Contains protein domain (PF00068) - Eukaryotic protein kinase domain	kinase	29331826, 35698052, 284509, 284906, 284907, 284908, 284909, 284511, 284910, 55812038, 284758, 284763, 284764, 284689, 35695917, 285022, 33857109, 18108374, 284631, 284635, 284638, 284568
1506	84143219 (3011, 3012)	Novel Protein sim. GBank gi 1304201 db BAA061701 - (D29786) alternatively spliced product [Rattus norvegicus]		Contains protein domain (PF00018) - SH3 domain	glycoprotein	85274572, 56182575, 56994075, 22278997, 22278998, 22278999, 284091, 284092, 60432049, 284259, 52845080, 29331822, 29331827, 284108, 29331830, 284908, 58182435, 284110, 284511, 284512, 55812038, 21908754, 87168559, 284800, 285017, 285018, 284681, 18108354, 284368, 284687, 284689, 21908785, 29148627, 21908788, 21908789, 29148629, 52844150, 33657023, 18108378, 65274791, 58182323, 284558, 284559, 18108385, 87168518, 60432113, 22279000, 284565
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gi 5689513 db BAA83040.1 - (AB029011) KIAA1088 protein [Homo sapiens]			helicase	284639
1508	11618758 (3015, 3016)	Novel Protein sim. GBank gi 5031975 ref NP_005875.1 pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284593
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gi 113161 sp P28814 ACOR_ALCEU - ACETON CATABOLISM REGULATORY PROTEIN			UNCLASSIFIED	284591, 33109954, 284563
1510	95362643 (3019, 3020)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII			UNCLASSIFIED	284259, 29331822, 285007, 18108374, 284558
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gi 4558353 gb AAD23014.1 AC00858 - (AC00858) putative extragenic suppressor protein [Arabidopsis thaliana]		Contains protein domain (PF01163) - RIO1/ZK632.3/MJD444 family	UNCLASSIFIED	284259, 29331822, 29331824, 29331827, 284509, 284907, 284510, 284511, 285007, 284512, 285008, 87168559, 284286, 285022, 33657023, 35695855, 284637, 284638, 284563
1512	85345380 (3023, 3024)	Novel Protein sim. GBank gi 4558353 gb AAD23014.1 AC00858 - (AC00858) putative extragenic suppressor protein [Arabidopsis thaliana]				52845156, 18108386, 56994075, 60432289, 285008, 60433358, 60433438, 21908754, 87168474, 87168559, 285018, 284762, 284763, 284687, 21908765, 21908789, 27486262, 35695783, 18108374, 35696423, 284555, 18108385, 18108387, 18108388, 87168518, 284482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gi 1330384 U58761 - C01F1.6 gene product [Caenorhabditis elegans]				35696052, 284905, 284806, 284907, 284908, 284909, 284910, 284591, 284766, 284689, 284692, 284629, 284636

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC006585 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35698286, 56994075, 264259, 52645080, 29331822, 29331825, 35698052, 28331830, 52644045, 58182435, 285008, 60433358, 60433436, 55812038, 21908754, 52646317, 52644296, 87168474, 87168559, 264448, 52644229, 21908765, 21908768, 21908767, 21908768, 35695917, 285020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486284, 27486285, 35695783, 18108376, 35698423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163538 (3028, 3030)	Novel Protein sim. GBank gi 3679501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33368 comes from this gene; cDNA EST EMBL:D33365 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi 488015 (L27479) - X123 (Homo sapiens)		UNCLASSIFIED	265008, 56182323, 22278002
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi 3415134 (AF082024) - Phyb1 (Pimpinella brachycarpa)			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi 728838 sp P39185 ALU8_HUMAN - III ALU SUBFAMILY SX WARNING ENTRY IIII	tm7		66714117, 264508, 264509, 284905, 264510, 264810, 264591, 284595, 264268, 264768, 264769, 18108374, 264638, 264638, 264486 264569, 264489, 60432049, 265009, 33657402, 264598, 21908754, 285019, 264369, 21908765, 21908768, 21908789, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22278002
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi 526268 emb CAB45771.1 - (AL080198) hypothetical protein [Homo sapiens]			
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi 2662161 db BAA23712 - (AB007800) H10452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. (Homo sapiens)	UNCLASSIFIED		18108392, 60432049, 264259, 29331824, 265007, 60433356, 285010, 21908768, 264636
1521	86970606 (3041, 3042)	Novel Protein sim. GBank gi 5052351 gb AAD38518.1 AF13542 - (AF13542) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108394, 264259, 66714117, 285011, 264603, 285019, 18108384, 35698423, 264557, 264558, 18108388
1522	78980687 (3043, 3044)	Novel Protein sim. GBank gi 3776587 (AC005388) - Strong similarity to F2187.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. (Arabidopsis thaliana)		UNCLASSIFIED	29331824, 285018, 285020, 265021
1523	91005151 (3045, 3046)			UNCLASSIFIED	65274572, 21908768, 264693
1524	80203723 (3047, 3048)				
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi 4759040 ref NP_004283.1 PRIN1 - ras inhibitor		UNCLASSIFIED	264112, 21908754, 263974
				UNCLASSIFIED	284883, 264687, 264688, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906765, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gi 2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432048, 29331822, 60432289, 264908, 66712502, 60433438, 87185559, 265017, 264288, 21906768, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130818 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265018, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gi 4408683 gb AAD20053 - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263894, 56182575, 22278995, 35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264389, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906768, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22279002, 264563, 264584, 264486, 264567
1530	95012765 (3059, 3060)	Novel Protein sim. GBank gi 2828710 (AF043842) - matrin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264908, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264583, 264586, 264488
1531	95418351 (3061, 3062)	Novel Protein sim. GBank gi 1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264087, 264259, 29331822, 29331825, 29331826, 28331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264389, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 283981, 60170394, 56182323, 83373044, 60432113, 264568

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gll3874716[emb]CAA91265] - (Z88494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D87438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689	
1533	94238830 (3065, 3066)	Novel Protein sim. GBank gll1490324[emb]CAB01543] - (Z78141) unknown [Mus musculus]			shud	29331824, 29148499, 284807, 284112, 285008, 285011, 285017, 285018, 284762, 18108351, 263987, 20281149, 18108374, 263981, 284566	
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gll81286[pir]S22897 - extensin - Vohox carterl (fragment)			UNCLASSIFIED	284905, 284807, 284766, 284637	
1535	90836732 (3069, 3070)					65274572, 22278997, 284259, 60432049, 29331822, 60432289, 29331827, 29148499, 285008, 285008, 60170831, 60433438, 33109854, 87168559, 285018, 18108357, 21908788, 29148829, 285021, 285022, 18108377, 58182323, 60432113, 22278000, 22279002	
1536	87802856 (3071, 3072)	Novel Protein sim. GBank gll106024[pir]B32891 - finger protein 2, placental - human	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor		294888, 18108357, 18108394, 21906767, 21906768, 29148829, 35896286, 285020, 285021, 52844150, 264693, 68714117, 29331825, 29331826, 284508, 284905, 20281149, 284809, 18108374, 35898423, 35895855, 285009, 284634, 284636, 284638, 18108385, 56528488, 285017, 285018, 284583, 284762, 18108351, 284448, 284369, 284766	
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gll387633[emb]CAB02098] - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426112.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 284259, 29331828, 285006, 285007, 60433356, 60433438, 284601, 18108351, 284448, 284369, 284288, 33857023, 65274620, 33857109, 60432113	
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gll403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds.], gene product [Gallus gallus]	Contains protein domain (PF00098) - Eukaryotic protein kinase domain	kinase		18108394, 18108397, 284909, 285008, 285009, 285010, 18108351, 284638, 18108382, 18108385, 18108388	

1539	95337828 (3077, 3078)	Novel Protein sim. GBank gij321841 [emb]CAA19575.1 - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease gamma subunit, len:264aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E():6.4e-2...		nuclease	22278994, 22278986, 35696286, 56994075, 22278987, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33659970, 56182435, 265009, 33657402, 60433358, 60433438, 55612038, 21908754, 87189559, 285017, 265018, 265019, 18108351, 284288, 52644229, 18108359, 21908764, 21908767, 21908768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486281, 18108370, 18108376, 35696423, 55811578, 65274791, 284558, 56182323, 60170394, 83373044, 87188518, 60432113, 22278000, 22278002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gij5052634 [gb]AAD38647.1 [AF145672] BcDNA, GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264368, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gij5052348 [gb]AAD38515.1 [AF135016] protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21908769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264586, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gij5305702 [gb]AAD41778.1 [AF126866] - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264636, 18108391, 18108382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gij728632 [sp]P39189 [ALU2_HUMAN - III] ALU SUBFAMILY SB WARNING ENTRY III		nuclease	264108, 33109854, 265019, 264683, 35695917, 264690, 264692, 33657109
1544	87757285 (3087, 3088)	Novel Protein sim. GBank gij3483182 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nud_recpt	35696288, 56994075, 22278999, 35696052, 60433358, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87188518, 22278000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gij1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811578
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86999584 (3093, 3094)	Novel Protein sim. GBank gij2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3095, 3098)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1 - (AB028014) KIAA1091 protein [Homo sapiens]		eph	60424178, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 284905, 284908, 264908, 264909, 285008, 284511, 285008, 60431735, 60433356, 21908754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264389, 56181562, 264789, 21908765, 21908768, 21908769, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56528486, 60432113, 22279002, 264563, 264566
1550	95201907 (3098, 3100)	Novel Protein sim. GBank gi 544483 sp P33530 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPRI PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	lm7	65274572, 60432289, 265008, 264910, 285011, 265017, 265019, 264788, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi 4758566 ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 284906, 264907, 264908, 285007, 264512, 284910, 21906754, 265018, 265019, 264681, 284764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	284259, 29331828, 68712502, 264764, 264288, 264688, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi 4589570 dbj BAA76807.1 - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	dehydrogenase	56182576, 35696286, 29146499, 264509, 284907, 264908, 264909, 56182435, 285006, 285008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274781, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233068 (3107, 3108)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 285007, 285009, 60432228, 33657402, 55812038, 265011, 265018, 264681, 264389, 264686, 264767, 264768, 21906785, 21906789, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170384, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gij2257465[dbj BAA21392] - (AB004534) p1015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 28331826, 35698052, 264508, 264805, 284908, 264807, 284908, 52844045, 264909, 264910, 60432228, 60433356, 55812038, 264758, 264759, 33857084, 265011, 87168559, 264801, 265018, 265019, 264763, 264764, 264288, 264786, 264788, 21806765, 35698423, 265022, 264891, 33657023, 35698423, 35698555, 264635, 264555, 264636, 264638, 264639, 18108385, 58526488
1556	91229268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35698052, 264630, 35698423, 265018, 264632, 264682, 28331822, 265020, 265011
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gij3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zfc3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q08003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	60432288, 264509, 264908, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264789, 264690, 263878, 264634, 264635, 264639, 264584, 264486
1558	84840376 (3115, 3116)	Novel Protein sim. GBank gij5360105[gb AA042871.1 AF155105] putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278994, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264808, 264909, 60433356, 21806754, 265017, 265018, 264448, 21806767, 265021, 265022, 33857023, 33857108, 18108370, 55811576, 83373044, 87168558, 22278900, 22279002
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gij112808[sp P02750 A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432288, 35698052, 84107, 264110, 21806754, 33109954, 87168559, 264760, 264763, 21806764, 21806765, 21806769, 265021, 264690, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gij3880146[emb CAA82704] - (Z98319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86608159 (3121, 3122)				264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	283987
1563	85508894 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gij1168287[sp P45953 ACQV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	18108394, 35698288, 264259, 29331822, 60432288, 35698052, 29331828, 264508, 68712502, 264908, 56182435, 265007, 264910, 80170831, 21806754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21806765, 21806768, 265021, 60170815, 264692, 35698423, 35698555, 264557, 58182323, 60432113, 22278902, 264482

1565	87783381 (3128, 3130)	Novel Protein sim. GBank gij129726[sp]P05307[PDI_BOVIN] - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264598, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gij3880445[emb]CAA20329] - (AL031288) VM108R.1 [Caenorhabditis elegans]		inf	22278996, 22278998, 264259, 26331822, 29331824, 60432288, 29331827, 66712502, 264908, 265008, 18108351, 52844228, 21908765, 21908767, 21908768, 21908769, 33657109, 264555, 264639, 264482
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gij492889[gb]AAD34110.1[AF15187] - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	56182575, 21908769, 264692
1568	87848761 (3135, 3136)	Novel Protein sim. GBank gij4827083[ref]NP_005072.1[pZNF1 - zinc finger protein 142 (clone pHZ-49)]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21908767, 21908768, 264691, 264693, 22279000, 22278002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gij5689451[dbj]BAA83009.1] - (AB028880) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21908765, 21908768, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264563, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gij1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gij4507731[ref]NP_001061.1[pTUBG - tubulin, gamma polypeptide]	Contains protein domain (PF00081) - Tubulin/Filz family	tubulin	22278996, 35698286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35698052, 264508, 264805, 56182435, 264510, 265007, 264758, 265011, 18108351, 264446, 264288, 264369, 21908765, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35698423, 35695855, 264834, 264555, 264558, 18108384
1572	81201664 (3143, 3144)			UNCLASSIFIED	35698052, 264805, 264808, 264908, 264910, 264758, 264786, 35695917, 264637
1573	80207068 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4758334 ref NP_004256.1 pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278998, 22278997, 22278998, 264259, 28331825, 28331827, 29146498, 29146499, 264107, 264907, 264909, 2644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264882, 264763, 264784, 18108354, 264389, 264288, 264685, 264768, 264686, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 28146629, 264680, 264681, 264683, 20281089, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264566
1575	95340018 (3148, 3150)	Novel Protein sim. GBank gi 3881810 emb CAA94856 - (Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL:CO8700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00038) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 28331825, 60432269, 28331828, 264909, 265008, 265009, 265008, 265010, 87188559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811857, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 85274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314018 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264568, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265008, 264910, 21906754, 265010, 265011, 87188559, 264761, 264762, 264288, 264766, 264769, 264681, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264488
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2489130 ep P70315 WASP, MOUSE - WISKOTT- ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	224511, 265011, 264881, 264388, 264888, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 28331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 dbj BAA25190 - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	35698286, 264908, 264908, 60433438, 55811386, 264369, 264685, 33657023, 264595, 264596, 264557, 87188518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD18986 - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278998, 35696052, 28331830, 52644045, 55812038, 87188474, 265018, 264448, 265022, 264638, 56526488, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 28331822, 29331824, 29331826, 56182435, 264595, 55812038, 87188559, 265017, 264288, 21906764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	85358052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb CAB46678.1]- (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 26331827, 264509, 264905, 264906, 264907, 264908, 264910, 264762, 264288, 264788, 264768, 264632, 264555, 264639, 56526488, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578958[emb CAB51351.1]- (AL050306) dJ47587.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21908766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gb AAD44482.1]- (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	- dehydrogenase	60424179, 52646842, 65274572, 56182575, 22278995, 35698286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424268, 60432289, 29331827, 29331828, 35698052, 28146488, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21908765, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810784, 55811578, 35698423, 85274781, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22278902
1585	67626117 (3168, 3170)	Novel Protein sim. GBank gij4240132[db BAA74846.1]- (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	- phosphatase	35698286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 265008, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 284604, 264369, 264288, 264685, 264769, 18108359, 21908765, 18108384, 18108370, 264629, 263972, 18108383, 18108386, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF089993) - No definition line found [Caenorhabditis elegans]			285017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617128 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryzotagus curvicaulus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264587
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pir S52680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265008, 264758, 21908754, 264761, 264762, 21906765, 21908769, 60170815, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pir I48746 - semaphorin C - mouse (fragment)]		UNCLASSIFIED	65274572, 264480, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264586, 265011, 264688, 21908766, 21908768, 55811957, 27488285, 264639, 18108385, 56526488, 60432113

1580	95319825 (3179, 3180)			UNCLASSIFIED	284489, 22278998, 284259, 29331824, 29331825, 29331826, 29331827, 285006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264785, 264288, 52844229, 21906785, 21906787, 21906788, 21906789, 285021, 264682, 27486285, 35695783, 56528488, 60432113, 22279000, 22278002, 284564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank		MHC	284259, 284905, 29331830, 284595, 285017, 284448, 264288, 284690, 284629, 87168518
1592	87882533 (3183, 3184)	gi 4557748 ref NP_000237.1 pMHC2 - MHC class II transactivator			
1593	94891661 (3185, 3186)			UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906788, 18108370, 35898423, 22279000, 264585, 284587
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	284488, 29331827, 284905, 264906, 284907, 284908, 264809, 284910, 284592, 264593, 284757, 264602, 284604, 284760, 284681, 284288, 264788, 284788, 28148629, 35895917, 264692, 264628, 264829, 264630, 284632, 264634, 284635, 284636, 284639, 284583, 284584, 284588
1595	79819425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	29331828, 284908, 55811957
1596	79833828 (3191, 3192)	Novel Protein sim. GBank		UNCLASSIFIED	28146498, 284758, 263987
1597	86971857 (3193, 3194)	gi 5257114 gb AAD41244.1 AF09448 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	- cyto450	284092, 29331824, 284508, 264682, 284389, 284686, 264630, 284583
1598	87862839 (3195, 3196)	Novel Protein sim. GBank			284259, 284834
1599	87849829 (3197, 3198)	gi 4508787 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	52845080, 29331824, 29331826, 284511, 265009, 265011, 284805, 284448, 284764, 265020, 264692, 284693, 18108370, 284635, 18108385
1800	80056002 (3198, 3200)				29331826, 264603, 284691, 284563
1801	15023248 (3201, 3202)			UNCLASSIFIED	284635
1802	86926987 (3203, 3204)	Novel Protein sim. GBank	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED - struct	28146499, 284112, 284762, 18108351, 28146827, 263974
1803	80502072 (3205, 3206)	gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus] chicken		collagen	284490, 29331824, 264807, 264809, 264511, 265008, 284592, 265010, 285011, 264782, 284784, 264389, 264288, 284687, 264789, 284693, 264828, 284634, 284636, 284555, 284596, 284638, 264557, 284558, 284559, 18108385
1804	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4768831 gb AAD28633.1 AF11682 - (AF116827) unknown [Homo sapiens]		ATPase-associated	18108385, 263977

1805	91221129 (3209, 3210)				struct	284905, 284508, 284908, 284907, 284908, 284909, 284604, 284768, 284768, 284692, 284693, 33657108, 284629, 35695855, 284635, 284636, 284637
1806	94312703 (3211, 3212)	Novel Protein sim. GBank gij4505313[ref]NP_003794.1[pm]YOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct		22278998, 22278999, 284259, 33657402, 285017, 18108351, 284448, 21908767, 21906789, 52844150, 284691, 87168518
1807	10871805 (3213, 3214)	Novel Protein sim. GBank gij5174473[ref]NP_005888.1[pm]PP1 - Intracellular A particle-promoted polypeptide		transcriptfactor		284689
1808	80428900 (3215, 3216)	Novel Protein sim. GBank gij2224629[db][BAA20802] - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED		284084, 284808, 284907, 284909, 284910, 284591, 284603, 284768, 284693, 284634, 284635, 284637, 284639
1809	94311572 (3217, 3218)	Novel Protein sim. GBank gij4684073[emb][CAB43213.1] - (AL049934) hypothetical protein [Homo sapiens]				52844507, 52845158, 52846365, 52846842, 56182575, 22278994, 56994075, 35698288, 22278997, 22278998, 22278999, 284259, 52845080, 29147820, 29331828, 35696052, 33696970, 284508, 284509, 284907, 52844045, 56182435, 284510, 284511, 284512, 33657402, 21906754, 52846317, 33109954, 52844228, 87168474, 285017, 285018, 285019, 18108351, 284448, 284288, 284769, 52844229, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 285020, 285021, 285022, 52844150, 33657023, 33657108, 52845129, 27488281, 27488282, 35695763, 284628, 18108370, 18108376, 35698423, 284638, 52844332, 18108387, 87168518, 22278000, 284563, 284486
1810	85488200 (3219, 3220)	Novel Protein sim. GBank gij283920[pm]S27839 - lensin - chicken		UNCLASSIFIED		284593, 284757, 55812038, 285018, 285020, 284691, 284692, 284693, 284631, 284634, 284635, 284555, 22279000, 284584
1811	94122843 (3221, 3222)	Novel Protein sim. GBank gij107284[pm]A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	peroxidase		35698288, 21908765, 284691, 35698423
1812	85748031 (3223, 3224)	Novel Protein sim. GBank gij3874846[emb][CAA94337] - (Z70307) Similarity to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL:C09951 comes from this gene; cDNA EST EMBL:C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED		284488, 284508, 18108370, 18108387, 284486
1813	82247354 (3225, 3226)			UNCLASSIFIED		284759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gij480673 gb AAD27726.1 AF13285 - (AF132851) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 284908, 284512, 285009, 285011, 285017, 285018, 285019, 18108351, 284883, 284288, 284766, 21906767, 21908768, 21908769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 58182323, 83373044, 284566
1615	86121909 (3228, 3230)	Novel Protein sim. GBank gij5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278998, 35696286, 22278997, 29331822, 35696052, 29331828, 284508, 284908, 284909, 58182435, 284511, 285017, 285019, 284766, 284767, 284768, 285020, 284891, 284828, 284632, 284635, 284555, 284556, 58182323, 284558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gij3676260 emb CA801698 - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C08081 comes from this gene; cDNA EST yk399f2.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	284488, 52844507, 52845156, 52846365, 52846842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52845080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 35695970, 284905, 284909, 284594, 52846317, 21906754, 33857084, 52844296, 87168474, 87168559, 285017, 285018, 285019, 284681, 284448, 284684, 52844229, 21906764, 284689, 21906765, 21908766, 21908769, 35695917, 285020, 265021, 52844150, 33657023, 52845129, 33657109, 33657182, 27486281, 27486262, 33657349, 27486265, 35695763, 18108376, 35698423, 35695855, 284557, 52844332, 284558, 18108385, 87168518
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gij486053 sp P34878 YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHH zinc finger domain	peptidase	35696052, 284905, 284509, 284907, 284908, 284510, 284511, 284784, 284766, 284768, 284689, 284693, 18108374, 284635, 284636, 284638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gij424023 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		strucd	35696286, 22278999, 284082, 29331824, 29331825, 35696052, 33657084, 21908765, 27496264
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gij5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	52846842, 65274572, 22278999, 284259, 29331822, 29331824, 28331825, 29331826, 29331827, 29331828, 35696052, 56182435, 285007, 285008, 284910, 60170831, 60432229, 60433356, 60433438, 285019, 284448, 284288, 284686, 21908768, 285021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 58182323, 58528488
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gij1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	284684

1621	87078708 (3241, 3242)	Novel Protein sim. GBank gi 3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	284910	18108382, 65274572, 18108398, 22278996, 22278997, 22278999, 29146488, 29146489, 284905, 284908, 284909, 284828, 52844045, 284592, 60433398, 21808754, 284602, 285017, 284389, 21908788, 55811957, 285021, 60170815, 284835, 284557, 60170394, 83373044, 18108385, 22279000, 22279002, 284588
1622	94741738 (3243, 3244)	Novel Protein sim. GBank gi 731086 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV22		ribosomal prot		18108398, 284259, 284909, 56182435, 87168474, 284448, 21808788, 35895917, 284691, 87168518, 284563
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gi 3875660 emb CAB05478 - (Z83104) cDNA EST EMBL:TO0015 comes from this gene; cDNA EST EMBL:D33665 comes from this gene; cDNA EST EMBL:D38540 comes from this gene; cDNA EST YK240f8.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED		68714117, 29331825, 284908, 285008, 284758
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gi 4589622 dbj BAA76833.1 - (AB023208) KIAA0988 protein [Homo sapiens]		kinase		264489, 22278984, 22278995, 22278998, 35896286, 22278997, 22278998, 22278999, 284092, 284259, 29331824, 29331825, 29331827, 29331828, 284102, 284106, 284508, 33657084, 265017, 265018, 18108351, 284683, 284369, 284288, 21808785, 21908786, 21808787, 21908789, 35895917, 285021, 284691, 65274820, 18108368, 283972, 18108378, 35898423, 284631, 264834, 22279000, 22279002
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gi 5878070 gb AAD48844.1 AF16090 - (AF160904) BcDNA HL05938 [Drosophila melanogaster]				52844507, 52845156, 52846385, 52846842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 68714117, 29331828, 60432289, 29331827, 29331828, 35896052, 284908, 68712502, 284908, 285008, 285009, 60432228, 60433356, 60433438, 21808754, 52846317, 52844296, 285011, 87188559, 284604, 285018, 284448, 284389, 284288, 284788, 52844228, 284689, 21808785, 21908788, 35895917, 285021, 285022, 52844150, 33657023, 65274620, 27486281, 27486282, 27486285, 35895783, 283972, 52844332, 60170394, 87168518, 60432113, 284587
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gi 5878070 gb AAD48844.1 AF16090 - (AF160904) BcDNA HL05938 [Drosophila melanogaster]				
1627	83368773 (3253, 3254)	Novel Protein sim. GBank gi 3688087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED		284288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gi 3688087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph		284288, 284886, 264767, 22278002

1628	84893841 (3257, 3258)	Novel Protein sim. GBank gi 4240175 dbj BAA74868.1 - (AB020850) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87778027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22279002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gi 1915892 emb CAA69955 - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33657023, 264693, 29331822, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264756, 18108385, 264563, 264784, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gi 2558501 dbj BAA22898 - (D83850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264768, 264691, 264692, 29148499, 264509, 264905, 264907, 264511, 264512, 264482, 264681, 264763, 264682, 264683, 264486, 264259, 264907, 264908, 264909, 264626, 264629, 264631
1633	87773683 (3265, 3266)				265007, 264637, 22278002
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gi 4867229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struct	
1635	84232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52844045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264388, 21908765, 21908768, 265021, 264690, 264482
1636	80413227 (3271, 3272)			UNCLASSIFIED	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)	Novel Protein sim. GBank gi 455751 ref NP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gi 3420051 AC004680 - unknown protein [Arabidopsis thaliana]			21908765, 21908767, 22278998, 35696286, 22278999, 264259, 264692, 264693, 29331824, 33657109, 264508, 264908, 18108370, 264628, 265007, 33657402, 21908754, 264602, 264604, 264764, 264683, 264568, 264288
1639	94322184 (3277, 3278)	Novel Protein sim. GBank gi 5420389 emb CA846680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265008, 265009, 264757, 264758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21908767, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 264558, 264639, 83373044, 18108385, 87168518

1640	94143185 (3279, 3280)	Novel Protein sim. GBank gj 2842469 emb CAA16847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 80432049, 80432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21908765, 21908766, 21908768, 35695917, 265021, 60170815, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	67625160 (3281, 3282)			UNCLASSIFIED	29146499, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gj 1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278899, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564
1643	94131766 (3285, 3286)				29331825, 29331827, 29331828, 21906754, 265019, 264286, 264683, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1644	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264783, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264583, 264584, 264585, 264586, 264587
1645	95013558 (3289, 3290)			UNCLASSIFIED	264685, 264693
1646	95362691 (3291, 3292)	Novel Protein sim. GBank gj 1076802 pir S49915 - extensin like protein - maize		UNCLASSIFIED	22278894, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 80432289, 264508, 60433356, 80433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486281, 27486285, 33657349, 60432113, 264583, 264584
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gj 5002573 emb CAB44338.1 - (Y17468) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264908, 264908, 264369, 21908768, 60170815, 264639, 22279000
1648	67642098 (3295, 3296)		Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264558, 56182323, 264558, 18108385

1649	95347628 (3297, 3298)	Novel Protein sim. GBank gij1854065jemb CAA58337 - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 86712502, 264808, 52644045, 264809, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21908754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264883, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644228, 264689, 21908765, 21908766, 21908767, 21908768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35698423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264565, 264566, 264487
1650	87418539 (3298, 3300)	Novel Protein sim. GBank gij3647335jemb CAA21059 - (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			265011, 264602, 21906767, 18108374, 18108377, 18108385
1651	91639773 (3301, 3302)	Novel Protein sim. GBank gij4884270jemb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21908754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21908765, 21908766, 21908768, 21908769, 265022, 264692, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56528486, 22279000, 22279002, 264564
1652	86598822 (3303, 3304)	Novel Protein sim. GBank gij1857837 (U73200) - p118Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	strud	22278997, 29146498, 56182435, 21908754, 264369, 21908765, 21908768, 21908769, 265020, 52644150, 33657108, 22279000, 22279002
1653	94255893 (3305, 3306)	Novel Protein sim. GBank gij3776054jemb CAA08273 - (AJ004899) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264809, 265008, 265009, 60432229, 60433356, 60433438, 21908754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274781, 18108384, 60432113, 264567
1654	79756471 (3307, 3308)			UNCLASSIFIED	33657109, 264565

1655	85689348 (3309, 3310)	Novel Protein sim. GBank gij3355717[emb CAA73496] - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52844507, 35896286, 22278998, 22278999, 29331824, 29331825, 29331828, 33858970, 284808, 52844045, 284511, 284810, 52846317, 284288, 52844229, 33657023, 33857109, 52844332, 284557, 58182323, 58526486, 60432113
1656	79862287 (3311, 3312)	Novel Protein sim. GBank gij1890141[dbj BAA18947] - (D83208) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 284563
1657	87771894 (3313, 3314)	Novel Protein sim. GBank gij4557645[ref NP_001524.1 pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_mia_bind	29331827, 285009, 21908768, 21908767, 285020, 285022, 33857109, 284638, 58526486, 284482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072[emb CAA87060] - (Z48937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal protenylitic L21 protein	UNCLASSIFIED	52846365, 35896286, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 28146488, 284905, 284908, 52844045, 285008, 60433358, 284757, 60433438, 21908754, 285011, 18108351, 284448, 284389, 284288, 284766, 284768, 21908765, 21908767, 21908768, 21908769, 28148629, 285021, 285022, 18108362, 283988, 283971, 18108374, 35898423, 18108383, 22279000, 284482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij539218[pir S38038] - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52846317, 21908766, 21908767, 21908768, 87188518, 22278996, 285020, 22278999, 87188559, 284603, 285017, 284631, 285018, 285019, 22278002, 284482, 284635, 284585
1660	94315313 (3318, 3320)	Novel Protein sim. GBank gij2497012[sp Q10010 YSV4_CAEEL - HYPOTHETICAL 28.6 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	284488, 35898286, 284258, 35898052, 284508, 284509, 284905, 284908, 284907, 284908, 284909, 284510, 284511, 285008, 285007, 284512, 285008, 284910, 284592, 284586, 285010, 284600, 284602, 285017, 285018, 284605, 284760, 284764, 284288, 284766, 284688, 284768, 284689, 21908768, 35895917, 284690, 33657023, 284693, 33857109, 284629, 35898423, 35895855, 284634, 284635, 284555, 284636, 284637, 284556, 284638, 284559, 18108385, 18108388, 284583, 284483, 284584, 284585, 284586, 284488, 284567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - UNCLASSIFIED RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	264488, 2227898, 264259, 29331824, 29331828, 29331827, 29331828, 264509, 68712502, 29331830, 264808, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 264448, 264766, 264768, 264768, 21906768, 21908769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264584, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27		18108392, 29331822, 29331828, 20281100, 264106, 265008, 265007, 265008, 18108348, 21908766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi4884136 emb CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - kinase WW domain	52845156, 56182575, 22278994, 22278995, 35686286, 22278998, 56984075, 22278997, 22278998, 22278998, 264259, 29331822, 29331826, 29331827, 29331828, 33658970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 265021, 265022, 264691, 33657023, 264683, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22278900
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi13043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]	UNCLASSIFIED	264488, 263984, 35698288, 29331824, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264789, 21908764, 21908765, 21908767, 35695917, 265021, 264534, 60170815, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35698423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264556, 83373044, 87168518, 264563, 264588, 264486

1665	91226952 (3329, 3330)	Novel Protein sim. GBank gj1083506[pri][S50085 - slabadesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	Immunoglob	264488, 28331826, 28331828, 284509, 284506, 284907, 284909, 284510, 284511, 284910, 284592, 284593, 284595, 284758, 284596, 284600, 284760, 284762, 284764, 284766, 284768, 284629, 284630, 284634, 284636, 83373044, 284564, 284566, 284567, 284488
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gi 3913431 sp Ox2843 DDX8 SCHPO - PUTATIVE PRE- MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	56994075, 22278999, 264259, 29331824, 29331826, 28331827, 28146488, 285009, 33109954, 87188559, 265018, 264288, 284688, 21908767, 21908769, 284691, 33857182, 18108370, 18108374, 18108385, 22279002
1667	91228655 (3333, 3334)	Novel Protein sim. GBank gj5689535[dj][BAA83051.1] - (AB028022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	284259, 28331822, 28331826, 284905, 284906, 284908, 264510, 285009, 284595, 284758, 285011, 87188559, 285017, 285018, 285019, 284448, 284766, 284688, 21908765, 21908767, 21908769, 265020, 285021, 60170815, 284690, 284692, 284693, 18108368, 18108370, 283972, 59810784, 284555, 83373044, 60432113, 22279000, 22279002
1668	88085135 (3335, 3336)	Novel Protein sim. GBank gj2076894[gj][AAB53983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE- bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	56714117, 284508, 284509, 284906, 284907, 284908, 284511, 284910, 284764, 284687, 284689, 33857109, 35898423, 35898555, 284632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gj3875371[jemb][CAA85414.1] - (Z38946) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D84658 comes from this gene; cDNA EST EMBL:D68829 comes fr...		UNCLASSIFIED	28331825, 33109954, 284369, 284767, 284689, 33857109, 83373044
1670	87628008 (3339, 3340)			UNCLASSIFIED	284259, 28331824, 28331827, 60433438, 285022, 284638
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gi 462451 sp P34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	35898286, 22278997, 28331825, 284909, 21906754, 285017, 285018, 285019, 284682, 284683, 284768, 284688, 21908768, 21908767, 21908768, 21908769, 284691, 284555, 284556, 22279000, 284566 284906, 284909, 284632, 18108381
1672	86281834 (3343, 3344)	Novel Protein sim. GBank gj1814270 (U74586) - double- stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	

1673	88095137 (3345, 3348)	Novel Protein sim. GBank gjl2078694[gbjAAB53883.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE_bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	264488, 264569, 18108394, 56994075, 22278996, 264259, 35898052, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33857023, 264692, 264693, 33857109, 264628, 264629, 18108374, 35898423, 35898555, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264638, 264563, 264482, 264564, 264565, 264566, 264567, 264488
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gjl5262467[embjCAB45693.1] - (AL080082) hypothetical protein [Homo sapiens]		kinase	29331822, 29331824, 264908, 52644045, 60433358, 87188559, 264448, 264288, 264888, 264691
1675	87608466 (3349, 3350)	Novel Protein sim. GBank gjl3128366 (AF010498) - 50S ribosomal protein 19 [Rhodobacter capsulatus]		UNCLASSIFIED	56181886, 35898286, 22278997, 22278998, 264259, 29331824, 29331827, 35898052, 66712502, 264784, 264288, 264686, 264687, 35895917, 265020, 264690, 264693, 35895763, 18108370, 35898423, 35895855, 264637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gjl4184065[gbjAAB05327] - (AF111091) latrophilin 3 splice variant 0bar [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21908785, 265020, 265022, 35895855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gjl3327046[dbjBAA31591] - (AB014516) KIAA0816 protein [Homo sapiens]		UNCLASSIFIED	264908
1678	88868829 (3355, 3356)			UNCLASSIFIED	29331824, 264102
1679	91214108 (3357, 3358)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35898286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108356, 18108359, 21908785, 29148627, 29148628, 264690, 18108381, 18108382, 18108384, 18108385, 18108386, 264628, 18108379, 35898423, 35895855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gjl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	85274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21908754, 265018, 264288, 21908769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gjl5689537[dbjBAA83052.1] - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811857, 264690, 33857023, 35898423, 83373044, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264603

1683	94316213 (3365, 3368)	Novel Protein sim. GBank gil503171[ref]NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263894, 35688286, 35688052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264388, 264766, 264768, 35695917, 264692, 33657109, 35696423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264583, 264566
1685	94323182 (3368, 3370)	Novel Protein sim. GBank gil1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Guanylate kinase	UNCLASSIFIED	60424178, 52846842, 22278994, 35696286, 22278998, 264259, 52845080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264368, 264689, 21908765, 21906767, 21908768, 21908769, 265021, 264892, 85274620, 33657109, 27488282, 264635, 52844332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gil2244707[dbj]BAA21115.1 - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264567
1687	94718400 (3373, 3374)	Novel Protein sim. GBank gil4680879[gbj]A027729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264556, 18108361, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gil4240193[dbj]BAA74875.1 - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264589, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433436, 55812038, 265017, 265018, 264448, 264764, 264288, 264688, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gil3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264389, 21908766, 264692, 264639, 87168518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gil2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264788, 33657109, 29331827, 26148629, 264510, 264106, 264810, 264109, 264508, 60170831, 264563, 264905, 264584, 264691, 264637, 264628, 264907, 264908, 33657023, 264587, 264766, 263974
1692	86108709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gil121271[spj]P02207[GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	26331826, 264508, 264905, 264907, 264585, 265010, 265011, 21908766, 33657023, 264629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gll5453932[re]NP_008225.1[pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 16 kDa subunit	mapolymerase	35698286, 22278898, 22278898, 22278899, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29148499, 284905, 284908, 52844045, 284511, 285008, 285007, 285009, 284592, 80433356, 21906754, 285010, 285011, 18108351, 264763, 264682, 264448, 264883, 264288, 264768, 264689, 21906768, 80170815, 264691, 264692, 284693, 18108370, 18108374, 263978, 35698423, 35698585, 284556, 18108381, 18108385, 87188518, 264482, 264488 284634
1685	94718325 (3388, 3390)	Novel Protein sim. GBank gll4880679[gb]AAD27729.1[AF132954] CGI-20 protein [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gll4220517[emb]CAA22890] - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278987, 264259, 265010, 18108351, 264764, 21908768, 18108370 264882
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gll505652 [U10382] - GP386 glycoprotein [Homo sapiens]	glycoprotein		
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gll5052031[gb]AAD38411.1[AF155739] axotrophin [Mus musculus]			56994075, 22278988, 22278989, 264509, 33657402, 264758, 87188474, 87188559, 265017, 265018, 264448, 264687, 29148627, 21908769, 29148829, 265020, 265022, 33657023, 264558, 87188518, 22278902 35698286, 264635
1699	87424793 (3397, 3398)	Novel Protein sim. GBank gll543344[pir]S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED nuc_recp	29331824, 52844045, 265008, 265009, 263969, 263971
1700	87859161 (3398, 3400)	Novel Protein sim. GBank gll387743[emb]CAA98652] - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		UNCLASSIFIED MHC	264092, 284110, 263977 22278995, 22278987, 264092, 29148498, 29148499, 264107, 264508, 264907, 264110, 284112, 265008, 80170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21906765, 35695917, 265021, 80170815, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263976, 35695955, 264555, 263981, 80170394, 18108385, 58528486, 87188518, 60432113 264908, 265017, 264628, 264629, 264638
1701	88570488 (3401, 3402)	Novel Protein sim. GBank gll451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264389
1702	87765082 (3403, 3404)	Novel Protein sim. GBank gll1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gll4519621[dbj]BA75670.1] - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264566 22278986, 22278988, 264259, 264509, 265018, 264764, 264685, 264688, 21906768, 21906769, 265022, 264691, 284559, 22278900
1704	86622978 (3407, 3408)	Novel Protein sim. GBank gll1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	
1705	87785175 (3409, 3410)	Novel Protein sim. GBank gll4519621[dbj]BA75670.1] - (AB017614) OASIS protein [Mus musculus]			
1706	87790967 (3411, 3412)	Novel Protein sim. GBank gll3123034[sp]Q15011Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gi4321664[gb AAD15797] - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108396, 22278997, 264259, 29147820, 29331826, 29146498, 284905, 284908, 285008, 284593, 284595, 264758, 284596, 285018, 284780, 18108351, 284786, 284889, 284693, 18108370, 35698423, 55811576, 284558, 87188518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gi5174591[ref NP_005947.1 pMT-HF - 5.10-methylphenetetrahydrofolate dehydrogenase, 5.10-methylphenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	synthase	56182575, 22278998, 58994075, 284259, 29331822, 28331824, 28331826, 28331827, 28331828, 29146498, 29146499, 28331830, 285009, 60170831, 33857402, 33108854, 87188559, 265019, 18108351, 284448, 21908785, 21908767, 21908768, 29148627, 29148629, 29148784, 60170615, 52644150, 33857023, 33857109, 18108374, 55811576, 284558, 18108385, 22278900, 284563
1709	80222583 (3417, 3418)			UNCLASSIFIED	284107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gi5031735[ref NP_005760.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase		UNCLASSIFIED	284556
1711	81013729 (3421, 3422)			sulfotransferase	85274572, 29331824, 29331826, 284788, 60431528, 35698423, 60432113, 284563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gi5454168[ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	kinase	56984075, 264093, 264259, 29331822, 284099, 29331824, 29331827, 284107, 284110, 284511, 264592, 285011, 285018, 284683, 284686, 284889, 285020, 33857023, 283987, 33857109, 283974, 35698423, 35698555, 284630, 284636, 284558, 284568
1713	9413453 (3425, 3426)	Novel Protein sim. GBank gi160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00843) - B-box zinc finger.	UNCLASSIFIED	22278995, 284508, 284758, 18108351, 18108370, 283974, 18108374, 284634, 58182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 284757, 21908765, 285020, 285021, 284892, 58528486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gi5689537[db BAA3052.1 - (AB028023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	284509, 284905, 284908, 284907, 284908, 284909, 284910, 284991, 285011, 284786, 284788, 284789, 284891, 284892, 284632, 284634, 284635, 284636, 284637, 284558, 284638, 284584
1716	87400448 (3431, 3432)	Novel Protein sim. GBank gi4589468[db BAA76761.1 - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 284108, 284909, 285007, 284600, 285019, 284886, 285020, 284893, 55811576, 284558, 60432113, 22278902

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749 - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264568, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265008, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264688, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391, 265011, 264681, 264682, 264684, 264688, 264689, 21908765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14989 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0938)		UNCLASSIFIED	264639, 18108388, 18108391, 265011, 264681, 264682, 264684, 264688, 264689, 21908765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108386, 65274572, 35696286, 22278997, 60432049, 58182181, 66714117, 60432289, 29331828, 35696052, 29331828, 264906, 29331830, 58182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264789, 21908786, 21908789, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657348, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 58182323, 264559, 264584, 264486, 56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21908754, 265011, 264801, 264760, 264762, 264288, 264766, 264686, 18108357, 264689, 21908785, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264558, 264638, 264639, 56182323, 87168518
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 pr J551939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	22278894, 22278999, 29331822, 265008, 265007, 265008, 55812038, 21908754, 60174639, 285011, 87168559, 18108351, 18108354, 21908765, 21908786, 21908788, 21908789, 265020, 33657109, 18108370, 18108374, 264558, 60170394, 83373044, 18108395, 264486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 488646 emb CAB43381.1 - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	22278894, 22278999, 29331822, 265008, 265007, 265008, 55812038, 21908754, 60174639, 285011, 87168559, 18108351, 18108354, 21908765, 21908786, 21908788, 21908789, 265020, 33657109, 18108370, 18108374, 264558, 60170394, 83373044, 18108395, 264486
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi 5688375 dbj BAA82868.1 - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - Tudor domain	kinase	56894075, 29331824, 29331828, 265009, 18108351, 21908786, 265020, 33657023, 18108374, 83373044

1723	95358181 (3445, 3448)	Novel Protein sim. GBank gij4426962[gijAAD20633] - (AF126082) Art-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33658970, 33657349, 29146489, 264508, 264807, 18108370, 264629, 264808, 264809, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432228, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87188518, 87188474, 265010, 265011, 87188598, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264587, 264488, 264389, 264786
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gij2340182 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264805, 18108359, 264893, 264628, 264631, 264636, 264555, 264556, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - homeobox Ank repeat	homeobox	35686288, 264259, 29331822, 35686052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264784, 264288, 264798, 264788, 21906769, 35685917, 264628, 35686423, 264630, 264631, 264632, 264635, 264636, 264638, 87188518, 264566
1726	85754255 (3451, 3452)	Novel Protein sim. GBank		UNCLASSIFIED	29148498, 264683, 264689
1727	85286362 (3453, 3454)	gij4689348[gijAAD27861.1]AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264805, 265011, 264689, 21906768

1728	95349515 (3455, 3456)	Novel Protein sim. GBank gij4406549[gbjAAD20027] - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35696286, 22278997, 22278998, 22278999, 284094, 60432049, 284256, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 284905, 284906, 284907, 29331830, 66712502, 284908, 56182435, 284511, 285008, 285009, 60432229, 60433356, 33657402, 60433438, 284759, 21906754, 87168474, 285010, 285011, 87168559, 265017, 265018, 265019, 55811150, 264681, 284448, 284682, 284763, 284683, 284288, 284684, 284369, 284685, 284766, 264687, 284769, 21906784, 284689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 284535, 284891, 284692, 33657023, 284693, 33657109, 18108370, 284628, 263972, 284629, 18108374, 18108376, 55810784, 65274791, 35695855, 264631, 264634, 264635, 60431850, 284636, 284638, 60170394, 284639, 83373044, 56526466, 87168518, 60432113, 22279000, 22279002, 284564, 284566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gij854085[emb[CAAS8337] - (X63413) U88 [Human herpesvirus 6]	UNCLASSIFIED	284906, 284907, 284908, 284511, 284555, 83373044, 284596, 284566
1730	85483474 (3459, 3460)		UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 284908, 284909, 285011, 284784, 284629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank gij831600[pir][S47094 - hypothetical protein - rabbit]	UNCLASSIFIED	52846842, 284907, 284909, 56182435, 55811366, 87168559, 265018, 285019, 284760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gij4240231[dbj[BAA74894.1] - (AB020678) KIAA0871 protein [Homo sapiens]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 284591, 33657402, 60433356, 285019, 21906788, 21906789, 35695917, 285020, 265021, 284636, 56182323
1733	97617178 (3465, 3466)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	synthase	284907, 284910, 33657402, 265010, 284681, 284683, 284684, 284685, 284769, 284691, 284692, 284693, 284628, 284636, 284556
1734	87785261 (3467, 3468)			284693

1735	88318638 (3468, 3470)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016		264488, 18108384, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265006, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108384, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264583, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gi 4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED		264490, 264259, 68714117, 68712502, 56182435, 265006, 265008, 264910, 60433358, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi 2143607 pir S68695 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	kinase	26331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi 2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED		264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		UNCLASSIFIED		35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gi 4809 emb CAA44309 - (X62452) YCR601 [Saccharomyces cerevisiae]	Acyl-CoA dehydrogenase	traffic	264604, 21908764, 18108384, 264629, 35695855, 264638
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi 4883898 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	Contains protein domain (PF01383) - FYVE zinc finger	UNCLASSIFIED	60432229, 264759, 265017, 264767, 264688, 264689, 21908769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi 4505183 ref NP_003687.1 pMLD - membrane fatty acid (lipid) desaturase	UNCLASSIFIED		264908, 264910, 264758, 265011, 264631, 264638, 264586
1743	86966475 (3485, 3486)				265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi 728323 sp P39189 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III	UNCLASSIFIED		22278998, 264508, 264907
1745	20280075 (3489, 3490)		UNCLASSIFIED		264558
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi 731756 sp P38673 YHY6_YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-K1 INTERGENIC REGION	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	65274791, 264639, 264559
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi 1658503 (U75467) - Atu [Drosophila melanogaster]	transcript factor		52648842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264398, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482

1748	88003580 (3495, 3498)	Novel Protein sim. GBank gil4504511 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00684) - eph DnaJ central domain (4 repeats)	264489, 56182575, 28331824, 56182435, 264112, 285007, 265019, 264784, 21908768, 285020, 284891, 55811576, 284635, 264555, 284556, 264557, 264559 264106
1749	83363081 (3487, 3488)	Novel Protein sim. GBank gil5650780 gb AAD45948.1 AF15196 - (AF15196) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - oncogene Regulator of G protein signaling domain	
1750	94321664 (3498, 3500)	Novel Protein sim. GBank gil4996894 gb AAC28444.2 - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]		
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gil2760161 dbj BAA241841 - (AB010054) outer arm dynein light chain 2 [Anthrax crassipina]	Contains protein domain (PF00560) - ATPase associated Leucine Rich Repeat	33657402, 264288, 52644150, 263974, 83373044
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gil3915482 sp P74348 YG29_SVNY3 - HYPOTHETICAL 38.0 KD PROTEIN SLR1829	Contains protein domain (PF00849) - deaminase RNA pseudouridylylase synthase	264510, 264593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gil2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - phosphatase Acyltransferase	56994075, 22278996, 264908, 60170831, 264682, 264784, 264389, 264288, 264685, 264687, 21908768, 264692, 264693, 65274620, 85274791, 35685855, 264637, 264584
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gil731421 sp P39881 YEH4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION	transport	264498, 35686286, 264509, 264908, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264804, 264782, 264783, 264685, 264768, 264691, 264628, 35686423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264593, 264584, 264565, 264586, 264567, 264686
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gil1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED	
1756	92862614 (3511, 3512)	Novel Protein sim. GBank gil4432860 gb AAD207081 - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]		52648842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 28331827, 33858970, 285006, 265009, 60432229, 60433356, 60433438, 33109954, 21908754, 285017, 285016, 285019, 264448, 264369, 264288, 21908765, 21908766, 21908767, 21908768, 21908769, 285020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168516, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gil5441615 emb CAB46856.1 - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00086) - dna_ma_bind Zinc finger, C2H2 type	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264768, 21908768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612971 (3515, 3518)	Novel Protein sim. GBank gl 3881040 emb CAA16403 (AL021497) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278998, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33857402, 33109854, 87168474, 264600, 265017, 265018, 21908769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52844332, 22279002, 264583
1759	36994372 (3517, 3518)			UNCLASSIFIED	264759
1760	87328716 (3519, 3520)	Novel Protein sim. GBank gl 5262748 emb CAB45688.1 - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35696052, 264805, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264784, 264766, 264768, 264769, 21806765, 55811957, 35695917, 264680, 264692, 264628, 264629, 55811576, 35696423, 264632, 264634, 264636, 264557, 264639, 60432113, 264585, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gl 127749 sp P10569 MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00818) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gl 3169158 (AC004770) - BC268730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21808765, 21908768, 21908767, 21908768, 265021, 264680, 33857109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gl 4809026 gb AAD30062.1 - (AF132858) suppressor of G2 allele of stop1 homolog [Homo sapiens]			56181886, 28331825, 35696052, 264805, 264908, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35696423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gl 1360969 pir CGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264286, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	81230081 (3529, 3530)	Novel Protein sim. GBank gl 468606 pir S35503 - finger protein neuralized - fruit fly [Drosophila melanogaster]		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21908754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21908766, 21908767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [DUGT]			glycoprotein	52845158, 87188558, 80170815, 33857023, 284893, 33857109, 27488281, 284555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 178443 emb CAA18263.1 - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]			UNCLASSIFIED	285017, 265018, 264686, 264768, 265020, 284692
1768	80253216 (3535, 3536)				UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)				UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 115204 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin		- complement	264498, 264768, 284769, 56182575, 55811937, 284690, 264691, 35696052, 284905, 284509, 284906, 264907, 284628, 284908, 284909, 284910, 284634, 284635, 284636, 284558, 284757, 264758, 55812038, 85274444, 284760, 264563, 284762, 284764, 284884, 284766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914181 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT [O-GLCNAc TRANSFERASE P110 SUBUNIT]	Contains protein domain (PF00515) - TPR Domain		- transferase	264758, 264600, 284369, 55811957, 265020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHCNEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHC zinc finger domain			22278998, 29331828, 33109954, 285018, 265019, 284784, 21906785, 265020, 285021, 284558
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel		65274572, 56182575, 22278998, 356960286, 22278999, 284259, 29331824, 60424289, 29331825, 60432289, 35696052, 284108, 284509, 284908, 284907, 29331830, 284908, 52844045, 284511, 265008, 265007, 265008, 80170831, 60433438, 284758, 55811386, 87188559, 285017, 264604, 265019, 55811150, 284288, 56181562, 284688, 21906788, 21906787, 21906789, 21906789, 55811957, 265020, 265022, 52844150, 284691, 33857023, 284692, 284693, 60431528, 35696423, 35695855, 284636, 56182323, 18108387, 56528486, 22278000, 22278002, 264563, 264564, 284585, 284586, 284587
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 2495669 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED		65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906787, 21906788, 21906789, 265020, 284681, 284636, 56182323, 22279002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gl 1469195 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331828, 60432289, 29331828, 35696052, 29331830, 68712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21908754, 55858542, 87168559, 264601, 265017, 265018, 265019, 264782, 264448, 264288, 264689, 21908765, 21908768, 21908787, 21908768, 265020, 265021, 265022, 264691, 33857023, 264692, 33857109, 27488281, 33857349, 18108370, 18108377, 35696423, 55811578, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87168518, 60432113, 22278000, 22278002, 264482, 264486, 264910
1776	94133758 (3551, 3552)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gl 3219839 sp P87115 YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.08C IN CHROMOSOME I	nuc1_rept		56894075, 29331828, 285008, 87168474, 265017, 265018, 264781, 55811150, 264784, 56181562, 264689, 21908765, 21908768, 21908789, 35695917, 264690, 33857023, 35695783, 60431528, 35696423, 55811578, 35695855, 22278000, 22278002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gl 3875648 emb CAA91454.1 - (Z88581) Similarity to Human rab13 protein (PIR Acc. No. A49847). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...	UNCLASSIFIED		29331828, 29331827, 35696052, 264512, 265007, 285009, 265017, 265018, 264782, 18108351, 264769, 21908765, 21908768, 21908787, 21908768, 21908789, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]	UNCLASSIFIED		29148827, 35696286, 29147620, 265008, 265007, 265008, 18108385, 65274727, 264482, 264389, 264786
1780	87023497 (3559, 3560)		UNCLASSIFIED	Contains protein domain (PF00807) - Apidaecin	264107, 33857108, 56526486
1781	84047477 (3561, 3562)		UNCLASSIFIED		264508, 264908, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gl 729225 sp P4123 CTXN_RAT - CORTEXIN			284259, 28331822, 264508, 264905, 264908, 284907, 264908, 265007, 265009, 264910, 264591, 264758, 264784, 264288, 264788, 264789, 264635, 264636, 264637, 264639, 264583
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gl 2257543 dbj BAA21436 - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]	interferon		264788

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gij1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PI domain	35696286, 264259, 35696052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264388, 264766, 264687, 264788, 264688, 21908768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35698423, 264631, 264632, 264635, 264637, 264636, 264639, 18108385, 22279000, 22279002, 264555, 264556, 264486 65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 80433356, 55811150, 264683, 264389, 264687, 52644229, 21908767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gij4589552[dbj]BAA76798.1] - (AB023171) KIAA0854 protein [Homo sapiens]	UNCLASSIFIED	
1786	85298465 (3571, 3572)	Novel Protein sim. GBank gij117768[sp]P26770CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)	UNCLASSIFIED	264908, 35698423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gij3877175[emb]CAA90338.1] - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL:D88896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264905, 264908, 264808, 264595, 264784, 264786, 264692, 60431528, 264629, 264636, 264564, 264566
1788	91228778 (3575, 3576)		UNCLASSIFIED	264488, 63373044
1789	88094528 (3577, 3578)	Novel Protein sim. GBank gij2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3578, 3580)			35696052, 264909, 264908, 264907, 264908, 264808, 265008, 264910, 264758, 265011, 265019, 264784, 264788, 264789, 264828, 264635

1781	95197258 (3581, 3582)	Novel Protein sim. GBank gij2114321dbjBAA200371 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	284488, 284886, 284887, 284768, 18108394, 284789, 18108397, 284259, 284891, 284682, 33657023, 284893, 284509, 284905, 284906, 284628, 284907, 284629, 284908, 284909, 284510, 285008, 284511, 285008, 284630, 285009, 284631, 284910, 284632, 284634, 284635, 284555, 284636, 284592, 284637, 284593, 284638, 18108381, 284639, 284758, 285010, 285011, 284602, 22279000, 284604, 284760, 284564, 284681, 284762, 284565, 284763, 284683, 284566, 284764, 284288, 284684, 284567, 18108354, 18108391, 284685, 284766
1782	87792690 (3583, 3584)	Novel Protein sim. GBank gij4337106jgbAAD180821 - (AF129758) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 284259, 284508, 285007, 33657402, 87188559, 284369, 33657023, 35695855, 20281071, 284559, 18108387, 87168518
1783	95337877 (3585, 3586)	Novel Protein sim. GBank gij5579331jgbAAD45504.1 AF14573 - (AF145732) endoplasmic reticulum alpha-mannosidase 1 [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase_associated	65274572, 22278995, 22278996, 22278997, 22278998, 284093, 284259, 29331824, 86714117, 80432289, 29331827, 29331828, 284103, 284105, 29331830, 265007, 284910, 285009, 60170831, 60433356, 21906754, 285010, 285017, 285018, 284681, 284682, 284288, 52644228, 21908785, 21908786, 21908787, 21908788, 21908789, 285020, 285021, 265022, 60170815, 52844130, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 80432113, 22278000, 284482, 284584
1784	87759806 (3587, 3588)	Novel Protein sim. GBank gij4914604jembjCAB43677.1 - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01788) - Putative snRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278996, 284259, 29331822, 29331824, 29331825, 29146498, 29146499, 284508, 284905, 52844045, 284112, 265006, 265008, 284910, 60433356, 284757, 55812038, 87188474, 285011, 285017, 18108351, 284763, 284448, 284683, 284369, 21908785, 21908786, 21908787, 21908788, 28148784, 35695817, 60170815, 33657023, 284629, 18108374, 18108376, 35696423, 35695855, 284556, 284557, 284638, 284558, 18108385, 284584, 284632, 284635, 284636, 284595, 284596, 284907, 284586, 284909
1785	79747856 (3589, 3590)			UNCLASSIFIED	
1786	86599486 (3591, 3592)	Novel Protein sim. GBank gij585084jbpjQ07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)		glycoprotein	284488, 284907, 284909, 284594, 284595, 284766, 284687, 21908785, 21906787, 284628, 284630, 284359

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gl 1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprot	22278998, 22278997, 22278998, 22278999, 28331822, 284910, 60170831, 21908754, 52644229, 21908765, 21908768, 21908769, 35695917, 285022, 52844150, 284691, 33657023, 263967, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gl 28328056 BAA24608.1 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 58984075, 22278997, 22278998, 22278998, 264259, 29331826, 60432289, 28331828, 33658970, 265008, 60432229, 284757, 60433438, 21908754, 33657084, 87168559, 285017, 18108351, 284682, 284448, 264288, 21908765, 21908768, 21908767, 21908768, 21908769, 35695917, 265020, 285021, 33657023, 33657182, 27486261, 27486265, 33657348, 263973, 18108374, 55611576, 35695855, 18108385, 87168518, 22279000, 284486
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gl 5689541 dbj BAA83054.1 - (AB029025) KIAA1102 protein [Homo sapiens]		eph	284908, 21806754, 21908767, 21908769, 285020, 33657023, 284692, 264693, 284404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank gl 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	284691, 284556, 284566
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gl 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			52844045, 285007, 284632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gl 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35686286, 66714117, 284508, 264509, 58182435, 264512, 18108351, 284688, 55811957, 284692, 55811576, 35695855, 284486
1803	95080725 (3605, 3606)	Novel Protein sim. GBank gl 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			284688, 284488, 264687, 284488, 264768, 284769, 284689, 21908769, 35686288, 35695917, 264259, 284691, 284692, 284693, 20281099, 18108384, 35696052, 284508, 284509, 284805, 284906, 18108370, 284628, 284907, 66712502, 284908, 284909, 18108374, 18108376, 35696423, 35695855, 284510, 284511, 285006, 285007, 284512, 285008, 284910, 264631, 264632, 264634, 284635, 284591, 284636, 284637, 284592, 284638, 284593, 284639, 284594, 83373044, 284758, 284586, 18108385, 18108387, 285011, 284760, 284563, 18108351, 264762, 284564, 284448, 284585, 284763, 284683, 284764, 284588, 284288, 284486, 264567, 284765, 284766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3879914[emb]CAA98538.1]- (Z74043) predicted using GeneFinder; cDNA EST EMBL-C13850 comes from this gene; cDNA EST EMBL-C11575 comes from this gene; cDNA EST yk3434.5 comes from this gene [Caenorhabditis elegans]			52648365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21908754, 264766, 21908765, 21908768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264594, 264596
1805	95330375 (3608, 3610)	Novel Protein sim. GBank gij5453644[ref]NP_008461.1[pEBBP - estrogen-responsive B box protein]			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264887, 52644229, 35698423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gij4589676[dbj]BAA76857.1]- (AB023230) KIAA1013 protein [Homo sapiens]	stud		264094, 264105, 264908, 35698423, 265008, 265007, 265008, 264555, 264592, 265011, 265018, 264389
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4884079[emb]CAB43235.1]- (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35696286, 66714117, 35696052, 68712502, 264592, 60433438, 52644298, 285010, 264683, 264369, 264689, 55811957, 35695917, 33857109, 35695763, 55810764, 18108376, 35698423, 35695855, 58182323, 264563, 264594, 264467
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1918827 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88086316 (3619, 3620)	Novel Protein sim. GBank gij1352944[sp]P47179YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35698052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33857402, 264757, 264595, 264758, 264596, 264759, 264800, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264789, 264689, 265021, 264690, 264691, 264693, 264626, 264629, 18108374, 264630, 264631, 264632, 264634, 264835, 264636, 264637, 264638, 264639, 264563, 264586, 264486, 264587
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gij2134984[pir]j37275 - death-associated protein kinase (EC 2.7.1.-) - human	kinase Ank repeat	Contains protein domain (PF00023)	264488, 264259, 264508, 264509, 264905, 264908, 264907, 58182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264768, 264688, 264769, 264534, 60170615, 33857023, 264629, 264631, 264638, 264563, 264482, 264483
1812	78245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21908769

1813	88090972 (3625, 3626)	[Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein (Homo sapiens)]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 284259, 29331824, 66714117, 29331828, 35886052, 264509, 284805, 284806, 264907, 284908, 66712502, 264909, 265007, 264910, 284591, 284593, 55612038, 265011, 285018, 284760, 284682, 264764, 284683, 264368, 284768, 284768, 284768, 21908768, 21908768, 284691, 284693, 18108374, 35695855, 264634, 284635, 284637, 284639, 284558, 22279000, 22279002, 284558
1814	88178047 (3627, 3628)	[Novel Protein sim. GBank gi 3843608 (AC005395) - hypothetical protein (Arabidopsis thaliana)]		UNCLASSIFIED	284488, 35696288, 22278998, 284092, 284094, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 285009, 60432229, 60433356, 87168474, 87168559, 284389, 264288, 21908765, 35695917, 285021, 285022, 33657023, 33657109, 18108374, 35696423, 264638, 56526486, 284482
1815	85296473 (3629, 3630)	[Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)]		snrcl	22278999, 284508, 284509, 284907, 264908, 284910, 265011, 264760, 264768, 264634, 284636
1816	83738845 (3631, 3632)	[Novel Protein sim. GBank gi 1176623 sp P41848 YO98_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III]		UNCLASSIFIED	18108394, 18108397, 284508, 284907, 284908, 284909, 285008, 284591, 265011, 265017, 264687, 264688, 285022, 264891, 18108362, 18108368, 18108370, 18108374, 18108379, 284635, 284557, 284564, 284567 284488, 22278997, 22278999, 60432049
1817	88095268 (3633, 3634)	[Novel Protein sim. GBank gi 376637 emb CAA21429 - (AL031807) hypothetical protein [Schizosaccharomyces pombe]]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	284488, 22278997, 22278999, 60432049, 60170831, 265017, 265018, 285019, 18108351, 264682, 52644229, 21908765, 21908767, 21908768, 52644150, 33657023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	[Novel Protein sim. GBank gi 3878121 emb CAA94370 - (Z70310) predicted using GeneFinder: Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...]	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	264686, 21908769, 264693, 264632
1819	87758572 (3637, 3638)	[Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner]		UNCLASSIFIED	22278995, 22278997, 22278999, 284259, 29331826, 284908, 265007, 265008, 265009, 60432228, 285017, 285018, 285019, 284448, 284288, 21908768, 21908769, 285020, 18108381, 18108384, 22279000, 22279002, 284557

1820	87769455 (3639, 3640)				284905, 284907, 284984
1821	80431510 (3841, 3842)				284907, 284768, 263978
1822	91221523 (3843, 3844)	Novel Protein sim. GBank gl 4884130 emb CAB43272.1 - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 284259, 29331824, 29331825, 29331826, 35698052, 29331828, 284908, 29331830, 60170831, 284591, 284593, 60433358, 284598, 285017, 285019, 18108351, 284763, 284683, 21908765, 21908787, 21908788, 21908789, 35695817, 285020, 285021, 33857023, 18108364, 18108370, 35695855, 22279000, 22279002, 284488, 284259, 284511, 284286, 264768, 284683, 35698423, 284634, 18108385, 284486
1823	85522330 (3645, 3646)			UNCLASSIFIED	
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gl 477072 pr A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - immunoglobulin domain	UNCLASSIFIED	284907, 284908, 284909, 284511, 284631, 284634, 284635, 284637, 284638, 284639, 284758, 284588
1825	87430125 (3849, 3850)	Novel Protein sim. GBank gl 3036803 emb CAA18493 - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432048, 264910, 284487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gl 4680885 gb AAD27732.1 AF132851 - (AF132851) CGI-23 protein [Homo sapiens]		ATPase-associated	52844507, 52645156, 52646842, 22278994, 22278998, 56994075, 284259, 60432049, 52845080, 35698052, 66712502, 52844045, 285008, 285009, 60432229, 60433356, 60433438, 52646317, 52644298, 285011, 87168559, 284448, 284288, 284369, 284688, 52644229, 284689, 21908785, 21908788, 285020, 60170615, 52844150, 33857023, 27486262, 27486264, 27486265, 35695763, 35698423, 35695855, 83373044, 87168518, 284404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gij4503571[ref]NP_001419.1[pENO1 - endolase 1, (alpha)]	Contains protein domain (PF00113) - Endolase	oncogene	264488, 52646842, 56182575, 22278996, 35996286, 22278997, 22278998, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265008, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433356, 60433438, 264758, 33109954, 21906754, 87188474, 265010, 265011, 87188559, 265017, 265019, 264761, 264762, 264448, 264784, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263872, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264567
1829	80167720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gj2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87168559, 265018, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657108, 33657182, 27466281, 27466282, 35695763, 263974, 35696423, 35695855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265018, 265022, 264693, 65274791 264602
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gj1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8.....			

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gij5174413[ref]NP_006028.1pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 284259, 28331822, 29331824, 60432289, 29331827, 35696052, 29146499, 284508, 284509, 284908, 284907, 66712502, 284908, 5284045, 284909, 284512, 285008, 284591, 284593, 80433356, 21908754, 33657084, 285011, 285017, 284604, 285018, 285019, 284681, 18108351, 284683, 284288, 284685, 284766, 284687, 21908785, 21908788, 21908787, 21908788, 21908789, 29148629, 285020, 285021, 284690, 284692, 33657023, 65274620, 33657182, 27486284, 33657349, 65274791, 284634, 284635, 284558, 284557, 284558, 284559, 18108385, 56528486, 87168518, 80432113, 22278000, 22279002, 264563
1834	80562790 (3667, 3668)				284238, 284907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 28331822, 29331826, 87168474, 284603, 21908788, 263978, 35895855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gij4759288[ref]NP_004288.1pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	28331825, 284908, 285018, 284784, 284686, 21908765, 284635
1837	94234287 (3673, 3674)	Novel Protein sim. GBank gij3334400[sp]Q24574UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146499, 285008, 285008, 285009, 285010, 284683, 21908765, 29148627, 29148628, 285020, 285021, 285022, 65274620, 18108370, 18108374, 284556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gij1362589[pi]A56154 - Abi substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00558) - WH1 domain		28331822, 285017, 284760, 285020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gij211731[emb]CAB09116.1 - (Z85620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 284601, 21908765, 21908768, 285021, 33657109, 284556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gij127560[sp]P23249[MV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	284683
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gij4572484[gb]AAD23834.1[AF123653] FEZ1 [Homo sapiens]			56182575, 28331824, 29331826, 60433356, 284764, 284286, 33657023, 283987, 18108370, 18108374, 284631, 284555, 284558, 284639

1842	90992645 (3683, 3684)	Novel Protein sim. GBank gij1326288 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	85274572, 29331822, 29331824, 29331825, 86714117, 29331826, 29331827, 284907, 284909, 52844045, 56182435, 284510, 285006, 285007, 285009, 284910, 60433356, 264757, 60433436, 55812038, 265017, 18108354, 264688, 284769, 33657023, 264693, 18108384, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 284563, 284594
1843	95292692 (3685, 3686)			UNCLASSIFIED	284488, 56182435, 284769, 29331826, 29331828, 284511, 285006, 285007, 284910, 264631, 264509, 284690, 264636, 264584, 284691, 60432229, 60432049, 284259, 284629, 33657023, 284488, 264909, 284587, 284595, 284768
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gij2498887 [sp]Q09232 [YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III]		UNCLASSIFIED	264908, 285022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gij1175494 [sp]Q09819 [YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I]	Contains protein domain (PF00628) - PHD-finger	transcript factor	264259, 29331824, 284907, 264908, 86712502, 284510, 285007, 285008, 55812038, 285018, 21908765, 52644150, 33657109, 284555, 284556, 284557, 56182323, 18108382, 83373044, 18108385, 284564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gij3881080 [emb]CAA21739] - (AL032857) similar to EGF-like domain; cDNA EST yk289a12.3 comes from this gene; cDNA EST EMBL.D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk289a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 284908
1847	67821497 (3693, 3694)	Novel Protein sim. GBank gij5059323 [gb]AAD38667.1 [AF151522] hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcript factor	22278997, 284259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gij5701854 [emb]CAB52191.1] - (AJ245417) G5b protein [Homo sapiens]		tm7	29331825, 29331826, 29331827, 265017, 284883, 284288, 284768, 264768, 21908767, 21908768, 284692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gij4503665 [ref]NP_001988.1 [pFBLN - fibulin 2 precursor]	Contains protein domain (PF00008) - EGF-like domain	ATPase associated	56182575, 285018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gij4589582 [db]JBAA76813.1] - (AB023186) KIAA0969 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 284908
1851	95418789 (3701, 3702)	Novel Protein sim. GBank gij220637 [db]JBAA014771 - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35686052, 264910, 60433438, 264688, 35685917, 265020, 52644150, 65274620, 52844332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174629 refNP_006090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 80432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52844045, 265007, 264810, 60432228, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22279002, 264563
1853	91222287 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 52645129, 29331827, 33656970, 33657349, 35695763, 264508, 264806, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265008, 264511, 264512, 264630, 265009, 264631, 264910, 264834, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265016, 264760, 264762, 264682, 264448, 264764, 264684, 264587, 264288, 264369, 264768
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi 2072984 (U83569) - putative p150 [Homo sapiens]		nuclease	264592
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi 4539520 emb CAB39984.1 - (AL035424) dA22D12.1 (novel protein similar to Drosophila Ketch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - Ketch motif	UNCLASSIFIED	18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 80432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 26148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi 3954978 emb CAA08945 - (AJ006276) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD18120 - (AF094508) dentin phosphoryn [Homo sapiens]	ATPase-associated	ATPase-associated	22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 80170394, 83373044

1858	87828311 (3715, 3716)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	284757
1859	84407484 (3717, 3718)	Novel Protein sim. GBank gi 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			22278986, 29331824, 285007, 33109954, 285019, 284369, 21906788, 29148784, 27486261, 52644332, 22278002 285019
1860	17828308 (3719, 3720)	Novel Protein sim. GBank gi 4009522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi 2143637 pir I B4505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		284887, 284259, 29331822, 29331824, 29331825, 265007, 285009, 284591, 33109954, 285010, 285019, 284369, 284288, 284686, 284691, 284693, 27486284, 18108370, 18108374, 283977, 55811576, 58182323, 284639, 22279000, 22279002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gi 125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35896286, 284259, 87168474, 284369, 21908768, 284558, 284583
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi 3820909 emb CAA09289 - (AJ010842) Dof protein [Drosophila melanogaster]	UNCLASSIFIED		284601, 284768, 29148627, 29148629, 284692, 284628, 284635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi 4322263 gb AAD15985 - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278989, 284259, 284907, 265018, 18108370, 284634, 284635, 284555, 284556, 284638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi 2485727 sp Q93073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278989, 284490, 29331822, 68714117, 68712502, 265008, 285007, 285008, 285009, 284591, 80433438, 285010, 285019, 284760, 284448, 284768, 29148627, 29148629, 285020, 285022, 18108385, 80432113
1866	87268816 (3731, 3732)	Novel Protein sim. GBank gi 5262617 emb CAB45748.1 - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 284768, 18108377, 21906785, 21908768, 35896423, 58182575, 21908769, 29148628, 35896286, 35895917, 285021, 284510, 284511, 284512, 284534, 284535, 60170831, 52644150, 284555, 284691, 284259, 284556, 284692, 284557, 33657023, 60433358, 29331822, 284559, 284595, 29331824, 18108385, 21908754, 33857182, 29331827, 35896052, 33856970, 87168518, 285017, 80431602, 22279000, 284508, 284509, 18108351, 284907, 284682, 264567, 18108372, 284785, 284486 284094
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi 3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	

1868	87357459 (3735, 3738)	Novel Protein sim. GBank gj13881525[embjCAA93884] - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D32554 comes from this gene; cDNA EST yk22463.5 comes from this gene; cDNA EST yk35710.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278998, 28331825, 29331828, 265008, 285009, 33857402, 87188474, 18108351, 21908765, 21908768, 21908769, 285020, 285021, 60170615, 27486284, 264628, 18108374, 264631, 18108385, 87188518, 22279000, 22279002, 264568, 264587
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gj14826772[refjNP_004981.1]pIGFA - insulin-like growth factor binding protein, acid labile subunit	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264800, 18108351, 264883, 264768, 264769, 35695855, 264634, 264558, 264639, 18108385, 264563, 264488
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gj1869859[embjCAB06722] - (Z88099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	28331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264688, 264688, 21906768, 21906769, 35695917, 80170815, 264692, 18108388, 35695763, 35696423, 85274791, 264638, 264639, 58528488
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264805, 264595, 264768, 264635, 264636, 264563, 264486
1872	80233355 (3743, 3744)	Novel Protein sim. GBank gj12460318 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264585
1873	80213890 (3745, 3746)				264509, 264512, 265009, 285011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	85351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264638, 264637, 264638, 33857402, 264558, 18108385, 264600, 264604, 264764, 264597, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gj14599520[dbjBAA76782.1] - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gj1263810[bbj122920] - collagen alpha chain [Riftia pachyptila=tube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 28331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264768, 18108378, 264558, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gj13883358[gbAAC83924.1] - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264688, 264768, 263878, 264693, 264639, 265010, 264583, 264905, 264908, 264907

1878	95351058 (3755, 3758)	Novel Protein sim. GBank gij4510345jgb AAD21434.1 - (AC006921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	284569, 284488, 35898286, 56994075, 284259, 28331822, 29331824, 29331825, 35698052, 29331828, 28148498, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 284512, 285009, 284910, 33657402, 284594, 284758, 55812038, 285011, 284802, 284780, 18108351, 284782, 284881, 284682, 284784, 284389, 284288, 284786, 284887, 284788, 284789, 21908788, 35695917, 285021, 60170815, 33857023, 284892, 284893, 33857109, 27486265, 284628, 18108370, 284829, 18108374, 35698423, 284834, 284635, 284555, 284638, 284639, 83373044, 18108385, 56528488, 87168518, 284563, 284584, 284588, 284486, 284587
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gij4928643jgb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	284905, 284907, 284808, 265007, 264565, 284568
1880	91012878 (3759, 3760)	Novel Protein sim. GBank gij1550785jemb CAA69283 - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	284786, 284691, 284692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gij83144 pir B40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhouser or Becker)		UNCLASSIFIED	284509, 284905, 284808, 284909, 284910, 284782, 284887, 33657023, 284632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gij2384958 (AF022985) - No definition line found [Caenorhabditis elegans]			284908, 21908788, 18108370, 283974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gij1351218 sp P47228 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	284908, 284910, 87168559, 21908788, 284638

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gij4829843igb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181686, 22278998, 60432048, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264508, 264905, 264906, 264907, 264908, 264908, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33857402, 55812038, 264758, 55811388, 265010, 265011, 87168559, 264600, 265017, 264604, 265018, 264605, 264760, 55811150, 264761, 264682, 264763, 264683, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 28148784, 35695917, 264690, 264891, 33657023, 264692, 264693, 33857109, 18108370, 264628, 60431528, 264628, 263873, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 80432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264587
1885	57644280 (3768, 3770)	Novel Protein sim. GBank gij2507155lep P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264805, 264809, 265008, 264598, 264766, 265020, 264628, 60431528, 264634, 56528486, 264080, 264563
1886	86874082 (3771, 3772)	Novel Protein sim. GBank gij2654159igb AAC02577.1 - (AF045841) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264810, 265018, 264766, 21906786, 29148629, 264690, 264693, 264826, 264555, 264486
1887	94139138 (3773, 3774)	Novel Protein sim. GBank gij5174421 ref NP_006023.1 pCPNE - copine VI (neuronal)	Contains protein domain (PF00188) - ATPase associated C2 domain		29331822, 29331824, 29331825, 29331826, 29331827, 264908, 265007, 264681, 264768, 28148627, 264693, 18108384, 35696423, 65274781, 35695855, 264632, 56182323, 264639, 264583
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gij3319831 emb CAB1084.1 - (Z98048) dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255703 (3777, 3778)	Novel Protein sim. GBank gij1083308 pir jA56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - helicase SNF2 and others N-terminal domain		264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906785, 21906768, 21906769, 265021, 33857023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3778, 3780)	Novel Protein sim. GBank gij4240185 dbj BAA74876.1 - (AB020660) KIAA0853 protein [Homo sapiens]	UNCLASSIFIED		18108398, 29147820, 264807, 265009, 264600, 265018, 18108351, 264288, 264689, 21906785, 21906788, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264556, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	284886, 284788, 284687, 284682, 284683, 28331822, 29331824, 284508, 284905, 284906, 18108370, 284628, 284907, 284908, 284909, 18108379, 285007, 285008, 284910, 284632, 284591, 284639, 284596, 18108384, 285010, 285011, 284601, 284605, 284563, 284369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gij5688535jdbj[BAA8305.1.1] - (AB028022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Ar	struct	22278985, 284509, 87168559, 18108351, 284448, 284682, 285020, 284683, 18108374, 222789000
1893	88533826 (3785, 3786)			laminin	284569, 65274572, 22278997, 22278999, 284259, 29331822, 29331824, 68714117, 29331828, 284908, 285008, 285009, 284592, 285018, 284681, 284448, 284683, 18108354, 284369, 284684, 284685, 284788, 284687, 284689, 21908788, 285020, 285022, 60170815, 52844150, 284690, 284691, 284692, 33857023, 284693, 33857109, 284628, 18108374, 35695855, 284630, 284632, 284634, 284557, 284558, 80170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				284508, 284905, 284908, 284907, 284594, 284684, 284890, 284692, 284630, 284635, 284636, 284639, 284583
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gij5262574jembj[CAB45729.1] - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		58182575, 284259, 60432289, 28331826, 284107, 284905, 284908, 284910, 60170831, 284758, 285010, 285018, 284448, 284288, 284788, 33857109, 284628, 55810764, 18108379, 284634, 58182323, 58528486
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	284907, 285008, 284682, 284686, 21908788, 284629, 284631, 284634, 284555, 284259
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gij728836jspjP39193 ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III		cadherin	
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gij127560jspjP23246 MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 28331824, 29331825, 60432289, 28331827, 35688052, 29331828, 285008, 285019, 284681, 284682, 284448, 284389, 52844229, 21908785, 21908786, 21908788, 21908789, 60170615, 55810764, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gij2809819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00908) - Ammonium Transporter Family	glycoprotein	284258, 284508, 284909, 60432229, 284789, 21908785, 21908789
1900	87841858 (3799, 3800)	Novel Protein sim. GBank gij4102881 (AF017250) - vitellin precursor [Oreochromis aureus]		UNCLASSIFIED	284683

1901	95196847 (3801, 3802)	Novel Protein sim. GBank gij585859[spjP38378]S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52844507, 52645156, 18108398, 52646385, 52848842, 18108397, 56182575, 22278984, 22278985, 56984075, 35686286, 22278987, 22278988, 264490, 60432048, 284259, 29331822, 52645080, 29331824, 29331825, 68714117, 29331826, 60432289, 29331827, 29331828, 35686052, 33656970, 29146488, 264908, 264907, 29331830, 284908, 52844045, 264809, 264112, 265006, 284512, 265008, 264910, 265009, 60170831, 60432229, 60433358, 33857402, 60433438, 55812038, 264758, 33109854, 21808754, 33857084, 52844296, 87188474, 265010, 265011, 87188559, 265017, 265018, 265019, 18108351, 264448, 284288, 264886, 52644229, 21808765, 21808768, 21808767, 21808769, 55811957, 35895917, 285020, 285021, 52844150, 18108362, 33857023, 284693, 283987, 33657109, 33857182, 27486284, 33657349, 35885763, 18108370, 18108376, 55811576, 35888423, 35695855, 60431850, 264683, 263981, 52844332, 60170394, 83373044, 18108385, 87188518, 60432113, 264584, 284107, 263976
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gij4426613[gbjA020451] - (AF098786) SLM-I [Mus musculus]		dns_ma_bind	
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gij3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	284259, 28331825, 28331827, 264508, 264907, 265008, 60170831, 60433358, 60433438, 284759, 21808754, 264448, 264288, 265021, 265022, 33857023, 264693, 55811576, 264555, 284556, 22278000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gij1352911[spjP47147YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264508, 264905, 264808, 264907, 264908, 285007, 264910, 264886, 264788, 264687, 264789, 264693, 264628, 18108374, 264634, 264636, 264637, 264555
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gij3043714[dbjBAA25521] - (AB011187) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264769, 264689, 29148829, 35695917, 35896286, 264259, 264892, 18108362, 33857023, 29331824, 33857109, 28146489, 264508, 264509, 264905, 264906, 264907, 68712502, 264908, 264808, 35696423, 35895855, 264510, 284511, 284512, 264910, 264634, 264635, 264637, 264638, 33857402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264586, 264288, 264768
1906	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	85351144 (3813, 3814)	Novel Protein sim. GBank gij4928585igp AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278998, 35898288, 22278998, 22278998, 264259, 60432049, 29331822, 29331825, 60424289, 29331828, 35898052, 284593, 60433356, 21908754, 55811386, 55858542, 87168559, 265018, 264681, 264682, 264684, 264288, 21908765, 21908768, 21908788, 265020, 265022, 284690, 52844150, 264682, 33657023, 284693, 33657109, 35695855, 264636, 264638, 60432113
1908	85313641 (3815, 3816)	Novel Protein sim. GBank gij3986770 (AF109806) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181688, 22278998, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331828, 29331827, 29331828, 29146498, 264905, 264806, 264907, 264908, 86712502, 264909, 56182435, 284510, 264511, 285008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812036, 33109954, 52846317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264881, 264448, 264288, 264888, 264688, 264769, 21908765, 21908768, 21908767, 21908768, 21908769, 55811857, 29148629, 35695917, 265020, 265022, 264681, 264692, 18108384, 65274620, 33657109, 33657348, 35695783, 18108374, 263978, 55810764, 55811578, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22278000, 22278002, 264566, 264488
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gij2224653 dbj BAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264784, 264766, 18108370, 264634, 264637, 264488
1910	84216821 (3819, 3820)	Novel Protein sim. GBank gij1351218 sp P47228 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35698288, 22278998, 22278999, 35698052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264788, 264788, 264687, 264769, 35695917, 265021, 52844150, 264692, 264628, 18108370, 264628, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264488

1811	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC006530 - (AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - nuclease DNA mismatch repair protein	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 264906, 265007, 264591, 55612038, 87168559, 264448, 264368, 21908765, 21908768, 265022, 264681, 264693, 18108385, 55811376, 264556, 18108385, 18108388
1812	95413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1 - (AB028874) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - UNCLASSIFIED Zinc finger, CCHC class	18108397, 56182575, 56181886, 22278894, 22278985, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 86714117, 35996052, 264805, 264908, 264907, 264908, 52844045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265018, 264760, 18108351, 264681, 264369, 264684, 264288, 264688, 264788, 21908785, 21908786, 21908787, 21908788, 21908789, 55811957, 265020, 265021, 265022, 60170615, 264682, 33657023, 264693, 18108376, 55811576, 35996423, 65274791, 264637, 56182323, 83373044, 56526486, 22279002, 264563, 264568
1813	95305548 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2		56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265008, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264368, 264288, 264685, 264686, 264789, 21908785, 21908786, 21908788, 21908789, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1814	83423882 (3827, 3828)	Novel Protein sim. GBank gi 4569604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - struct EF hand	56182575, 29331824, 35996052, 264806, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264688, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1815	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82891.1 - (AB028882) KIAA1039 protein [Homo sapiens]	UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264908, 265008, 265017, 265019, 264786, 264789, 264688, 264628, 264635, 264637, 264639, 83373044, 264565
1816	79840761 (3831, 3832)			264683, 264639

1817	87821680 (3833, 3834)	Novel Protein sim. GBank gi 5889391 dbj BAAD2979.1 - (AB028950) KIAA1027 protein [Homo sapiens]		struct	284769, 284689, 21908785, 21908788, 22278986, 284259, 284691, 284693, 29331824, 29331825, 29331826, 29331828, 284905, 284906, 284628, 284907, 284908, 284908, 284510, 284630, 284910, 284634, 284635, 284638, 284637, 284638, 283981, 284639, 284758, 18108385, 21908754, 285011, 284604, 284563, 18108351, 284782, 284783, 284568, 284784, 284786
1818	95302795 (3835, 3836)	Novel Protein sim. GBank gi 5281517 gb AAD41524.1 AF15483 - (AF154831) PV-1 [Rattus norvegicus]		struct	284488, 18108392, 18108357, 21908785, 21908787, 21908788, 56182375, 21908789, 22278994, 35698286, 35698917, 22278996, 22278997, 285021, 285022, 284534, 284690, 284691, 284692, 33857023, 284693, 29331824, 29331825, 33857109, 29331826, 52845129, 35698052, 29331828, 27488282, 27488284, 35698783, 284508, 284905, 284508, 284906, 284628, 284907, 18108370, 284908, 284628, 284909, 18108372, 18108374, 283978, 35698423, 35698555, 284510, 284511, 285006, 285007, 284512, 285008, 284631, 285009, 284910, 284634, 284635, 284555, 284636, 284556, 284637, 284557, 284593, 284638, 284594, 80170394, 284595, 284559, 284598, 83373044, 284758, 52846317, 18108385, 52844286, 58528486, 87188518, 285010, 285011, 87188559, 284600, 284601, 284602, 285017, 284603, 284604, 285018, 284605, 284760, 284761, 284482, 284584, 18108351, 284762, 284682, 284585, 284448, 284784, 284586, 284488, 284587, 284369, 284288, 284786, 284487, 284885
1819	94143847 (3837, 3838)	Novel Protein sim. GBank gi 3878584 emb CAB01237 - (Z77687) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO8753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 28331822, 285007, 60170831, 60432228, 80433438, 284448, 284882, 284288, 5811957, 33857023, 33857109, 65274791, 58182323, 22279002
1820	91228953 (3839, 3840)	Novel Protein sim. GBank gi 1808231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g830485) and H12888 (NID:g877888) [Homo sapiens]		UNCLASSIFIED	284510, 284511, 284512, 284586
1821	79555226 (3841, 3842)	Novel Protein sim. GBank gi 4560897 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	284693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi136595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELIN I (LVI); PHOSVITIN (PV); LIPOVITELIN II (LVI)]; YGP40]		UNCLASSIFIED	284688, 284688, 284490, 18108370, 284909, 18108374, 285008, 284557, 284564, 18108351
1923	84323588 (3845, 3846)	Novel Protein sim. GBank gi119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	284488, 284489, 22278995, 284094, 284259, 35986052, 284509, 284905, 284906, 284907, 284908, 68712502, 284908, 284511, 284512, 285007, 284910, 285008, 284591, 284592, 284593, 284594, 284595, 284758, 284598, 284759, 285011, 285017, 285018, 285019, 5581150, 284681, 284782, 284448, 284784, 284286, 284369, 284786, 284787, 284688, 284687, 284788, 284789, 56181562, 284689, 21908766, 284691, 33857023, 284693, 65274620, 33857109, 18108370, 284628, 284629, 35896423, 284630, 284631, 284632, 284634, 284555, 284638, 284637, 284638, 284639, 284558, 83373044, 87188518, 284563, 284564, 284565, 284566, 284567, 29331826, 284906, 284908, 284595, 285017, 285018, 285019, 285021, 284681, 284683, 284637, 18108385, 284585
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi13877655 emb CAA86657 - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75184 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3848, 3850)	Novel Protein sim. GBank gi14981803 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	22278995, 22278996, 22278997, 284259, 29331824, 66714117, 29148498, 284909, 5264045, 285008, 285009, 284758, 285011, 285017, 284605, 284448, 284288, 284692, 33857109, 18108374, 60170394
1926	88084739 (3851, 3852)	Novel Protein sim. GBank gi12246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		strucd	284905, 284908, 284907, 284910, 284593, 285018, 284760, 284764, 284288, 284692, 284693, 283976, 284631, 284634, 284637, 284583
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi13043632 dbj BAA25480 - (AB011126) KIAA0554 protein [Homo sapiens]			284689, 284631
1928	87798054 (3855, 3856)	Novel Protein sim. GBank gi1665761 dbj BAA13371 - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00183) - Extracellular link domain	inf	284488, 284259, 285017, 285021, 284682
1929	86987236 (3857, 3858)	Novel Protein sim. GBank gi15001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/hypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	284508, 284591, 33857402, 285017, 284788, 284632, 284556, 284639

1930	87888128 (3859, 3860)	Novel Protein sim. GBank gij1708230[sp]P52983[NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35686286, 29331828, 284905, 284907, 284808, 284909, 284511, 284910, 284758, 284601, 285017, 285019, 284605, 284760, 284764, 284766, 284686, 284769, 285022, 35698423, 284638, 60432113
1931	87797279 (3861, 3862)	Novel Protein sim. GBank gij404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	284906, 284908, 60432229, 284758, 284764, 284288, 285020, 284692, 284634, 284637, 284684, 284691, 284635
1932	15030972 (3863, 3864)			UNCLASSIFIED	284595
1933	11813868 (3865, 3866)			struct	56182575, 56182435, 284510, 284757, 284758, 55812038, 55811386, 285018, 55811150, 21806785, 284691, 284631, 284635, 284637
1934	84426360 (3867, 3868)	Novel Protein sim. GBank gij4115748[dbj]BAA36494 - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		UNCLASSIFIED	284886, 285011, 284511, 284905, 18108351, 284584, 284681, 284259, 18108370, 284586, 284764, 284389, 284585
1935	87752511 (3869, 3870)				60432289, 285007, 285010, 285011, 285018, 33657109, 18108374
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gij4827040[ref]NP_005110.1pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			
1937	94847141 (3873, 3874)	Novel Protein sim. GBank gij543187[pir]S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21908767, 35685917, 60170615, 284693, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gij4344431[gb]AAD2340.1AC00695 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	284488, 28146488, 284905, 284559
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gij500958[dbj]BAA03210 - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278899, 60432289, 56182435, 60433356, 285017, 21908765, 21908766, 21908768, 55811957, 27488284, 35688423, 60432113, 284584
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gij1946300[emb]CAA73132 - (Y12528) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	284488, 28331822, 284448, 284683, 284288, 285020, 33657023, 284631
1941	94147177 (3881, 3882)	Novel Protein sim. GBank gij4206388 (AF080570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56894075, 22278898, 284259, 28331824, 28331827, 284905, 285008, 33657084, 285017, 285018, 284288, 284687, 21908765, 21908766, 21908767, 285020, 52644150, 27488284, 83373044, 18108387, 60432113, 22278002, 284585
1942	87841870 (3883, 3884)	Novel Protein sim. GBank gij4927204[gb]AAD33049.1JAF13391 (AF133911) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	284488, 18108398, 28331825, 27488281, 284509, 18108370, 18108374, 284482
1943	84325288 (3885, 3886)	Novel Protein sim. GBank gij3122852[sp]O15736[TIPD_DICD1 - TIPO PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278898, 28331822, 28331827, 35686052, 284511, 285008, 284592, 60432228, 285017, 285018, 285019, 284684, 284692, 33657109, 85274791, 284638

1944	94232858 (3887, 3888)	Novel Protein sim. GBank gi 1799570 dbj BAA13432 - (D87671) TIP120 [Rattus norvegicus]		UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432228, 60433356, 33657402, 60433438, 264598, 33109954, 21908754, 87168474, 87168558, 265017, 265018, 265019, 18108351, 264368, 264686, 264768, 21908765, 21908766, 21908767, 21908769, 35695917, 265020, 265021, 60170815, 264692, 33657023, 18108370, 18108374, 35698423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563, 264486, 22278996, 264510, 264511, 18108351, 264683, 264486, 264567
1945	87641672 (3888, 3890)	Novel Protein sim. GBank gi 4927204 gb AAD33048.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	
1946	87443980 (3891, 3892)	Novel Protein sim. GBank gi 2498104 sp Q27869 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN		UNCLASSIFIED	
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gi 3914801 sp Q54888 PPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)		nsopolymerase	27488264, 264637, 87168518, 264583, 22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264268, 264768, 264688, 21908768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22278998, 264909, 60170831, 264591, 264594, 235010, 265011, 264784, 264369, 264689, 264631, 264638
1948	85189174 (3895, 3896)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243458) proteophosphoglycan [Leishmania major]		strud	
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gi 3876766 emb CAA93466.1 - (Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	Contains protein domain (PF00857) - Isochorismatase family	UNCLASSIFIED	264389, 264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264508, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264583, 55811150, 18108351, 264389, 264288, 18108354
1950	87788531 (3899, 3900)	Novel Protein sim. GBank gi 2628753 dbj BAA23424 - (AB008782) sulfate transporter [Arabidopsis thaliana]	Contains protein domain (PF00916) - Sulfate transporter family	transport	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52648317, 265018, 265019, 264369, 21908765, 21908767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gi 4929633 gb AAD34077.1 AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	reductase	264591, 264593, 264594, 264595, 264555, 264558, 264557, 264558, 264595

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gi 168715 sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	284259, 284558
1954	91228025 (3907, 3908)	Novel Protein sim. GBank gi 4240271 dbj BAA74914.1 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	284486, 283994, 18108394, 35696286, 22278998, 29331822, 86714117, 29331828, 29331827, 284508, 264905, 264906, 264907, 264908, 264909, 264510, 285008, 265007, 265008, 264910, 285009, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264786, 264789, 35695917, 285020, 265021, 264691, 33857023, 284692, 33857109, 284628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264486, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 264508, 29331830, 265008, 285009, 264591, 55812038, 87188474, 265017, 265018, 265019, 264448, 264788, 21908765, 21908766, 21908767, 55811957, 265020, 265021, 52845129, 33857109, 27486284, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gi 1665821 dbj BAA134071 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	284488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 285010, 285018, 18108351, 264788, 56181562, 264689, 21908786, 21908789, 265022, 264691, 264628, 18108374, 55810784, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22278900, 22279002, 264583, 264584

1857	94326510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA78856.1 - (AB023228) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52648842, 56182575, 22278987, 22278988, 22278998, 28331824, 68714117, 29331827, 28146488, 284593, 33657402, 33109954, 87188474, 285018, 284448, 284388, 284288, 284788, 21908768, 21908767, 21908768, 21908769, 285020, 265021, 284692, 85274620, 27488264, 33657349, 27486285, 35695855, 22278002, 284482
1858	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020876) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278998, 284092, 284094, 284259, 80432049, 28331824, 58182181, 86714117, 284107, 284109, 284909, 284511, 60170831, 60432229, 21908754, 285010, 21908769, 35695917, 285022, 65274620, 263987, 283978, 35888423, 284631, 284632, 284634, 284635, 18108385, 22279000, 22279002, 284583, 285019
1859	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860 - (Z98056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1860	80308608 (3919, 3920)	Novel Protein sim. GBank gi 227485 dbj BAA21515 - (D64159) 3-7 gene product [Homo sapiens]		strut	284905, 284808, 284807, 284908, 284909, 285006, 285007, 284910, 284595, 285017, 284804, 285018, 18108351, 284764, 284369, 284768, 284768, 21908765, 18108388, 284628, 18108378, 284635, 284638, 284637, 284638, 284488
1861	16292807 (3921, 3922)				284635
1862	81008385 (3923, 3924)				
1863	90938017 (3925, 3926)	Novel Protein sim. GBank gi 3721653 dbj BAA33581 - (AB012833) acyl-CoA synthetase 5 [Rattus norvegicus]		UNCLASSIFIED eph	65274572, 284592, 284593, 285019, 284691, 65274572, 18108398, 35886286, 28331825, 60432289, 28331827, 284828, 285008, 285008, 60433356, 60433438, 21908754, 285020, 285021, 33657023, 33657109, 27488285, 35895855, 284555
1864	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1 - (AL080169) hypothetical protein [Homo sapiens]		cadherin	284488, 284092, 284259, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 285007, 285008, 284910, 284592, 284593, 284594, 284595, 284758, 284600, 284803, 284804, 284805, 284780, 284782, 284448, 284764, 284288, 284685, 284768, 284768, 284769, 21908768, 284691, 284692, 284693, 18108370, 284628, 284829, 18108374, 284630, 284631, 284634, 284638, 284637, 284638, 18108382, 83373044, 18108385, 284483, 284584, 284585, 284586, 284488, 284587
1865	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36284 - (AB001773) PEM-6 [Clona savignyi]	Contains protein domain (PF01428) - ANI-like Zinc finger	ubiquitin	284488, 284510, 284760, 284768, 284486

1866	94192058 (3831, 3832)	Novel Protein sim. GBank gi4929707 gb AAD34114.1 AF15187 - (AF15187) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264884, 264786, 264685, 264688, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264567
1867	87386123 (3833, 3934)	Novel Protein sim. GBank gi2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	29331824, 265010, 265017, 264288, 21906784, 263981, 56528488
1868	88095841 (3835, 3936)	Novel Protein sim. GBank gi2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00009) - EGF-like domain	oncogene	35698286, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264784, 264885, 264786, 264787, 264889, 264691, 264693, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264584, 264585, 264586, 264587
1869	84328529 (3837, 3938)	Novel Protein sim. GBank gi2911274 (U20328) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1870	80596048 (3839, 3940)	Novel Protein sim. GBank gi4050087 (AF108907) - S164 [Homo sapiens]		UNCLASSIFIED	264808, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi134208 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264486, 264489, 22278998, 264259, 60432049, 86714117, 29331828, 60432289, 29331827, 35698052, 264508, 264905, 264508, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264598, 264600, 264604, 264605, 264760, 18108351, 264448, 264784, 264288, 264786, 264788, 264769, 21908785, 33657023, 264692, 18108370, 264629, 35698423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264583, 264584, 264585, 264586, 264486
1872	87815444 (3943, 3944)	Novel Protein sim. GBank gi4519623 dbj BAA75871.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644296, 265018, 265019, 264781, 264688, 21908788, 21908789, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35698423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264784, 264583

1975	94316479 (3949, 3950)				UNCLASSIFIED	264488, 66714117, 28331826, 29331828, 56182435, 285008, 284757, 55812038, 285010, 285017, 284389, 55811957, 65274781, 35695855, 58182323, 60432113, 284259, 35696052, 285018, 265020, 285021, 33657109, 58526486
1976	95358914 (3951, 3952)				UNCLASSIFIED	284908, 264598, 285021, 264566
1977	94652684 (3953, 3954)	Novel Protein sim. GBank glj2499528[sp]Q07782[NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)]			homeobox	
1978	87447645 (3955, 3956)	Novel Protein sim. GBank glj103421[pir]jA33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)			transcription factor	60170831, 264568
1979	87627708 (3957, 3958)	Novel Protein sim. GBank glj2244815[emb]CAB10238.1] - (Z97336) hypothetical protein [Arabidopsis thaliana]			UNCLASSIFIED	29331828, 28146498, 284905, 264907, 285007, 285009, 285010, 285018, 264888, 18108358, 21906768, 35695917, 265020, 60170815, 284693, 18108368, 18108370, 284631, 284635, 264556, 284558, 18108384, 22279000, 284585
1980	86577059 (3959, 3960)	Novel Protein sim. GBank glj4759280[ref]NP_004642.1]pUSP1 - Ubiquitin carboxyl-terminal hydrolase, X-linked			ubiquitin	284489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank glj4406683[gb]AAD20060] - (AF131849) Unknown [Homo sapiens]			UNCLASSIFIED	22278995, 22278997, 22278999, 264258, 29331825, 29331828, 29146498, 29146499, 264107, 284908, 284910, 284595, 21906754, 285010, 285017, 285018, 285019, 264448, 284288, 21906767, 33657023, 27488284, 18108370, 18108374, 18108378, 284630, 284631, 284635, 18108385, 87168518, 22279000, 264482, 284584
1982	80995367 (3963, 3964)	Novel Protein sim. GBank glj5689523[db]jBAA83045.1] - (AB028016) KIAA1093 protein [Homo sapiens]				65274572, 29331825, 35696052, 33656970, 284908, 285008, 55811386, 284780, 264686, 284691, 27488264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank glj3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcription factor	22278998, 35698286, 284259, 29331822, 20281099, 29331824, 60432289, 29331827, 284509, 284905, 264906, 284907, 66712502, 284808, 32844045, 284908, 284510, 284512, 284910, 285009, 264591, 284592, 60433356, 60433438, 264758, 285010, 284600, 284603, 284604, 284780, 264762, 264763, 284764, 284766, 264687, 264768, 284769, 21908765, 55811957, 35695917, 284690, 264692, 284693, 284628, 264629, 283978, 18108379, 35698423, 35895855, 20281071, 284832, 284634, 284635, 264555, 264636, 284637, 284638, 284639, 83373044, 18108389, 22279000, 22279002

1984	85760889 (3967, 3968)	Novel Protein sim. GBank gij286695fembjCAA17174.1] - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811957, 56894075, 285020, 285021, 22278999, 285022, 284259, 29331822, 33637182, 29148499, 264628, 18108370, 284908, 264629, 55811576, 35695855, 285008, 285007, 264591, 21906754, 33637084, 285010, 285017, 265019, 264288
1985	85636897 (3989, 3970)	Novel Protein sim. GBank gij5712131gbjAAD7379.1]AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 284637, 58182323, 18108385, 264584
1986	80200507 (3971, 3972)			UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443gbjAAD31319.1]AF14457 - (AF144573) Mx-Interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21906768, 33637023, 284892, 284893, 18108377, 264835, 60170384, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 284907, 284908, 284909, 264910, 264591, 264593, 264758, 264764, 284686, 284768, 285021, 284692, 284828, 284628, 35695855, 284630, 284635, 284636, 284637, 284638, 284639, 284483
1989	81225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc97 homolog GCP2 [Homo sapiens]		tubulin	60432049, 80432289, 52844045, 56182435, 264112, 265007, 33637402, 52844229, 21906765, 21906768, 21906769, 55811957, 33637023, 263987, 33637109, 18108370, 22279000, 22279002
1990	85698888 (3979, 3980)	Novel Protein sim. GBank gij57011727dbjBAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287dbjBAA74922.1] - (AB020706) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaplin N terminal region	glycoprotein	18108394, 56182575, 22278994, 34688286, 58994075, 22278997, 22278999, 29331822, 29331824, 29331825, 80432289, 29331828, 264508, 264906, 264907, 284908, 58182435, 284510, 285007, 21806754, 33109954, 87168474, 265017, 265018, 285019, 264762, 18108351, 264763, 284683, 284369, 284288, 284685, 264765, 264687, 264769, 21906765, 21906768, 21906769, 55811957, 285020, 80431528, 263974, 18108379, 35695855, 284555, 264557, 264639, 83373044, 18108384, 87188518, 80432113, 22279000, 22279002, 264584, 264488
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- struct	29331827, 264908, 284907, 284909, 285007, 284603, 264768, 264686, 264768, 21906768, 284628, 284635, 264636, 18108385, 56526486, 264568, 264567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	284592, 35698423

1994	94329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45922.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (P1D:g2359287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymarase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265008, 60432229, 33657402, 60433356, 284757, 60433438, 284758, 33109954, 285011, 285017, 285018, 285019, 264684, 264369, 264685, 264686, 264768, 21908765, 21908787, 21908788, 21908789, 265020, 264890, 18108362, 264893, 85274820, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526486, 22279000, 22279002, 264584, 264488, 18108386, 22278994, 56894075, 22278998, 35688286, 22278997, 22278999, 264259, 29147820, 56182181, 29331824, 60432229, 29331826, 29331827, 35696052, 29146498, 264905, 264907, 66712502, 56182435, 285006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 55858542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264883, 264764, 264286, 264766, 264686, 264768, 264769, 56181562, 264689, 21908765, 21908789, 21908787, 28148827, 21908788, 21908789, 29148629, 28148784, 265020, 265021, 264690, 18108381, 264893, 27486262, 27486264, 27488285, 18108370, 60431528, 18108374, 18108377, 35688423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264559, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87188518, 264404, 60432113, 264587, 264584
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	
1996	80254185 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020 - (X88028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2842034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 dbj BAA76839.1 - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264885, 264555, 264567

1999	94324903 (3997, 3998)	Novel Protein sim. GBank gij5225312jgbjAAD40846.1jAF07244 - (AF07244) cathepsin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424289, 29331827, 29331828, 35696052, 285008, 284512, 55811386, 285010, 285018, 285019, 55811150, 18108351, 264763, 284682, 284369, 284685, 284686, 56181582, 265020, 264891, 33857023, 264693, 33857109, 27486284, 18108370, 18108378, 35895855, 264634, 264635, 264636, 264555, 284557, 56182323, 18108382, 264559, 83373044, 60432113, 22278000, 264563, 264564, 284566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gij723232jipjQ10155jYATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME 1	UNCLASSIFIED	UNCLASSIFIED	52846365, 52846842, 22278894, 22278895, 22278898, 35696286, 22278897, 22278898, 22278999, 284259, 52845080, 29331822, 29331826, 29331827, 29331828, 35896052, 264106, 29331830, 52844045, 285007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21808754, 52844286, 265017, 265018, 265019, 264761, 264389, 284288, 52844229, 21908785, 21908786, 21908787, 21908788, 21908789, 35895917, 265020, 265021, 60170815, 52844150, 33657023, 65274620, 52845128, 27486281, 27486282, 27486284, 35695763, 35698423, 35695855, 264631, 52844332, 56182323, 60170394, 83373044, 56528486, 22279002, 284586, 284587
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gj107560jipjJB38637 - Ras inhibitor (clone JC265) - human (fragment)	UNCLASSIFIED	UNCLASSIFIED	264769, 52844228, 65274572, 21908768, 22278896, 35696286, 35695917, 265020, 22278999, 284534, 284490, 284259, 284692, 60432289, 33657109, 35698052, 284508, 284509, 18108370, 80431528, 18108374, 35698423, 65274781, 35695855, 264510, 264511, 264512, 285009, 284634, 284636, 284555, 264556, 284636, 284557, 264558, 284558, 60433438, 83373044, 284769, 18108385, 285011, 284800, 264801, 60432113, 264603, 264604, 264605, 264448, 284288, 284765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gij729433jipjP38657IER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-80 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	- isomerase	284807, 285006, 284910, 284603, 284682, 284629, 18108374, 284556, 284557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gj186388jipjJAZ7040 - neurofilament triplet M protein - chicken (fragment)	UNCLASSIFIED	UNCLASSIFIED	284805, 284906, 284908, 284910, 284598, 285017, 18108351, 284692, 284629, 284634, 284585

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1 - (AL048998) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645158, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35686286, 22278997, 22278998, 22278999, 60432049, 264259, 52845080, 29331824, 29331828, 29331827, 35686052, 29331828, 33656870, 29331830, 264908, 264592, 60433356, 33657402, 52846317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265018, 264763, 264683, 264288, 52644228, 21908765, 21908768, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52845129, 33857109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 56526486, 87168518, 60432113, 264483, 264488, 264908
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22613 - (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424288, 66714117, 35698052, 264806, 66712502, 264909, 264510, 60433356, 85656542, 265010, 265018, 265019, 264882, 264448, 264288, 264768, 26148627, 21906769, 26148784, 35695917, 60170815, 264691, 33657023, 65274620, 33657109, 55810784, 55811578, 35695855, 87168518, 60432113, 264563, 264482
2007	94325558 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BA23712 - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	264488, 265394, 35696052, 264508, 264905, 264906, 264807, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264780, 264782, 264784, 264788, 264885, 264767, 264768, 264789, 55811957, 35695917, 265020, 264691, 264693, 264628, 264828, 65274791, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264586
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257 - (Y07860) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264788, 35695855

2009	85748240 (4017, 4018)	Novel Protein sim. GBank gi 3882305 dbj BAA34512.1 - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264881, 264683, 21908788, 264891, 33857182, 33857349, 264631, 87168518, 264404, 22279002, 264583
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gi 5262829 emb CAB45753.1 - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	- eph	52844507, 52845158, 52846365, 52846842, 18108397, 65274572, 22278994, 56994075, 35986286, 22278998, 22278997, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432228, 60433356, 21906754, 52846317, 33109954, 52844286, 87168474, 87168559, 265017, 265018, 265019, 264881, 264885, 264687, 52844229, 264689, 21906785, 21908788, 21908787, 21908788, 35895917, 265020, 52844150, 264681, 264692, 33857023, 293987, 52845129, 35895783, 18108376, 35898423, 65274791, 35895855, 264631, 264634, 60431850, 264637, 264638, 52844332, 60170394, 18108385, 87168518, 22279002, 264584, 264585, 264586, 264587, 58182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35898052, 284908, 68712502, 265008, 265007, 265008, 265010, 265011, 265017, 265018, 264681, 264448, 264683, 264389, 264288, 264685, 264788, 264687, 21906785, 21908787, 21908788, 21908789, 265020, 285022, 264691, 33857023, 65274820, 33857109, 264628, 264557, 264559, 83373044, 87188518, 80432113, 22279002
2011	94328148 (4021, 4022)	Novel Protein sim. GBank gi 3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87188539, 265019, 264682, 264288, 264686, 21906784, 265020, 265022, 33857023, 264693, 33857109, 55811576, 264632, 264558, 58182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2012	8772137 (4023, 4024)	Novel Protein sim. GBank gi 1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87188539, 265019, 264682, 264288, 264686, 21906784, 265020, 265022, 33857023, 264693, 33857109, 55811576, 264632, 264558, 58182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gi 4507985 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- dna_ma_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21908787, 265020, 264692
2014	87347840 (4027, 4028)	Novel Protein sim. GBank gi 127720 sp P20938 MYP0_HETFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	264488, 28331826, 264807, 264636, 264555, 264639, 264558

2015	86094922 (4029, 4030)	Novel Protein sim. GBank gl 81286 pir S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35698286, 264259, 35698032, 264508, 264908, 264907, 264510, 264512, 87188474, 265010, 264681, 264288, 264689, 264628, 35698423, 35698555, 264638, 264583, 264584
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gl 285046 pir S26413 - t-complex protein Top-10 - mouse		sluod	284102, 284508, 264110, 265009, 33108954, 21908768, 265021, 33657109, 27486282, 263972, 18108374, 263976, 264555, 264584
2017	79464293 (4033, 4034)			UNCLASSIFIED	284685, 264636
2018	79637087 (4035, 4036)	Novel Protein sim. GBank gl 124735 sp P18175 INVO_PIG - INVOLUCRIN			264683
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gl 2143910 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gl 2078483 (U43200) - antifreeze glycopetide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22278002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gl 585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21808754, 21908788, 33857023, 33857109, 27488261, 87188518
2022	95295685 (4043, 4044)	Novel Protein sim. GBank gl 4218005 (AC008135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			284757, 284787, 60170615, 18108385
2023	87722876 (4045, 4046)	Novel Protein sim. GBank gl 5410230 gb AAD2992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264782, 264789, 264634, 264636, 87188518, 60432113, 22279000, 264482, 264585
2024	87896443 (4047, 4048)				60433438, 265017, 264686, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gl 4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Calthrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 60170615, 264558
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gl 1655689 emb CAA68032 - (Y07752) pterophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87188559, 264288, 264688, 264689, 21808768, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264584, 264568, 264587
2027	80249001 (4053, 4054)			UNCLASSIFIED	263976, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gl 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - ubiquitin-HECT-domain (ubiquitin-transferase).	52644507, 52645156, 52646842, 56182575, 56984075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35686052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21908754, 52646317, 52644286, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21908765, 21908766, 21908787, 21908788, 21908769, 55811857, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27488261, 27486282, 27488284, 27488265, 35695763, 264629, 55811576, 35698423, 35695855, 264635, 264636, 52644332, 264556, 83373044, 56529486, 22278000, 22279002, 264563
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gl 3599940 (AF017368) - faclogerital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - UNCLASSIFIED	265009, 264595, 85636542, 264555, 264556, 264557, 264558, 264559, 83373044
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gl 5630080 (gb AAD45825.1 AC004890) similar to HUB1; similar to BAA24380 (P D:2789430) [Homo sapiens]	Contains protein domain (PF00096) - transcript factor Zinc finger, C2H2 type	18108394, 56984075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21908769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2031	80245281 (4061, 4062)			264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gl 5688491 (db BAA83029.1) - (AB028000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - hydrolase Sulfatase	65274572, 35696286, 29331824, 264808, 265009, 264593, 265016, 264288, 264686, 264769, 21908766, 21908767, 29148827, 264828, 35698423, 264634, 264556, 18108381, 60170394, 264558, 83373044, 18108385, 264482, 264484
2033	85000809 (4065, 4066)	Novel Protein sim. GBank gl 2484828 (sp Q84886 CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2-6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)	synthase	56181562, 264628, 264632, 264555, 264556
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gl 4828984 (ref NP_005147.1 PROD1 - UNKNOWN	Contains protein domain (PF00076) - dna_ma_bind RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	22278998, 22278999, 264907, 29331830, 265008, 265016, 264681, 264682, 264684, 21908767, 21908768, 21908769, 33657109, 83373044, 56528488

2035	83553451 (4069, 4070)				264369, 264686, 265022, 26526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324633 (4073, 4074)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]	UNCLASSIFIED		65274572, 22278995, 22278996, 36994075, 3586286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331828, 29331828, 35698052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264584, 5812038, 33109954, 21906754, 87188559, 265017, 265018, 265019, 264762, 264389, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35895917, 265020, 265021, 285022, 52844150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gi 3880625 emb CAB07858 (Z93785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27558 comes from this ge...	UNCLASSIFIED	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	22278995, 22278996, 56994075, 264259, 29331824, 35698052, 264905, 264906, 52844045, 265007, 265009, 87188559, 265017, 18108351, 264448, 264389, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52844150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108378, 35698423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87188518, 22279000, 22279002, 264563, 264564, 264566
2039	95514626 (4077, 4078)	Novel Protein sim. GBank gi 2224653 dbj BAA20813 (AB002354) KIAA0358 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264809, 264510, 265008, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35698423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87188518, 284486
2040	95308417 (4079, 4080)		UNCLASSIFIED		264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gi 2500825 sp P70700 PRA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase		264488, 22278998, 35698052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35698423, 35698555, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gij4406590jgbjAAD20040] - (AF131786) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 284259, 29331826, 35696052, 29331828, 264508, 264509, 284907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 285019, 264681, 264764, 264368, 264765, 264684, 264288, 264766, 264688, 52844229, 284769, 21908765, 35695917, 264535, 52844150, 264691, 264692, 18108365, 27486281, 27486282, 27486285, 18108374, 35698423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264583, 264584, 264586
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gij5052554jgbjAAD38607.1jAF14563 - (AF145632) BcDNA.GH08032 [Drosophila melanogaster]	Contains protein domain (PF00122) - transport E1-E2 ATPase		284488, 52844507, 52846385, 56994075, 22278997, 22278998, 20281171, 264258, 29331822, 29331824, 66714117, 29331828, 29331828, 33656970, 29146488, 264508, 264908, 52844045, 58182435, 265008, 33657402, 21908754, 52644296, 87188559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 60170815, 264691, 33657023, 264693, 65274620, 33657108, 33657182, 27486281, 27486282, 33657349, 35695783, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 58182323, 264558, 83373044, 18108385, 56526486, 87188518, 60432113, 22279000, 264587
2044	87106827 (4087, 4088)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264689, 21908765, 21908769, 265020, 264692, 264482, 264588
2045	79635532 (4089, 4090)				264692
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gij4406698jgbjAAD20082] - (AF131852) Unknown [Homo sapiens]			264259, 284806, 264683, 22279002
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gij4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278998, 29147620, 29331824, 29146498, 264508, 265007, 285008, 265019, 264605, 264681, 29148627, 29148628, 265021, 33657023, 18108365, 33657108, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84506378 (4095, 4096)			UNCLASSIFIED	264909
2049	88094680 (4097, 4098)	Novel Protein sim. GBank gij4589656jgbjBAA76850.1] - (AB023223) KIAA1008 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264908, 264907, 264908, 264909, 264910, 264603, 264783, 21908767, 21908768, 264628, 264634, 264637, 22279002, 264584, 264565, 264566, 264567

2050	79633835 (4089, 4100)			UNCLASSIFIED	264693	264488, 264259, 264509, 264508, 264907, 264768, 18108374, 35698423, 264563, 264566, 264488
2051	87780188 (4101, 4102)			UNCLASSIFIED		
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gl 45298889 gb AAD21812.1 - (AF134728) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain	kinase		264488, 263394, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264368, 264766, 264686, 264768, 264769, 52844229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695955, 264630, 264631, 264632, 264634, 264635, 264636, 264558, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567, 264488, 263394, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264368, 264766, 264686, 264768, 264769, 52844229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695955, 264630, 264631, 264632, 264634, 264635, 264636, 264558, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gl 2985449 emb CAA75113 - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED		264488, 263394, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264368, 264766, 264686, 264768, 264769, 52844229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695955, 264630, 264631, 264632, 264634, 264635, 264636, 264558, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567
2054	85358937 (4107, 4108)	Novel Protein sim. GBank gl 3876326 emb CA802090 - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain			264488, 263394, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264368, 264766, 264686, 264768, 264769, 52844229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695955, 264630, 264631, 264632, 264634, 264635, 264636, 264558, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gl 5353746 gb AAD2226.1 AF15913 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED		264488, 263394, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264368, 264766, 264686, 264768, 264769, 52844229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35698423, 55811576, 35695955, 264630, 264631, 264632, 264634, 264635, 264636, 264558, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264488, 264567

2056	88177396 (4111, 4112)	Novel Protein sim. GBank gi 4826960 ref NP_005042.1 pOARS - glutamine-IRNA synthetase	Contains protein domain (PF00749) - IRNA synthetases class I (E and Q)	- synthase	284488, 52845156, 56182575, 22278994, 35898286, 56994075, 22278996, 22278998, 22278999, 60432049, 284259, 29331824, 60432289, 29331827, 29331828, 33656970, 284104, 284908, 284808, 285006, 285008, 60170831, 264591, 60432229, 60433438, 18108348, 21908754, 33857084, 52844296, 67168474, 265010, 67168559, 265017, 265018, 284760, 18108351, 264681, 264682, 284448, 264883, 284389, 284288, 264685, 284687, 264888, 284689, 21906765, 21906766, 21906767, 21906769, 55811957, 35895917, 265022, 33657023, 18108362, 33657108, 18108368, 33657182, 27486281, 27486284, 27486285, 33657348, 264628, 18108370, 284628, 18108374, 18108377, 18108379, 35896423, 55811578, 20281152, 284638, 284952, 18108385, 18108388, 87188518, 284482, 284565, 284588, 284587, 52846842, 52848385, 56182575, 35898286, 22278996, 22278997, 22278998, 284093, 52845080, 35896052, 29331828, 33656970, 265009, 52846317, 55811388, 52844296, 52644229, 21906769, 35895917, 265021, 60170815, 52844150, 33657109, 33657182, 27486281, 27486282, 35895763, 35896423, 35895855, 52844332
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	285007, 265008, 284591
2058	88278896 (4115, 4116)	Novel Protein sim. GBank		UNCLASSIFIED	29331825, 284682, 284686, 284691, 284693, 22278002
2059	78866684 (4117, 4118)	gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gi 2811122 (U87316) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 28331824, 29331828, 284910, 55811957, 18108370, 55811578

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gij2496947[sp]Q09298[yQO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EED8.9 IN CHROMOSOME II	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85858542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264688, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56528486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gij4502091[ref]NP_001139.1pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	strut	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264782, 264565, 264784, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gij4589562[dbj]BAA78603.1 - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00817) - RasGEF domain	oncogene	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264584, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gij1754515[dbj]BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 26331828, 35696052, 264509, 265007, 265008, 60432229, 60433436, 21906754, 265010, 265011, 87168559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108368, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22278000, 22279002, 264566, 264488
2065	95082238 (4129, 4130)	Novel Protein sim. GBank gij2507144[sp]Q04205TENS_CHICK - TENSIN		kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433358, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002, 56182575, 264259, 264906, 264784, 264289, 56182323, 264567
2066	85783402 (4131, 4132)	Novel Protein sim. GBank gij160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	

2067	95303882 (4133, 4134)				35698286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35686423, 35695855, 264558, 264404, 264563, 264488
2068	84344754 (4135, 4136)				264687
2069	84319177 (4137, 4138)	Novel Protein sim. GBank gi 3152862 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	60424179, 56182575, 22278995, 22278998, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656870, 264509, 264905, 56182435, 265009, 60433356, 87186559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906787, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87186516, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gi 5712131 gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35695817, 264805, 264628, 264808, 264638
2071	86846116 (4141, 4142)	Novel Protein sim. GBank gi 3551531 dbj BAA33016 - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265008, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	81718428 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264480, 60432049, 264259, 29331822, 29331824, 29331828, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27825684 (4145, 4146)	Novel Protein sim. GBank gi 1504026 dbj BAA13212 - (D86978) similar to C.elegans protein (Z37093) [Homo sapiens]		UNCLASSIFIED	264556
2074	84324767 (4147, 4148)	Novel Protein sim. GBank gi 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264809, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gij5138930jgblAAD40382.1) - (AF093680) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696288, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35698052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265008, 33837084, 264760, 264448, 264288, 264766, 264767, 264689, 21908768, 21908787, 21908769, 285021, 285022, 60170615, 33657023, 27486282, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)		UNCLASSIFIED		264592
2078	87539384 (4155, 4156)	Novel Protein sim. GBank gij4220590jdbjBAA74579j - (Q87908) nuclear protein np85 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger		29331825, 265017, 265018, 264288, 265020, 265021, 264634, 58528488
2079	88085916 (4157, 4158)	Novel Protein sim. GBank gij4240255jdbjBAA74906.1) - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281089, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gij2408021embjCAB16219.1) - (Z98162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264082, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94947186 (4161, 4162)	Novel Protein sim. GBank gij5524734jgblAAD44360.1)AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278998, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21908767, 21908768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gij3880558embjCAA94234j - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278998, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21908754, 265018, 265019, 264448, 264288, 264685, 21908769, 265020, 265022, 264691, 18108370, 85274791, 264631, 264555, 264563
2084	95186298 (4167, 4168)	Novel Protein sim. GBank gij728836spjP39193jALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	UNCLASSIFIED		285018, 264763, 264683, 264691

2085	94889476 (4169, 4170)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) pherophorin-S [Volvox carter]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264783, 264369, 264688, 264693, 18108370, 58182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936 - (Z48125) similarity to Trichostromyces colubiformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D38148 come...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264809, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35698423, 35695955, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264488
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi 3880830 emb CAA16334.1 - (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70897 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		UNCLASSIFIED	264488, 22278994, 35696286, 22278986, 29331827, 35696052, 33657402, 21908754, 33108954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21908765, 21906768, 21908767, 21908768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486285, 35698423, 35695855, 83373044, 87168518, 22279000, 264587
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin		18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278987, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 28331822, 20281099, 28331824, 28331825, 28331826, 29331827, 29331828, 35696052, 33696870, 29146498, 29146499, 264102, 264106, 264107, 264108, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265008, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21908754, 33657084, 55811385, 52644286, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21908765, 21908768, 21908767, 21908768, 29148827, 21908769, 55811957, 29148828, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690

2090	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264688, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265022, 80170615, 33857023, 35698423, 35695955, 264952, 18108387, 22279000
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gij4580997[gbjAAD24571.1]AF121081 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264488
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265008, 265007, 265009, 264910, 264598, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264680, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2094	91230928 (4187, 4188)	Novel Protein sim. GBank gij4929551[gbjAAD34036.1]AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35698286, 265017, 265018, 265019, 18108388
2095	95351528 (4189, 4190)	Novel Protein sim. GBank gij1383238[pirj]A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF000035) - Double-stranded RNA binding motif	dna_ma_bind	35696286, 52844045, 265008, 265007, 265008, 87168559, 18108351, 21906769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94118760 (4191, 4192)	Novel Protein sim. GBank gij3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278998, 22278997, 22278999, 264259, 60432289, 29331828, 35698052, 264107, 264508, 264509, 264905, 264806, 264907, 264908, 52844045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433358, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52844150, 264691, 264692, 33657023, 264693, 27486261, 35695783, 264628, 264629, 35698423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264488, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi 5174501 ref NP_000051.1 pLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	Transcript factor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170615, 264892, 33657109, 18108370, 264636, 264483 56994075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi 4758209 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412827 (4197, 4198)	Novel Protein sim. GBank gi 2695659 (AF028954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332856 (4199, 4200)	Novel Protein sim. GBank gi 3881189 emb CAB16514 - (Z98281) similar to ADP-ribosylation factor; cDNA EST EMBL-C08179 comes from this gene; cDNA EST EMBL-C08337 comes from this gene; cDNA EST EMBL-C09829 comes from this gene; cDNA EST yk4... comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nuc_rept	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264908, 265008, 265009, 264910, 264591, 60432229, 60433356, 33857402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264782, 264448, 264369, 264288, 18108355, 264886, 21908785, 21906787, 21908788, 21906769, 265020, 265021, 33857023, 18108374, 35896423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002 264091, 29331824, 264105, 265007, 285010, 18108380
2101	87782604 (4201, 4202)	Novel Protein sim. GBank gi 4589468 dbj BAA78761.1 - (AB012809) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi 3874148 emb CAA97423.1 - (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35886286, 264259, 35896052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264805, 264780, 18108351, 264448, 264784, 264288, 264787, 264788, 21908789, 35895917, 18108374, 264634, 264555, 264559, 264563, 264482, 264486
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi 4240159 dbj BAA74858.1 - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35896052, 29331828, 68712502, 265008, 60170631, 264595, 33109954, 85658542, 87168559, 285017, 265019, 264448, 21908785, 21908788, 265022, 33857023, 27488262, 33857348, 35895783, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264584
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gl 1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g8.3; coded for by C. elegans cDNA CEMSE10F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65n8.3; coded for by C. elegans cDNA yk65n8....		UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33857402, 60433356, 264595, 60433438, 264758, 33657084, 87188474, 265010, 87188559, 265017, 265018, 265019, 264782, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21908785, 21908786, 21908787, 21908788, 21908789, 35695917, 285020, 285022, 80170615, 52844150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274781, 35695855, 264635, 60170394, 264638, 264558, 18108385, 18108387, 56526486, 87188518, 60432113, 264564, 264566, 264567
2106	83365475 (4211, 4212)				265008, 265019
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gl 3881524 emb CAA93883 - (Z70038) ZK1087.4 [Caenorhabditis elegans]			264906, 264639
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gl 3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264908, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264784, 264786, 264787, 264788, 264789, 264693, 264628, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264486
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264789, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gl 481043 pir S37671 - bat2 protein - human		UNCLASSIFIED	264594
2111	87818418 (4221, 4222)	Novel Protein sim. GBank gl 2143639 pir I56542 - calmodulin-binding protein - rat		UNCLASSIFIED	264788, 35695917, 264630, 264587, 264486
2112	87283783 (4223, 4224)	Novel Protein sim. GBank gl 426629 gb AA020459 - (AF100960) protocadherin [Rattus norvegicus]	Contains protein domain (PF00069) - struct		264508, 264606, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gl 3327184 db BAA31660 - (AB014585) KIAA0685 protein [Homo sapiens]	Eukaryotic protein domain (PF00028) - cadherin		265008
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gl 3327184 db BAA31660 - (AB014585) KIAA0685 protein [Homo sapiens]	Cadherin domain		66714117, 28331826, 29331827, 60433438, 55812038, 265017, 265019, 264688, 21908789, 55811957, 265020, 265021, 33657109, 60170394, 264558
2115	80883785 (4229, 4230)	Novel Protein sim. GBank gl 4757890 refNP_004328.1 pC8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264689, 264691, 264692, 60432113

2116	88258387 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35696286, 22278999, 56182181, 28331824, 29331825, 29331827, 35696052, 284907, 56182435, 285008, 264591, 55812038, 55811386, 87168558, 264288, 264389, 21908769, 28148629, 33857023, 35895763, 55811576, 35898423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 284511, 285009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 58526486, 284482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1078307 [prij]B56573 - nuclear pore complex glycoprotein p82 - African clawed frog		glycoprotein	284259, 284905, 284807, 284808, 284510, 284511, 285009, 284910, 285010, 284602, 284288, 264768, 264683, 283987, 263972, 284638, 284559
2119	86988317 (4237, 4238)	Novel Protein sim. GBank gij4321407 [gbj]AAD15748 - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87788395 (4239, 4240)	Novel Protein sim. GBank gij488527 [refj]NP_005480.1 [pNSP3 - novel SH2-containing protein 3]	Contains protein domain (PF00017) - eph		264091, 264259, 28331826, 28331828, 265017, 284804, 284288, 264685, 265020, 284691, 18108370, 55810764, 264555, 284638, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij4757728 [refj]NP_004886.1 [pAGTA - angiotensin vasopressin receptor AII/AVP-like]		UNCLASSIFIED	284601, 264766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gij4929551 [gbj]AAD34036.1 [AF151799] CGI-40 protein [Homo sapiens]			18108384, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 284907, 56182435, 265007, 284910, 265010, 265018, 284886, 265020, 55811576, 284555, 264637, 18108382, 83373044, 18108383, 18108384, 58526486, 284585, 284587
2123	86787988 (4245, 4246)	Novel Protein sim. GBank gij2224551 [dbj]BAA20784 - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108388, 264757, 285011, 18108351, 284691, 284634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij5689455 [dbj]BAA63011.1 - (AB028882) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 284908, 284907, 264591, 284639, 284583
2125	85354041 (4249, 4250)	Novel Protein sim. GBank gij728831 [spj]P39188 [ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]		UNCLASSIFIED	284259, 284509, 264907, 284511, 85658542, 284763, 21908765, 35895917, 264638, 284488
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij4539264 [embj]CAB38853.1 - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284488, 284489, 28331827, 35696052, 264905, 284509, 284808, 284809, 284510, 265009, 284591, 264592, 284593, 33857402, 284594, 284595, 284596, 284759, 284601, 284803, 285018, 284804, 284605, 284780, 284681, 284782, 284683, 284784, 284684, 284288, 264685, 264689, 60170815, 33857023, 33857108, 55810764, 284635, 284636, 284637, 264638, 284639, 83373044, 284564, 284568

2127	81118652 (4253, 4254)	Novel Protein sim. GBank g k468435 gb AAD31315.1 AF143236 apoptosis related protein APR-2 [Homo sapiens]			35696288, 29331828, 35696052, 284508, 284509, 284905, 284806, 284907, 284908, 284909, 284510, 285006, 284511, 284512, 285007, 285009, 284910, 284758, 285011, 284800, 284601, 284604, 284782, 284783, 284786, 284687, 284788, 284789, 284689, 35695917, 284690, 284691, 284692, 284693, 284629, 18108374, 35695855, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 18108385, 284563, 284564, 284567, 56182575, 35696288, 56182181, 29331824, 60432289, 35696052, 284905, 284907, 66712502, 284908, 284909, 284510, 284512, 285009, 284910, 284591, 55812038, 285018, 284784, 284288, 284389, 284687, 284788, 55811957, 284692, 18108388, 284628, 284632, 284634, 284635, 284637, 56182323, 284639, 18108384, 18108388, 284563, 284567
2128	87414262 (4255, 4256)				66714117, 284828, 284595, 55812038, 55811150, 55811857, 284693, 18108374, 283878, 65274791, 18108381, 83373044, 22279000 283981
2129	95102089 (4257, 4258)		UNCLASSIFIED		
2130	95417144 (4259, 4260)	Novel Protein sim. GBank g j2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		
2131	85723065 (4261, 4262)	Novel Protein sim. GBank g j1068886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	potassium_channel		
2132	85361086 (4263, 4264)	Novel Protein sim. GBank g j5689373 db BAA82973.1 - (AB028944) KIAA1021 protein [Homo sapiens]	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies) Contains protein domain (PF00122) - E1-E2 ATPase		284488, 22278998, 264259, 29331827, 29331828, 35696052, 284509, 284805, 284908, 284907, 284909, 284909, 284510, 285008, 284511, 285007, 284910, 284591, 284592, 284595, 284758, 21908754, 33108954, 87168474, 265011, 284600, 284601, 284605, 285018, 284760, 18108351, 284681, 284782, 284784, 284288, 284684, 284786, 284686, 284687, 284788, 284789, 284888, 21908789, 284690, 52644150, 284691, 284693, 18108370, 284828, 284629, 18108372, 18108374, 35696423, 35695855, 284631, 284634, 284635, 284638, 284555, 284637, 18108380, 284639, 284558, 56182323, 56526486, 284564, 284565, 284566, 284567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gij4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	50424179, 52646365, 52646842, 56994075, 35986286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331828, 29331828, 35990552, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109954, 21908754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264369, 264288, 52644228, 56181562, 21906785, 21906786, 21906787, 21906788, 21906789, 55811957, 35985917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35986423, 65274791, 35985855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264583, 264588
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gij3875351jembj(CAB09415) - (Z96047) DY3.6 [Caenorhabditis elegans]			56181688, 35986286, 21906754, 55811386, 265011, 265017, 18108351, 264765, 264786, 264688, 21908788, 35985917, 265020, 33657023, 264628, 35985855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	86078813 (4269, 4270)	Novel Protein sim. GBank gij5689559jdbj(BAA03063.1) - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278998, 29331828, 35986052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87188559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35985763, 264629, 35985855, 264631, 264635, 264638, 264637, 56182323, 264639, 22279002, 264564
2136	84346479 (4271, 4272)	Novel Protein sim. GBank gij2662167jdbj(BAA23715) - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gij4894110jembj(CAB43262.1) - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264559, 264909, 33109954, 264763, 21908788, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gij5174779jgbj(AA0X0696.1) - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase_associated	264259, 29331828, 35986052, 264909, 265006, 265017, 265018, 18108351, 264288, 21908766, 33657023, 33657109, 264628, 18108374, 35985855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gij3650821jembj(CAA77135) - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 85658542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108364, 55811578, 83373044, 18108385, 56528486, 264482

2140	87645655 (4279, 4280)	Novel Protein sim. GBank gi 4417203 gb AAD204181 - (AC007019) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	284488, 284259, 29331824, 264104, 264109, 284508, 285006, 284759, 265018, 264448, 284288, 21906768, 55811957, 285021, 33657023, 27486265, 35698423, 284636, 284558, 284557, 284559, 284588
2141	79623886 (4281, 4282)		UNCLASSIFIED	265020, 284893
2142	80041222 (4283, 4284)		UNCLASSIFIED	283978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gi 2135766 pir S53362 - mudn 5AC (clone JER47) - human (fragment)	UNCLASSIFIED	22278997, 28331827, 284907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gi 2076483 (U43200) - antifreeze glycopetide AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	65274572, 284259, 28331824, 28331827, 284908, 284908, 284591, 285011, 87188559, 284600, 265019, 284288, 284768, 21906765, 21908787, 55811576, 35698423, 65274791, 22279002
2145	20564305 (4289, 4290)		UNCLASSIFIED	283978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gi 1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]	UNCLASSIFIED	284908, 60433356, 284688
2147	80432811 (4293, 4294)	Novel Protein sim. GBank gi 3080398 emb CAA18718.1 - (AL022603) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	284907, 284768, 284768, 18108365
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED	284593
2149	87382022 (4297, 4298)	Novel Protein sim. GBank gi 119863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	glycoprotein	28331824, 28331826, 35698052, 284758, 87188474, 265018, 52844150, 33657109
2150	84140059 (4299, 4300)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	22278998, 28331822, 28331824, 28331826, 284784, 284789, 21906768, 284488
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gi 5689407 dbj BAAB2987.1 - (AB028958) KIAA1035 protein [Homo sapiens]		22278998, 56984075, 22278999, 60432049, 284259, 29331822, 28331824, 28331826, 35698052, 28331828, 284508, 284511, 80433356, 284758, 284598, 33109954, 60174639, 265010, 265011, 87188559, 265017, 265018, 265019, 264448, 264288, 284688, 21906765, 21908768, 21908788, 285020, 60170815, 33657109, 33657182, 33657349, 18108370, 284635, 284557, 60170394, 18108385, 87188518, 22278000, 18108397, 18108388, 285007, 284591, 285011, 18108351, 18108386, 18108374, 18108388
2152	76321840 (4303, 4304)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gll4758704/rei NP_004216.1 pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 52646842, 22278986, 22278988, 22278989, 264259, 26331822, 35680052, 264508, 264508, 264905, 264906, 264807, 264908, 264908, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264389, 264766, 264687, 264789, 52644229, 21906786, 21906788, 35685917, 33657023, 33657109, 35685855, 264631, 264632, 264635, 264638, 264639, 18108385, 264483, 264564, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gll225150 prl 1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56894075, 264094, 265009, 265019, 264288, 21906787, 35695917
2155	87424072 (4308, 4310)			UNCLASSIFIED	18108392, 18108398, 22278986, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264688, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gll3970966 (AC004974) - spa-1- like; similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gll1076211 prl S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gll4650844 dbj BAA77027.1 - (AB026180) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain		264596
2159	80083728 (4317, 4318)	Novel Protein sim. GBank gll2879925 dbj BAA24826 - (AB007897) KIAA0437 [Homo sapiens]			29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4318, 4320)				264634
2161	87739131 (4321, 4322)	Novel Protein sim. GBank gll1504006 dbj BAA13202 - (D88966) similar to human ZFY protein. [Homo sapiens]		UNCLASSIFIED	265008
2162	94318526 (4323, 4324)			UNCLASSIFIED	65274572, 264508, 264805, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264683, 264784, 264288, 264766, 264686, 264788, 264789, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264586, 264587
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gll3876537 emb CAA98270 - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278988, 264093, 264683, 33657023, 65274820, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	84329169 (4329, 4330)	Novel Protein sim. GBank gij1086784 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278998, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 29331830, 56182435, 285009, 21908754, 33657084, 265011, 265019, 264448, 264288, 264369, 21908785, 21908788, 21908789, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22279002, 264587
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gij2706522[emb]CAA75816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]		ubiquitin	52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21908785, 21908787, 21908788, 21908789, 265021, 265022, 264693, 27466282, 35695783, 18108376, 56528486, 87168518, 264587
2167	87718864 (4333, 4334)	Novel Protein sim. GBank gij2224713[jdb]BAA20840] - (AB002384) KIAA0388 [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 29146498, 56182435, 265008, 265009, 264592, 264593, 33657402, 33109854, 265011, 265017, 265018, 18108351, 264369, 21908784, 21908785, 21908788, 29148627, 21908789, 52644150, 33657109, 35696423, 18108361, 18108384, 18108385, 60432113, 264587
2168	86999334 (4335, 4336)	Novel Protein sim. GBank gij4321407[gb]AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	66714117, 29331827, 264907, 264511, 264591, 265018, 264784, 264683, 264786, 264768, 264566
2169	87686937 (4337, 4338)	Novel Protein sim. GBank gij5106521[gb]AAD39741.1[AF10536] K-Ci cat transporter KCC4 [Homo sapiens]		UNCLASSIFIED	264629, 264555, 264559
2170	84141033 (4339, 4340)	Novel Protein sim. GBank gij5106521[gb]AAD39741.1[AF10536] K-Ci cat transporter KCC4 [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264908, 56182435, 60433438, 55812038, 264596, 55811388, 265018, 264782, 264763, 264448, 264764, 264684, 264286, 264788, 264685, 56181562, 264689, 55811857, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 67168518, 60432113, 264584
2171	80194050 (4341, 4342)			UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)			UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gij4309681[gb]AAD15478] - (AC006930) R33423.1 [Homo sapiens]		UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gij2493778[sp]Q08456[YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5]			264908, 35695855, 264555, 264557

2175	84325850 (4349, 4350)	Novel Protein sim. GBank g 1263287 (U47855) - fibrin-3 [Araeus diadematus]		UNCLASSIFIED	264488, 35686286, 20281099, 29331826, 80432289, 35686052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 285008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264800, 264803, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21806788, 55811957, 35685917, 265020, 265022, 264691, 264682, 33657023, 264693, 264628, 264629, 55811576, 35686423, 65274791, 35685855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264584, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank g 728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncopene	52644507, 52646842, 22278994, 35686286, 22278996, 22278999, 29331826, 29331827, 35686052, 29331828, 33656970, 29331830, 264910, 33657402, 264758, 52644296, 87188559, 265016, 264689, 21806785, 21906787, 21906788, 35685917, 52644150, 264890, 33657023, 33657109, 52645129, 33657182, 27466261, 27466262, 33657349, 18108376, 18108377, 35685855, 87188518, 60432113, 264404, 22279000, 264486
2177	64128942 (4353, 4354)	Novel Protein sim. GBank g 5454072 ref NP_006416.1 pSLU7 - step II splicing factor SLU7		kinase	18108392, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264786, 264689, 21906787, 21906788, 21906789, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2178	87601557 (4355, 4356)	Novel Protein sim. GBank g 1473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644286, 87188474, 18108370, 35685855, 22279002
2179	87316275 (4357, 4358)			UNCLASSIFIED	60424289, 264760, 264628, 264632

2180	95351397 (4359, 4380)	Novel Protein sim. GBank gij3122317[sp]p90648[KMHB_DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35698423, 35698585, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486, 29331827, 264369, 18108376, 264564
2181	85764830 (4361, 4382)	Novel Protein sim. GBank gij3024689[sp]Q15542[T2DA_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)]		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278996, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264784, 264288, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002 264760
2183	85460849 (4365, 4366)	Novel Protein sim. GBank gij3873408[gb]AAC7482.1] - (U17129) unknown [Rhodococcus erythropolis]		tnf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557 29331824, 264907, 66712502, 264757, 265019, 264288, 264682, 56526486
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gij3114713 (AF081346) - Edp1 protein [Mus musculus]			
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gij5106956[gb]AAD39908.1[AF11381] - (AF113815) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gij2864625[emb]CAA16872] - (AL021811) putative protein [Arabidopsis thaliana]		ATPase associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264766, 55811957, 33657023, 55811576, 56182323, 264563
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265018, 264762, 264681, 264766, 264769, 35695917, 264692, 35698423, 264631, 264635, 264637, 18108388, 264566, 264486, 18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gij5107816[gb]AAD0129.1[AF14941] - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gij3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263987

2190	87639197 (4379, 4380)	Novel Protein sim. GBank gi 132575 sp P29315 RINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278998, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52644286, 265010, 265018, 264685, 264686, 56161562, 21908769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gi 5327002 emb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264558, 264559, 264558
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gi 482600 sp P34400 MI10 CAEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		
2193	84140073 (4385, 4386)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181666, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274791, 35695855, 60431650, 56182323, 60432113, 264592
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gi 2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gi 2832783 emb CAA15685.1 - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /motif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278998, 22278999, 35696052, 265008, 21908754, 265017, 35695917, 265021, 265022, 35695855
2196	95091831 (4391, 4392)	Novel Protein sim. GBank gi 5262487 emb CAB45699.1 - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696266, 22278997, 22278999, 264259, 29331822, 68714117, 60432289, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21908765, 21908768, 21908767, 35695917, 265022, 264691, 33657023, 264893, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264638, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gi 4829567 gb AAD34044.1 AF151807 CGI-49 protein [Homo sapiens]			264768, 264768, 21908765, 21908768, 21908767, 29148827, 55811857, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264768, 63373044, 21908754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88060914 (4395, 4396)	Novel Protein sim. GBank gi 3548787 (AC005622) - R30853.1 [Homo sapiens]		UNCLASSIFIED	

2198	88054355 (4397, 4398)	Novel Protein sim. GBank glj2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]				284105, 284110, 284112, 284688, 55811957, 33857023, 284892, 283967, 20281071, 56526486
2200	87405385 (4389, 4400)	Novel Protein sim. GBank glj3043634(dbjBAA35481) - (AB011127) KIAA0555 protein [Homo sapiens]	struc			29331824, 284783, 284788
2201	94316872 (4401, 4402)	Novel Protein sim. GBank glj3913470(spj057314)DHXB_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00108) - short chain dehydrogenase			29331824, 35698052, 284905, 284907, 33857402, 55811388, 285017, 285018, 285019, 284288, 21908768, 35695917, 285020, 285022, 33857023, 33857109, 27486261, 18108370, 35698423, 35695855, 284555, 284558, 83373044, 87188518, 60432113
2202	81672385 (4403, 4404)	Novel Protein sim. GBank glj5262665(femb)CAB45767.1) - (AL080188) hypothetical protein [Homo sapiens]	UNCLASSIFIED			284489, 284259, 29331824, 60432289, 35698052, 284905, 284909, 284592, 285017, 285018, 285019, 18108351, 284782, 284448, 264389, 284288, 264768, 21908765, 21908768, 284890, 284691, 284692, 33857109, 284634, 284636, 284555, 284639, 284558, 284559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank glj1172845(spjP48629)R825_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - glycoprotein Ras family			52846385, 56994075, 284259, 29331822, 29331828, 29331827, 29331828, 284910, 285010, 285011, 87188559, 285018, 285019, 284605, 284288, 21908768, 35695917, 33857023, 284892, 33857109, 35695763, 18108378, 284638, 22279000, 284586, 284567
2204	88088871 (4407, 4408)	Novel Protein sim. GBank glj121036(spjP29348)GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED		
2205	84147588 (4408, 4410)	Novel Protein sim. GBank glj4589480(dbjBAA76788.1) - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - dna_rna_bind Zinc finger, C2H2 type			18108394, 18108397, 56182575, 60432049, 284259, 29331822, 29331824, 29331825, 29331828, 29331827, 284906, 285007, 285008, 285009, 60432228, 285010, 285011, 285018, 284883, 284288, 284369, 284886, 21908768, 21908768, 21908769, 284890, 284891, 284893, 18108388, 55811576, 65274791, 284634, 18108381, 18108384, 60432113, 22279002, 284563, 284586, 284591
2206	20820008 (4411, 4412)	Novel Protein sim. GBank glj4557753(rej)NP_000372.1pMID1 - midline 1 protein	Contains protein domain (PF00822) - SPRY domain	UNCLASSIFIED		29331822, 56182181, 29331827, 35698052, 52844045, 285008, 285019, 56181562, 55811957, 285021, 33857023, 35695763, 35695855, 60170394, 60432113, 284586
2208	86100830 (4415, 4416)	Novel Protein sim. GBank glj3986746 (AF105228) - tuftelin [Bos taurus]				284908, 285019, 18108351, 21906769
2209	87800420 (4417, 4418)		struc			284112, 285009, 284891, 18108385, 18108374, 284634, 20281166

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	284603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39184 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	284685, 284686, 18108365, 22278002, 284482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214 - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278998, 264092, 264094, 29331822, 66714117, 29331826, 29331828, 264907, 52844045, 285009, 60170831, 21908754, 87188559, 285017, 265019, 18108351, 284683, 18108354, 264389, 264786, 264687, 52644229, 21908765, 21908786, 21908787, 21908788, 265021, 33657109, 18108370, 18108374, 284638, 56182323, 18108384, 18108387, 87168518, 284585
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278998, 22278997, 35896052, 284805, 66712502, 264808, 264828, 58182435, 264112, 265008, 60431735, 60433438, 21908754, 265010, 285011, 285017, 265018, 265019, 18108351, 264785, 21908765, 21908788, 21908789, 265020, 265021, 284693, 264628, 263974, 263976, 18108378, 55811578, 264556, 264637, 284558, 83373044, 22278002, 284482, 264483

2214	85361453 (4427, 4428)	Novel Protein sim. GBank glj4504325[refJNP_000173.1]pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketocoyl-Coenzyme A (thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	284486, 52844507, 18108394, 56182575, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 284490, 60432049, 264259, 52645080, 28331822, 28147620, 28331824, 66714117, 28331825, 60432289, 28331826, 28331827, 35696052, 29331828, 20281100, 284509, 284907, 66712502, 264908, 29331830, 52844045, 56182435, 264510, 285008, 284511, 284512, 265007, 265008, 265009, 60170831, 284593, 60433358, 60433438, 33109954, 33657084, 52844298, 87188474, 285010, 285011, 87168559, 264601, 265017, 265018, 265019, 18108351, 284448, 284682, 264763, 284288, 284687, 52844229, 284689, 21906765, 21906768, 21906787, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170815, 264690, 52844150, 284691, 33657023, 264692, 18108364, 33657109, 33657182, 27486282, 27486264, 27486285, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35698423, 35695655, 264634, 284636, 52844332, 284638, 284558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22278002, 264482, 284584, 284585, 284586, 284908, 265008, 264555, 264558, 87188518
2215	85419206 (4429, 4430)	Novel Protein sim. GBank glj1847160 (AF000288) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614048 (4431, 4432)	Novel Protein sim. GBank glj1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388288) [Caenorhabditis elegans]		
2217	80589404 (4433, 4434)	Novel Protein sim. GBank glj5031707[refJNP_005503.1]pGARP - glycoprotein A repetitions predominant	UNCLASSIFIED	284683
2218	85518254 (4435, 4436)	Novel Protein sim. GBank glj387863[embjCAA88953] - [Z49128] similar to cAMP-dependent protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk485d8.3 comes from this gene; cDNA EST yk485d8.5 comes from this gene; cDNA EST yk492f4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00560) - Leucine Rich Repeat	284288, 33657109, 284556
2219	87614048 (4437, 4438)	Novel Protein sim. GBank glj1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388288) [Caenorhabditis elegans]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 284563
			Contains protein domain (PF01983) - TraB family	284682, 284683, 284688, 284689, 284693, 18108370, 18108378

2220	95354185 (4439, 4440)	Novel Protein sim. GBank gi 4507261 ref NP_003145.1 pSTAT - statherin			264488, 18108394, 18108395, 35695286, 264259, 264097, 60432289, 264508, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264758, 85858542, 265010, 264601, 264803, 265019, 264605, 264760, 264762, 264448, 264764, 264369, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264568, 264488, 264567
2221	88060827 (4441, 4442)	Novel Protein sim. GBank gi 3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425882 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	85091849 (4445, 4446)			UNCLASSIFIED	265010, 264885, 264890, 264683, 264628, 263974, 263976, 55811576, 264555, 264636, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gi 3876005 emb CAA04799 - (Z35719) cDNA EST EMBL:D87419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01858) - Domain of unknown function	UNCLASSIFIED	264258, 264509, 56182435, 265008, 265009, 265008, 264757, 21908754, 18108351, 264883, 18108374, 18108385
2225	85748484 (4449, 4450)	Novel Protein sim. GBank gi 1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]		transport	22278994, 22278995, 22278999, 52844045, 264600, 265019, 21908785, 21908789
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gi 4828524 emb CAB2852.1 - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 264806, 265007, 264681, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265008, 265008, 18108354, 29148629, 29148784, 27488261, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gi 806976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264081, 264082, 264084, 29331822, 29331825, 66714117, 264693, 263972, 264639, 83373044, 264583
2228	88060831 (4457, 4458)	Novel Protein sim. GBank gi 3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342815 (4459, 4460)	Novel Protein sim. GBank gij226154[prfj1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264788, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35698423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060837 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328_1 [Homo sapiens]		UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316[gblAAD41476.1(AF133124) transcription factor IIC63 [Homo sapiens]		transcript factor	18108394, 56182575, 22278995, 35698286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264369, 264288, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 26148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264584, 264908, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385, 56182435, 264369, 264686, 21906765, 265020, 264693, 264556, 56526486
2233	87755282 (4465, 4466)	Novel Protein sim. GBank gij4249733[gblAAD13760] - (AF109377) ldlBp [Mus musculus]			
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559[spjP54352]EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)	kinase		
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gij4972734[gblAAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675[prfjB53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	eph	264569, 264487, 264769, 21906765, 264259, 60432049, 264691, 29331828, 60432289, 20281149, 264908, 264907, 264511, 265008, 265009, 264634, 264635, 264638, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734[gblAAD34762.1] - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22278002, 264482, 18108351, 264288

2238	94998857 (4475, 4478)		Contains protein domain (PF00286) - Viral coat protein		284508, 264907, 284629, 284634, 284564
2239	87798688 (4477, 4478)				29331825, 285009, 284389, 33657109, 18108370, 18108374, 284557, 284559, 284488, 65274572, 56182575, 35686286, 22278997, 22278999, 284259, 29331827, 35690052, 284508, 52844045, 56182435, 284511, 285007, 285008, 265009, 60433356, 60433438, 55812038, 21908754, 33657094, 55811396, 285018, 265019, 18108351, 284683, 284288, 284788, 284687, 284688, 284789, 21908765, 21908768, 21908769, 35695917, 285021, 285022, 60170815, 52844150, 33657023, 33657182, 33657349, 35685763, 18108370, 35686423, 35685855, 67168518, 22279000
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gi2882311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	
2241	60091951 (4481, 4482)				
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gi2484312 sp P70541 E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)		UNCLASSIFIED synthase	22278995, 22278996, 22278997, 22278998, 284259, 29331822, 29331824, 29331826, 29331827, 29331828, 284509, 285007, 285009, 284596, 21908754, 265010, 265011, 285017, 265018, 265019, 284448, 284389, 284288, 52844228, 21908765, 21908768, 21908767, 21908768, 21908769, 285020, 285021, 33657109, 27488282, 27486284, 18108374, 35685855, 284634, 284637, 56182323, 63373044, 56528486, 67168518, 284564
2243	78802026 (4485, 4486)			UNCLASSIFIED	285008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gi2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]		UNCLASSIFIED	284604
2245	85316545 (4489, 4490)	Novel Protein sim. GBank gi470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	52845156, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331827, 284907, 284512, 60433438, 284758, 21908754, 265011, 284603, 284764, 284687, 21908767, 21908768, 21908769, 55811957, 265022, 284689, 284629, 35686423, 284638, 18108387, 60432113, 22279000, 22279002, 284568

2248	94848710 (4481, 4482)	Novel Protein sim. GBank gi 4986096 dbj BAA78326.1 - (AB028089) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696288, 22278996, 22278997, 22278999, 284259, 35698052, 284108, 284905, 284907, 285008, 285007, 285008, 80433438, 33108854, 87168559, 285018, 285019, 284288, 21908765, 21908767, 21908769, 21908769, 55811957, 35695917, 285020, 285022, 27486284, 18108370, 18108374, 85274791, 35695955, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gi 654063 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52845156, 52846385, 52845080, 35696052, 33656970, 52846317, 33657084, 285017, 21908768, 21908769, 35695917, 33657109, 52845129, 33657182, 27486261, 27486282, 33657349, 27486285, 18108387
2246	95412986 (4495, 4496)	Novel Protein sim. GBank gi 4758502 ref NP_004123.1 pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calthepsin	284488, 284259, 284907, 29331830, 284909, 285007, 285009, 284595, 21908754, 65274444, 284803, 285019, 284782, 284448, 284288, 284689, 21908768, 55811957, 265021, 284691, 18108374, 284634, 284635, 284636, 284555, 284638, 284557, 284558, 284559, 18108383, 83373044, 18108385, 284488
2249	84685662 (4497, 4498)	Novel Protein sim. GBank gi 4038461 AF107772 - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	284766, 284628, 284636, 284637
2250	79827508 (4499, 4500)	Novel Protein sim. GBank gi 3738140 emb CAA21241 - (AL031852) valyl-tRNA synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	284908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gi 3218467 emb CAA07090.1 - (AJ008529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	284259, 35696052, 284508, 58182435, 285009, 284592, 284593, 284780, 284448, 284694, 284288, 284690, 284628, 55811578, 284555, 284558, 284557, 284558, 284559, 284588
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gi 4929325 gb AAD33953.1 AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	284092, 284094, 284259, 29331822, 68714117, 28331828, 284102, 284103, 284104, 284105, 284109, 284112, 284511, 285007, 60433358, 285010, 18108351, 21908767, 21908768, 284691, 283974, 263977, 284488, 284587
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 285019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gi 4502847 refNP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284569, 18108394, 18108398, 56182575, 56994075, 35696296, 22278998, 284084, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 264108, 264508, 284509, 284808, 264907, 29331830, 66712502, 284908, 284909, 284510, 265006, 284511, 265007, 265008, 265009, 60170831, 60432229, 60433336, 60433438, 264758, 65858542, 265010, 265011, 87168558, 265017, 265018, 265019, 284448, 264764, 284288, 284369, 264768, 284686, 264768, 264769, 21908765, 21908767, 55811957, 264691, 33857023, 284692, 18108362, 65274620, 263989, 284628, 18108370, 60431528, 263972, 284629, 18108372, 18108377, 18108379, 55811576, 35696423, 35895855, 284630, 284634, 284635, 284636, 284556, 263981, 264638, 56182323, 60170394, 284558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 284482, 284584, 284585, 284486, 284587, 18108391
2255	81010546 (4509, 4510)	Novel Protein sim. GBank gi 5541865 emb CAB51072.1 - (AL098858) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	bind	65274572, 56182575, 22278997, 22278999, 284259, 29331822, 29331825, 29331828, 29331827, 29331828, 284508, 264905, 284908, 264907, 66712502, 284908, 56182435, 284510, 284511, 285008, 284593, 284595, 21908754, 33109954, 87168474, 265011, 265017, 265019, 284682, 264764, 284389, 284288, 264768, 284685, 284686, 284768, 21908765, 21908766, 21908768, 21908769, 265020, 60170815, 52644150, 284690, 284692, 284693, 33857109, 33657349, 264632, 284636, 52644332, 56182323, 22279000, 22279002 284768, 264689, 18108374
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gi 3327174 dbj BAA31655 - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 284681, 21908765, 21908768, 264587
2257	80086235 (4513, 4514)			UNCLASSIFIED	284808, 264592, 264764
2258	80900518 (4515, 4516)	Novel Protein sim. GBank gi 3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	

2259	95384155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB43278.1 - (AL050110) hypothetical protein [Homo sapiens]	UNCLASSIFIED	18108386, 65274572, 56182575, 22278897, 22278898, 264258, 29331822, 29331827, 284905, 66712502, 284908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87168559, 18108351, 264448, 264683, 264288, 264389, 56181582, 265021, 60170815, 264890, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482, 56182575, 265020, 284905, 264908, 264908, 35996423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264583
2260	88084119 (4518, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB008086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00009) - oxidase Thrombospondin type 1 domain	
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334526 emb CAA16138 - (AL021308) predicted using FGENEH [Homo sapiens]	UNCLASSIFIED	
2262	91698282 (4523, 4524)	Novel Protein sim. GBank gi 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]		56182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35996052, 264508, 66712502, 52644045, 56182435, 265008, 265008, 60433356, 55812038, 265010, 265017, 265018, 264288, 264369, 21908785, 21908787, 55811957, 35695917, 52644150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003872) - hypothetical protein [Arabidopsis thaliana]		22278894, 22278897, 264907, 264828, 52644150, 18108361, 264893, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657601 (U66220) - unknown [Nannocystis exedens]	UNCLASSIFIED	264686, 264488, 264768, 264769, 264681, 264508, 264905, 264509, 264908, 264907, 264908, 264809, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264638, 264757, 264758, 18108385, 265011, 264760, 264584, 264585, 264764, 264586, 264488, 264768
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir JA48018 - mucin 7 precursor, salivary - human	UNCLASSIFIED	264689, 264910, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Zinc finger, C2H2 type Contains protein domain (PF01305) - ribosomal protein L15 amino terminal region	22278895, 22278897, 22278899, 264258, 265008, 265007, 265009, 60433438, 21908754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21908785, 21908788, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264568, 264487

2267	87395638 (4533, 4534)	Novel Protein sim. GBank gi 3560229 emb CAA20687.1 - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35686286, 264259, 29331824, 29331825, 35686052, 29331828, 264905, 284508, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33857402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52844229, 35695917, 264691, 33657023, 18108382, 33657109, 35696423, 264634, 18108381, 87188518, 264568
2268	85683687 (4535, 4536)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		cadherin	264488, 264259, 284509, 264595, 265010, 265017, 264768, 18108385, 264488
2269	88177877 (4537, 4538)	Novel Protein sim. GBank gi 103418 p J17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	56182575, 60432049, 265007, 265009, 264591, 87188558, 264605, 18108351, 21908764, 265020, 264628, 60431528, 264638, 18108385, 18108387, 60432113, 264763
2270	80410327 (4539, 4540)				
2271	91010392 (4541, 4542)			cyto450	264909, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2272	84208220 (4543, 4544)			UNCLASSIFIED	264905, 264908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gi 4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278986, 22278989, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 285008, 264593, 60433438, 21906754, 265016, 264689, 21906765, 21906768, 21908767, 21908769, 265021, 265022, 60170815, 264691, 33657023, 264693, 33657109, 27486264, 18108378, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gi 1480112 emb CAA67881 - (X99842) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278987, 22278989, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 284511, 265008, 265009, 60170831, 264591, 21908754, 33109894, 265011, 265016, 18108351, 264448, 264288, 264684, 264768, 21908765, 21908768, 21908767, 21908769, 52644150, 264683, 18108384, 35695763, 18108374, 35696423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56528488, 87188518, 22279002
2275	88082501 (4548, 4550)	Novel Protein sim. GBank gi 3165406 (AC004755) - fos37502.2 [Homo sapiens]	Contains protein domain (PF00122) - transport E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)			UNCLASSIFIED	264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D48802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278999, 35898052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22279002
2278	94133078 (4555, 4556)	Novel Protein sim. GBank gi 2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108384, 22278997, 28331826, 60433356, 60433438, 21908754, 265018, 33657023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)				
2281	95283048 (4561, 4562)	Novel Protein sim. GBank gi 4240209 dbj BAA74928.1 - (AB020712) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33108954, 265010, 265019, 265020, 264092, 264259, 29331822, 29331824, 29331826, 35898052, 264107, 264906, 264909, 52844045, 265006, 33657402, 60433356, 264756, 265011, 265019, 264681, 264683, 264684, 264686, 21908765, 21908767, 21908768, 21908769, 60170615, 264680, 52844150, 18108382, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi 1537070 (U83840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87188474, 265019, 18108351, 21908767, 21908769, 55811957, 33657023, 52845128, 33657109, 33657182, 27486282, 263972, 55811576, 87188518, 20281189
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gi 2495729 sp Q82559 Y281 - HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35898286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35898052, 29148499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33108954, 33657084, 55811388, 87188474, 265010, 265011, 265018, 265019, 55811150, 264863, 264369, 264286, 264688, 21908765, 21908767, 21908768, 29148827, 21908769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810764, 18108379, 55811576, 35898423, 35895855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264567

2284	95414955 (4567, 4568)	Novel Protein sim. GBank gij2498797sp Q6431.1 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)			60424179, 52644507, 18108394, 52646842, 22278994, 35698286, 22278996, 22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 60432269, 29331826, 29331827, 35698052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87188559, 285018, 285019, 55811150, 264682, 264368, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35695917, 285020, 265021, 60170615, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35698423, 35695855, 60431850, 87188518, 60432113, 264482, 264584
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gj13342234 (U93809) - nuclear antigen EBNA-1 [Cercopithecina herpesvirus 15]	collagen		35698052, 264905, 264807, 264808, 264809, 264512, 265009, 264910, 264595, 264780, 18108351, 264682, 264783, 264685, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gj13873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]	kinase		35698286, 56182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87188474, 35695917, 264692, 55811576, 264555, 264557
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gj1630905 prj1542731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	UNCLASSIFIED	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gij728632 sp P39188 ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III!	Im7		22278995, 56994075, 22278997, 22278998, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21908765, 21908766, 21908767, 21908768, 33657023, 264557, 22279000, 22278002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gj12887497 (AC004144) - R34001_1 [Homo sapiens]	kinase	Contains protein domain (PF00400) - WD domain, G-beta repeat	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gj12887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00400) - WD domain, G-beta repeat	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gj13253120 (AC005175) - R31449_3 [Homo sapiens]	strucd		18108394, 264807, 265006, 265008, 33108994, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328834 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1 - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 56994075, 29331824, 29331825, 35696052, 56182435, 60433436, 55812036, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264389, 264288, 56181562, 264768, 21908765, 21908766, 21908767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 56182323, 56526466, 87168518, 22279000, 264567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	strud	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264806, 264808, 264511, 264512, 265009, 264810, 18108351, 264764, 264369, 264288, 264685, 264766, 265020, 265022, 264534, 35696423, 264631, 264637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565, 22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264662, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264488, 22278996, 60432289, 264682, 264683, 264689, 18108374
2294	86693580 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88864) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	263974, 263978
2295	95312200 (4589, 4590)			UNCLASSIFIED	264488, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264807, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812036, 21908754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21908765, 21908767, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 63373044, 18108385, 56526466, 264504, 264466
2296	80030781 (4591, 4592)			transcriptfactor	
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5688501 dbj BAAB3034.1 - (AB028005) KUA1082 protein [Homo sapiens]			

2288	95312207 (4595, 4598)	Novel Protein sim. GBank gij3875051[emb]CAB02849] - (Z81050) predicted using GeneFinder, similar to collagen; cDNA EST EMBL:D85564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424178, 56181686, 22278995, 35696288, 22278998, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 60424268, 35696052, 29331828, 66712502, 56182435, 264310, 265006, 60433438, 21806754, 33109854, 55811386, 265010, 265018, 55811150, 264762, 18108351, 264882, 264683, 264288, 264684, 264686, 264688, 56181582, 264689, 21808768, 21906787, 29148629, 55811957, 29148784, 35695917, 265020, 18108382, 33857023, 18108384, 33857109, 60431602, 18108370, 60431528, 18108374, 55810784, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22279000, 264482, 264587, 264488
2289	80193720 (4597, 4598)			UNCLASSIFIED	264389
2300	94124346 (4598, 4600)	Novel Protein sim. GBank gij2443888 (AC002294) - Unknown protein [Arabidopsis thaliana]			264488, 22278988, 22278989, 264259, 29331824, 66714117, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21808768, 21808767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22279002, 264583
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gij2143637[pir]I94505 - calcium-dependent actin-binding protein - rat		strod	264908, 264758, 265017, 21808765, 83373044, 264583
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gij2887497 (AC004144) - R34001.1 [Homo sapiens]		UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gij4884194[emb]CAB43220.1] - (AL049946) hypothetical protein [Homo sapiens]		Contains protein domain (PF00047) - strod immunoglobulin domain	264259, 60432049, 264907, 264909, 264910, 60432228, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gij2494162[sp]Q10005[YRY1 CAEEL - HYPOTHETICAL 38.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906787, 33857182, 33657348
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gij4972686[gb]AAD34738.1] - (AF132150) unknown [Drosophila melanogaster]			85274572, 22278988, 264908, 265006, 21906788, 264681, 264488

2308	95334840 (4811, 4812)	Novel Protein sim. GBank gi 4929585 gb AA034043.1 AF151806 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	284488, 22278995, 22278998, 35688288, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35688052, 284508, 284905, 284907, 29331830, 284908, 284909, 284510, 285006, 284511, 265007, 284512, 285008, 285009, 33857402, 21908754, 8568542, 285010, 285011, 284601, 285017, 285018, 284604, 285019, 18108351, 284448, 284288, 284786, 284789, 21908785, 21908788, 21908787, 21908788, 29148829, 29148784, 35695917, 285020, 285021, 285022, 33657023, 284892, 18108370, 18108374, 18108378, 35688423, 35685855, 284630, 284634, 284635, 284636, 284837, 284638, 284639, 18108382, 18108385, 18108387, 284563, 284566, 284488 284828
2307	79415283 (4813, 4814)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		UNCLASSIFIED	284828
2308	87608409 (4815, 4816)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35688288, 264259, 29331822, 29331824, 264112, 264512, 284757, 21908754, 284288, 284690, 27488284, 284631, 284634, 284404 18108397, 22278998, 22278997, 22278998,
2309	95357218 (4817, 4818)	Novel Protein sim. GBank gi 3878059 emb CAB17070 - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72844 comes from this gene; cDN...		glycoprotein	22278999, 60432049, 29331822, 29331828, 60432289, 68712502, 60432228, 60433356, 60433438, 65274444, 265010, 284600, 284681, 284448, 284683, 284288, 21908786, 21908788, 285020, 284691, 284892, 284893, 85274820, 85274781 284508
2310	79601668 (4819, 4820)	Novel Protein sim. GBank gi 2137337 pir j48281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	284508
2311	87721189 (4821, 4822)	Novel Protein sim. GBank gi 2137337 pir j48281 - gene mCBP protein - mouse		transcriptfactor	18108397, 56182575, 22278998, 56984075, 284259, 29331824, 29331827, 284508, 284907, 56182435, 284510, 284511, 285008, 284512, 285007, 285008, 285009, 60433438, 33108954, 265010, 285011, 284603, 265017, 18108351, 284782, 284883, 284288, 284369, 284688, 33857023, 20281149, 20281069, 284628, 283972, 55811578, 35688423, 20281071, 284632, 284638, 18108385, 18108387, 87168518, 222789000, 284563, 284488

2312	87549881 (4623, 4624)	Novel Protein sim. GBank gij2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278998, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812036, 33109954, 21908754, 87168474, 265018, 18108351, 264288, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 265022, 60170815, 33657023, 27486281, 27486284, 35696423, 35695855, 18108385, 22278000, 22278002 263981
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gij3043626[idjBAA25477] - (AB011123) KIAA0551 protein [Homo sapiens]			
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gij5586714[embjCAB51401.1] - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52844507, 52846365, 52846842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432229, 29331826, 29331827, 29331828, 35696052, 35656970, 52844045, 265008, 264593, 60433356, 60433438, 264756, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21908765, 21908766, 21908768, 35695917, 52844150, 33657023, 33657109, 52845129, 33657349, 35695763, 18108374, 35696423, 35695855, 52844332, 22278000, 22278002, 264563, 264567 264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385 52844507, 52645156, 52846365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52844045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433436, 21908754, 52846317, 33109954, 33657084, 52844296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52844229, 21908764, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 52844150, 33657023, 18108362, 52845129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52844332, 83373044, 18108385, 18108387, 87168518, 60432113, 22278000, 264566, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gij5531827[idjBAA044488.1] - (AF-078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - UBX domain		

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432229, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79859878 (4635, 4636)			UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gi 5262613 emb CAB45746.1 - (AL080155) hypothetical protein [Homo sapiens]			264488, 264568, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35896286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21908754, 52644298, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21908764, 21908765, 21908768, 21908767, 21908769, 21908789, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27488264, 33657349, 35895763, 18108370, 18108376, 18108379, 35896423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	81622426 (4639, 4640)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase		22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21908765, 18108372, 18108387, 22278002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gi 3873837 emb CAB02700 - (Z81029) Similarity to S.pombe hypothetical protein C104.09C (SW:Q10154); cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01062 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com....	UNCLASSIFIED		264488, 264687, 18108394, 264689, 21908765, 18108397, 18108398, 21908767, 21908768, 65274791, 22278995, 35895855, 22278998, 265021, 265022, 264510, 265008, 264511, 264512, 265008, 60170815, 264555, 264636, 264556, 18108381, 264259, 60432229, 33657023, 264557, 264558, 264893, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gi 5678957 emb CAB51685.1 - (AL109830) BACRTA4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264788, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gij2484162[sp]Q10005[RYR1_CAEEL - HYPOTHETICAL 38.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00228) - eph DnaJ domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 58182435, 264511, 265008, 60433358, 60433438, 55812038, 33109954, 21908754, 85658542, 87168474, 285011, 87168559, 285017, 285018, 284780, 264681, 18108351, 264369, 264288, 18108355, 284687, 264888, 21908785, 21908787, 21908788, 55811957, 35695917, 285021, 33657023, 18108362, 27486282, 55811576, 284631, 264555, 83373044, 87188518, 60432113, 22279002
2324	86833607 (4647, 4648)	Novel Protein sim. GBank gij5419865[emb]CAB46377.1] -	ATPase-associated	264592, 284593, 265020
2325	88165074 (4649, 4650)	(AL096732) hypothetical protein [Homo sapiens]		265020
2326	84390982 (4651, 4652)	Novel Protein sim. GBank gij231885[sp]P29981[CP4C_BLADI - CYTOCHROME P450 4C1 (CY1VC1)	Contains protein domain (PF00067) - cyto-50 Cytochrome P450	285006, 284759, 35695855, 56182323
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gij4240227[dbj]BAA74892.1] -	UNCLASSIFIED	
2328	83388428 (4655, 4656)	(AB020876) KIAA0869 protein [Homo sapiens] Novel Protein sim. GBank gij1245105 (U46463) - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 285010, 264766, 264768, 264789, 33657023, 264683, 264628, 264631, 264634, 264638, 264639, 264486
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gij1169343[sp]P42209[DIF8_MOUSE - DIFF8 PROTEIN	Contains protein domain (PF00735) - Cell division protein	60433438, 264595, 285017, 264786, 264692, 264629, 264635, 264638, 264638, 56182323, 60432113, 284568
2330	87335398 (4659, 4660)	Novel Protein sim. GBank	UNCLASSIFIED	285017, 264685, 60432113, 264088
2331	8680463 (4661, 4662)	Novel Protein sim. GBank gij5878136[gb]AA046874.1[AF160934 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	transport	265009
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gij2104452[emb]CAB08779] - (Z85387) unknown [Schizosaccharomyces pombe]	ATPase-associated	35696286, 22278998, 29331824, 60424269, 285008, 265008, 285018, 264448, 264764, 21908785, 35695917, 35695855, 264636, 22279000, 264568
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gij3879985[emb]CAA02891.1] - (Z68316) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST ...	UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263978
2334	84318788 (4667, 4668)	Novel Protein sim. GBank gij4966270[gb]AAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	56182575, 29331825, 21908788, 264636, 83373044

2335	80046103 (4668, 4670)	Novel Protein sim. GBank gij3283350 (AF062378) - calmodulin-binding protein SH-A1 [Mus musculus]	Contains protein domain (PF00812) - IQ calmodulin-binding motif	strucd	18108351, 21908769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gij19290505[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	264907, 35895917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gij4495063[emb]CAB39181.1] - (Z85986) dJ108K11.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]	UNCLASSIFIED		35698286, 22278999, 56182181, 29331825, 60424289, 96182435, 33657402, 55812038, 55811386, 265017, 265018, 285019, 21908788, 35895917, 264691, 33657023, 33657109, 263972, 35698423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gij224688[db]BAA20829] - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	UNCLASSIFIED	18108394, 29331822, 66714117, 60432289, 264908, 56182435, 265009, 60433438, 264596, 265010, 265018, 18108354, 264288, 264368, 55811857, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gij3873550[emb]CAA22127] - (AL033534) serine-rich protein [Schizosaccharomyces pombe]	UNCLASSIFIED		35698286, 264592, 284369, 264691, 264558
2340	90937716 (4678, 4680)				65274572, 22278994, 35898286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264788, 264685, 21908769, 35895917, 264691, 264692, 35698423, 87188518, 22279000
2341	87775281 (4681, 4682)	Novel Protein sim. GBank gij3874563[emb]CAB02797] - (Z81042) similar to Yeast hypothetical protein YFY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 264908, 264909, 264682, 22279000
2342	95334988 (4683, 4684)				264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35698052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433358, 87168474, 265017, 265018, 265019, 264448, 264369, 264288, 21908765, 21908766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810764, 35698423, 55811576, 264536, 264558, 18108385, 60432113, 264583, 264584, 264585, 264586, 264587, 264907, 264512, 265011, 264683
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gij4929741[gb]AAD34131.1[AF15189] (AF151894) CGI-136 protein [Homo sapiens]	UNCLASSIFIED		
2344	79953198 (4687, 4688)		UNCLASSIFIED		264758
2345	94319799 (4689, 4690)	Novel Protein sim. GBank gij2506307[sp]P13944[CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)]	Contains protein domain (PF00092) - von Willebrand factor type A domain	collagen	264488, 264259, 66712502, 264759, 83373044, 264566

2348	94131820 (4691, 4692)	Novel Protein sim. GBank gll1255411 (U53153) - one short region of weak similarity to S. cerevisiae protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to S. cerevisiae glucose repression mediator protein (SP:P14922) [Caenorhabditis elegans]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35698052, 29331828, 33857402, 60433356, 33109954, 87188559, 264803, 265019, 18108351, 264881, 264685, 21908768, 265021, 33657109, 55811578, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264768, 264687, 264688, 264691, 264692, 55811578
2348	95196133 (4695, 4696)	Novel Protein sim. GBank gll1929056[emb] [CAAT2805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]		kinase	18108394, 35696286, 264259, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264567, 264488
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gll4984106[emb] [CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35696052, 29146489, 264908, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21908754, 265010, 87188559, 265018, 265019, 264781, 264681, 264288, 18108357, 21908768, 21908767, 264691, 264692, 35695855, 87188518, 22278000, 22279002, 264482
2351	86968042 (4701, 4702)	Novel Protein sim. GBank gll728832[sp]P39189[ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII]		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gll731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.8 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638764 (4705, 4706)	Novel Protein sim. GBank gll1346955[sp]P48809[RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264638
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gll731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	81638786 (4709, 4710)	Novel Protein sim. GBank gij4938503[embjCAB43861.1] - (AL078465) hmrNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	56994075, 22278996, 35696286, 22278999, 284259, 29331825, 29331826, 29331828, 29148498, 284905, 284908, 265006, 284758, 87168474, 265010, 265017, 264887, 21908769, 21908767, 21906769, 284691, 284692, 263987, 18108370, 87168518, 22278900
2356	85327688 (4711, 4712)	Novel Protein sim. GBank gij5138920[gbjAAD40377.1] - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 284259, 29331824, 86714117, 29331825, 60432289, 35696052, 29331828, 284908, 66712502, 284512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 284758, 52646317, 33109854, 21908754, 55811386, 87168474, 265017, 265018, 284905, 285019, 264681, 264682, 264448, 284389, 264288, 264686, 284768, 21908765, 21908766, 21908767, 21908768, 21906769, 285021, 60170815, 33657109, 27486284, 35695763, 55810764, 18108378, 35698423, 55811576, 35698555, 60170394, 58182323, 83373044, 18108385, 56526486, 284404, 60432113, 22279000, 284482, 284563, 284566, 284486, 284567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gij492874[gbjAAD34131.1]AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	284488, 284769, 18108394, 284259, 29331822, 18108370, 18108374, 284510, 285017, 284482, 284563, 284762, 284565, 284566, 284389, 18108354
2358	8777078 (4715, 4716)	Novel Protein sim. GBank gij4218005 (AC008135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 284509, 284905, 284592, 18108351, 284661, 284682, 264768, 32833986, 18108374, 284556, 18108385, 284482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gij1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g8.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk15g12....		UNCLASSIFIED	35698286, 22278998, 284905, 284511, 285007, 285008, 60433438, 284286, 264686, 21908769, 265020, 284692, 35695855, 284558, 56526486, 284563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gij388154[embjCAA83779] - (Z89804) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22278900
2361	84232191 (4721, 4722)	Novel Protein sim. GBank gij746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 284512, 285009, 284757, 21908765, 65274620, 18108370, 60431528, 18108374, 284635, 60170394, 284482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gii1171083[sp]P19706[MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)]		UNCLASSIFIED	22278998, 264259, 29331822, 29331824, 60432288, 264509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21908765, 21908768, 21908769, 80432113, 22279000, 22279002 264907, 264626, 264635
2363	95006635 (4725, 4728)	Novel Protein sim. GBank gii854065[emb][CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gii5839830[gb]AAD45886.1[AF14601] - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	284488, 18108394, 264887, 18108398, 22278998, 56994075, 35698288, 22278997, 22278998, 264259, 86714117, 29331825, 35698052, 264509, 264905, 264906, 264907, 264908, 86712502, 264909, 264511, 265008, 264512, 265007, 265008, 33657402, 264758, 21908754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21908765, 21908766, 21908767, 35695917, 265020, 265021, 265022, 80170815, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35698423, 35695855, 264635, 264556, 264557, 264639, 80170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526488, 264482, 264584, 264486 22278998, 22278998, 22278999, 264907, 264908, 264910, 33857402, 264758, 264600, 264768, 264687, 264689, 21908765, 21908767, 21908768, 21908769, 265021, 33657023, 33657109, 83373044, 264566
2365	94140746 (4728, 4730)	Novel Protein sim. GBank gii1940045 (U48082) - transporter protein [Homo sapiens]		transport	
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264809, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21908766, 21908769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108386, 18108387, 264584, 264586 35698288, 21908768, 55810764, 85274791, 264587 264628
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gii1065457 (U40410) - C54G7.4 (gene product [Caenorhabditis elegans])	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	
2368	94322190 (4735, 4736)				

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gjl5360901[dbj]BAA82158.1]- (AB028343) a-helix coiled-coil rod homologue [Homo sapiens]		sinud	52644507, 52646842, 35696286, 264092, 284094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644298, 52644229, 264689, 21906765, 21906768, 35695917, 265020, 52644150, 263987, 33857109, 27486285, 35695783, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 18108386, 264909, 264598
2370	78804120 (4738, 4740)			UNCLASSIFIED	264389
2371	57280408 (4741, 4742)			UNCLASSIFIED	263967, 263981
2372	87642413 (4743, 4744)			UNCLASSIFIED	29331826, 265010, 265019, 35695917, 284634, 60432113
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gjl4589582[dbj]BAA76813.1]- (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	265008, 265007, 265008, 265009, 265011, 264786, 35695917, 35695855, 263981, 264557, 264585
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gjl5105131[dbj]BAA80445.1]- (AF000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exonuclease family	UNCLASSIFIED	60432049, 28331824, 264807, 52644045, 284512, 60433356, 21906754, 52644298, 87168559, 264448, 21906765, 21906768, 21906769, 33857023, 18108368, 55811576, 52644332
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gjl1351115[sp]P47758[SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	284259, 29331830, 264909, 264910, 265009, 80433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gjl2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase-associated	18108394, 85274572, 22278897, 22278899, 264095, 29331822, 29147620, 29331824, 68714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 264509, 265006, 265007, 265008, 265009, 60170631, 285010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21906767, 21906768, 29146627, 29146629, 265021, 33857023, 33857109, 18108370, 18108374, 18108378, 35698423, 264556, 83373044, 18108385, 18108386, 58526486, 22278000, 22278002, 264583
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gjl5257005[gbj]AAD41239.1]- (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 68714117, 29331825, 29331826, 60432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33857023, 264557, 56182323, 83373044, 18108385, 22278002, 264482
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gjl1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	265017, 264288, 21906768
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gjl3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	

2380	86923062 (4759, 4760)	Novel Protein sim. GBank gi 4502939 ref NP_001845.1 pcoll1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87808241 (4761, 4762)	Novel Protein sim. GBank gi 4455609 emb CA836555 - (AL031646) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) 'chromo' (Chromatin Organization Modifier) domain	helicase	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264883, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 5911576, 264636, 264567
2382	81225982 (4763, 4764)	Novel Protein sim. GBank gi 4325130 gb AADI7276 - (AF119716) dMi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00828) - PHD-finger	transport	29331824, 60432289, 264805, 264596, 21906754, 264769, 265022, 264693, 263987, 33657109, 264629, 264631, 264558, 83373044, 60432113, 264482
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi 1902982 hb BAA19005 - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	265008, 21906765, 21906766
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi 2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00585) - PDZ domain (Also known as DHR or GLGF).	strud	264488, 52644507, 52645156, 52646365, 35698286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644286, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 85274820, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2385	95419485 (4769, 4770)			UNCLASSIFIED	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278998, 264259, 52645080, 28331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18106370, 264631, 52644332, 22279000, 22279002, 264583, 264585, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gi 4929899 gb AAD34110.1 AF151873 CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906769, 29146629, 35695917, 265021, 264690, 33657109, 264628, 18106376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14897880 (4773, 4774)			UNCLASSIFIED	284834
2388	11424604 (4775, 4776)			UNCLASSIFIED	284595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gij4758058[refNP_004372.1]pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor		284488, 22278988, 22278989, 284508, 284905, 284906, 284907, 284908, 284909, 285008, 284511, 284512, 284910, 284591, 21908754, 284601, 284604, 284761, 18108351, 284764, 284288, 284768, 284788, 284789, 21908765, 21908768, 284892, 284893, 35898423, 284635, 284636, 284555, 83373044, 22279000, 284488
2390	94320912 (4779, 4780)	Novel Protein sim. GBank gij1644239[djBAA12223] - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	polymerase	52844507, 56182575, 22278995, 35896286, 22278996, 22278997, 22278998, 29331822, 29331825, 29331826, 35898052, 284905, 52844045, 285009, 284758, 284759, 33108954, 52844296, 85658542, 285011, 285017, 285018, 284605, 52844229, 21908765, 21908767, 21908768, 21908769, 35895917, 52844150, 33657023, 33657109, 33657349, 35895763, 18108370, 18108374, 18108376, 35896423, 35895855, 284555, 52844332, 56182323, 60170394, 83373044, 56528488
2391	80036184 (4781, 4782)			UNCLASSIFIED	283976
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gij4240168[djBAA74863.1] - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	35896286, 35896052, 284508, 284905, 284509, 284906, 284907, 284908, 284909, 284510, 284511, 284512, 284910, 285009, 284591, 284758, 284600, 284604, 284762, 284448, 284764, 284389, 284768, 284788, 284789, 284689, 35895917, 284828, 18108374, 283978, 35898423, 35895855, 284631, 284634, 284635, 284636, 284637, 284638, 60170394, 284639, 284565, 284486

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gi 4506667 ref NP_000983.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - ribosomal prot Ribosomal protein L10	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278998, 264093, 60432049, 264259, 29331822, 29147820, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 28146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264809, 56182435, 264112, 264113, 264510, 265008, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264768, 264686, 264687, 264688, 264689, 18108359, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 26146629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486262, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695655, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265008, 264592, 55811388, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21908765, 21908768, 21908769, 55811857, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264564, 264568, 264567
2394	94323266 (4787, 4788)	Novel Protein sim. GBank gi 4159888 (AC004808) - zinc finger protein from gene of uncertain exon structure; similar to Q99678 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00086) - dna_ma_bind Zinc finger, C2H2 type	
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi 5712756 gb AAD47836.1 AF16079 - (AF16079) calcium transporter Cat1 [Rattus norvegicus]	dna_ma_bind	264259, 29331824, 264810, 264288, 265021, 83373044, 18108387, 264563, 264566

2396	95096700 (4791, 4792)	Novel Protein sim. GBank gij1063222(pirj)B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52646365, 18108397, 56182575, 35696286, 22278997, 22278999, 80432048, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264108, 264907, 29331830, 68712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264766, 52644229, 21908786, 21908787, 265020, 265021, 60170615, 264892, 33657023, 65274820, 52645129, 33657182, 27486282, 27486284, 27486285, 264629, 18108374, 35696423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22278002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 28147820, 264805, 264907, 264908, 264809, 264910, 264758, 52644296, 264803, 264804, 264762, 264681, 264764, 18108357, 264769, 21908768, 264693, 264628, 264835, 264638, 264639, 264564
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gij3258609 (AC005178) - H53 GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gij786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56984075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 68714117, 60432289, 264906, 29331830, 56182435, 264112, 264810, 33109954, 21908754, 87168474, 264600, 265017, 265018, 265019, 264764, 264765, 21908765, 21908768, 21908767, 21908769, 35695917, 265020, 265022, 60170615, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22278000, 22278002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gij2352822(gbj)AAB69285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21908766, 52646842, 56984076, 33657182, 27486282, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gii2352822[gblAA869285.1] - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52644507, 52645156, 52644229, 264688, 21908784, 21908783, 52646385, 52646842, 21908786, 21908767, 21908768, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33857023, 52645080, 264693, 29331824, 33857109, 52645129, 29331826, 33857182, 29331827, 35696052, 27486261, 27486262, 33856870, 33857349, 27486285, 35695763, 264106, 264905, 35696423, 35695655, 265008, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644286, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264583, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gii4689258[gblAAD27832.1]AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]			
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gii4929575[gblAAD34048.1]AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35698052, 265018, 264686, 264693, 93373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gii2315798 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	35698286, 28331826, 35696052, 265008, 265018, 21908769, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gii464178dbj[BAA03581] - (D14853) polyprotein [Hepatitis C virus]		UNCLASSIFIED	35696286, 29331822, 265007, 21908754, 265017, 265018, 265019, 264783, 264369, 21908765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gii273363 (AF041382) - microtubule binding protein D-CLIP-180 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264108, 264908, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21908768, 21908769, 52644150, 264693, 52645129, 264628, 35698423, 264632, 56182323, 264639, 22279000, 22278002, 264583
2407	79465005 (4813, 4814)			UNCLASSIFIED	264685, 264686
2408	87391503 (4815, 4816)	Novel Protein sim. GBank gii423442[prr]S33513 - gene F1f protein - mouse		UNCLASSIFIED	264910, 265010, 264448, 264557

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gi 1176801 sp P45966 YNZ8_CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278985, 22278986, 22278987, 264087, 29331822, 29331824, 29331827, 29148498, 5264045, 60433438, 33857084, 87168474, 264780, 21906787, 29148627, 29148629, 52644150, 33857023, 263967, 20281089, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278988, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gi 4966262 gb AAC48052.2 - (UB4849) Contains similarity to Pfam domain: PF00646 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gi 3114713 (AF061346) - Ecdp1 protein [Mus musculus]		inf	29331824, 29331827, 29331828, 264784, 264389, 33857109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gi 5410336 gb AAD43038.1 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278988, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21908786, 265020, 33857109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gi 5262705 emb CAB45778.1 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264882, 264784, 264786, 264886, 264788, 264889, 265021, 33857023, 18108370, 264628, 35685855, 264632, 264634, 264635, 264636, 83373044, 264563, 264584, 264585, 264586, 264587, 264488
2414	94312580 (4827, 4828)	Novel Protein sim. GBank gi 1082340 pr J552863 - DNA- binding protein R kappa B - human		ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278986, 35696286, 22278987, 22278988, 22278989, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33856970, 29331830, 264909, 80433356, 33857402, 264594, 52646317, 21906754, 33857084, 265010, 87168559, 265017, 265018, 265019, 264389, 264684, 264887, 264888, 56181562, 21908764, 264689, 21908765, 21908786, 21908787, 26148627, 21908788, 265020, 265021, 60170815, 33857023, 264693, 52645129, 33857109, 33857182, 27486261, 27486262, 27486265, 33857349, 18108370, 60431528, 264629, 18108374, 18108376, 55810784, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002

2415	88088002 (4828, 4830)	Novel Protein sim. GBank gij423915[pir][A45439 - myosin I heavy chain - rat]	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	284259, 284908, 60433356, 33657402, 21908754, 285018, 264687, 284689, 21908768, 55811957, 285021, 264690, 264691, 33657023, 264693, 35698423, 56182323, 56526486
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944[pir][S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00153) - Mitochondrial carrier proteins		284094, 28331822, 28331824, 28331827, 284389
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gij1178572[sp][P45895]YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 28331824, 28331825, 60432286, 28331828, 264905, 264907, 264511, 265009, 60432229, 21908754, 87186559, 285019, 264682, 21908768, 21908769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264568
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gij284006[pir][S18732 - autoantigen, 64K - human]		struct	284589, 284762, 264448, 264691, 264631, 264634, 264555, 264556, 264636, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij1076211[pir][S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	28331824, 28331825, 28331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264584
2421	87805345 (4841, 4842)			UNCLASSIFIED	284908, 284768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij2224567[db][BAA20772] - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	transport	18108392, 18108394, 18108398, 284906, 265006, 265010, 18108351, 18108374, 18108385
2423	88056380 (4845, 4846)	Novel Protein sim. GBank gij4505153[refNP_002392.1]pMEKK - MAP/ERK kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284259, 60432049, 28331822, 28331826, 60432289, 28331828, 265008, 265009, 60433356, 21908754, 265017, 285018, 265019, 21908766, 21908768, 21908769, 265020, 285021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278997, 60432049, 284259, 28331828, 28331828, 264905, 68712502, 28331830, 60433356, 265011, 265019, 264768, 21908768, 55811957, 264692, 33657023, 33657108, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gij2077832[db][BAA19879] - (D88556) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gij2038368[gb][AA853003.1] - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21908767, 18108370, 18108374, 263976

2427	87622693 (4853, 4854)	Novel Protein sim. GBank gi 480695 gb AAD27737.1 AF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4L1 family	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264862, 264883, 264369, 264684, 264686, 264687, 264689, 21908766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		22278996, 22278999, 35696052, 21908754, 264288, 21908765, 21908768, 21908769, 35695917, 265020, 263972, 22278002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gi 601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	22278999, 29331824, 264806, 264809, 264511, 265009, 21908754, 265017, 265018, 265019, 264448, 264683, 264288, 21908765, 21908768, 265021, 264693, 18108381
2430	86948927 (4859, 4860)	Novel Protein sim. GBank gi 3860729 emb CAA14530 - (AJ235270) CELL DIVISION PROTEIN FTSJ (ftsJ) [Rickettsia prowazekii]	UNCLASSIFIED	264112, 264681
2431	87849884 (4861, 4862)	Novel Protein sim. GBank gi 3876367 emb CAA93287 - (Z69360) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45317); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yt295b9.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF01728) - FtsJ cell division protein	29331826, 29331827, 35696052, 29146499, 264905, 264806, 264681, 264288, 264689, 21908765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gi 2224593 db BAA20784 - (AB002324) KIAA0326 [Homo sapiens]	protease	264634, 264558
2433	80055082 (4865, 4866)	Novel Protein sim. GBank gi 2224593 db BAA20784 - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	264569, 264805, 265018, 264782, 264683, 264691, 264556, 264557, 264639, 264558
2434	18520148 (4867, 4868)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]	UNCLASSIFIED	264563
2435	20759044 (4869, 4870)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]	UNCLASSIFIED	264555
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]	UNCLASSIFIED	265008, 264756, 265010, 264689, 27486261, 263972, 18108374, 18108381
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gi 3641352 (AF091234) - putative transcription factor [Mus musculus]	UNCLASSIFIED	29331826, 265007, 265008, 265017, 264760, 264685, 264693, 264585
2438	94143473 (4875, 4876)	Novel Protein sim. GBank gi 3860014 (AF091086) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33857402, 21908754, 265011, 264760, 264784, 264885, 264686, 264788, 35695917, 33857023, 264893, 264831, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850850 (4877, 4878)	Novel Protein sim. GBank gij4263519 gb AAO15345 - (ACO04044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181888, 56994075, 22278996, 35698286, 22278997, 22278998, 264259, 52645080, 29331822, 56182161, 29331824, 60424268, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35698052, 29146498, 264509, 264905, 264906, 52644045, 60431735, 33109954, 21908754, 33657084, 55811388, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 33657023, 33657109, 33657182, 27486262, 27486284, 33657349, 27486285, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431650, 56182323, 60432113, 22278000, 22278002, 264587
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264639, 22278002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gij3024889 sp P56524 Y288 HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264628, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gij4506013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gij1170658 sp Q02875 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcription factor	
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gij4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	264259, 18108382, 18108383, 18108385, 22279000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gij2135950 p S58222 - PQ-rich protein - human			264259, 35696052, 264369, 18108361
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gij4753887 emb CAA05409.2 - (AJ002424) p85 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhib	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gij4885613 ref NP_005409.1 pST5j - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4898)			UNCLASSIFIED	22278998, 22278997, 22278999, 28331826, 35686052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486282, 263978
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III; ALU SUBFAMILY SQ WARNING ENTRY III		cadherin	284259, 264828, 265007, 264595, 265021, 56528486
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gi 1710021 sp P35280 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35686052, 264907, 66712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gi 1504034 dbj BAA13216 - (D86980) KIAA0227 [Homo sapiens]		isomerase	284102, 264112, 264688, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369908) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	ngfrecap	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gi 1076802 pir S49915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264592, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264686, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35686055, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gi 543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264486, 22278998, 264259, 35686052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21906768, 21906767, 21906769, 29148628, 35686017, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	86166700 (4911, 4912)	Novel Protein sim. GBank gi 2568630 (AC003079) - Ankyrin- like; 54% similar to 20223-40A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4813, 4814)	Novel Protein sim. GBank gij3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	58181686, 264805, 264907, 264511, 264596, 55811388, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 96526486, 264563
2458	85675304 (4815, 4816)	Novel Protein sim. GBank gij2384942 (AF022885) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264683, 264634, 264559
2459	87551913 (4817, 4818)	Novel Protein sim. GBank gij5441942 [gb]AAD3187.1 [AC004997] supported by mouse EST AA538043 (NID: g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4819, 4820)	Novel Protein sim. GBank gij4929701 [gb]AAD34111.1 [AF15187] - (AF151874) CGI-116 protein [Homo sapiens]		kinase	85274572, 35696286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33658970, 29146499, 264102, 264109, 60433438, 265017, 285018, 265019, 264288, 21806765, 21806768, 21806769, 35695917, 285020, 264691, 33657023, 27486261, 18108374, 35695855, 87188518, 60432113
2461	87645147 (4821, 4822)	Novel Protein sim. GBank gij4426862 [gb]AAD20633] - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264810, 18108351, 18108370, 18108374
2462	86980002 (4823, 4824)	Novel Protein sim. GBank gij5420387 [emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264809, 264758, 264684, 18108374, 264637, 18108385
2463	84386543 (4825, 4826)	Novel Protein sim. GBank gij5052516 [gb]AAD38588.1 [AF14561] - (AF145613) BcDNA GH03108 [Drosophila melanogaster]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219857 (4827, 4828)	Novel Protein sim. GBank gij5410300 [gb]AAD43021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 285017, 285018, 265019, 264762, 264448, 264764, 264288, 264766, 21806765, 21806768, 21806769, 21806768, 21806769, 265021, 33657023, 33657109, 18108370, 18108381, 80170394, 18108385, 22279002, 264486

2465	95357483 (4929, 4930)	Novel Protein sim. GBank gi 4508401 ref NP_002871.1 pRAF1 - v-rafl-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52845156, 52846365, 22278994, 22278995, 35696286, 22278996, 22278998, 284259, 29331822, 29331824, 29331825, 60424289, 60432289, 29331827, 35696052, 29331828, 284907, 29331830, 52844045, 284908, 56182435, 284511, 285007, 265008, 265009, 284910, 33657402, 60433438, 55812038, 21908754, 33109954, 285010, 265011, 87168559, 284800, 265017, 285018, 265019, 18108351, 284369, 284288, 284885, 284767, 21908785, 21908787, 21908768, 55811957, 35695917, 265020, 265021, 60170815, 52844150, 33657023, 52845129, 33657109, 27486261, 27486264, 35695763, 284628, 263972, 18108374, 35695855, 284636, 284637, 60170394, 56328486, 87168518, 60432113, 284563, 284584, 284568, 284487 284389
2466	85681388 (4931, 4932)	Novel Protein sim. GBank gi 4321619 gb AAD15788.1 - (AF051088) seven transmembrane domain orphan receptor (Mus musculus)			
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi 3513300 (AC005585) - F16801_1, partial CDS [Homo sapiens]		UNCLASSIFIED	56994075, 284908, 21908768, 33657023
2468	87814686 (4935, 4936)	Novel Protein sim. GBank gi 2143455 pir j58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	28331824, 52644045, 265008, 284910, 265019, 21908785, 21908769, 285021 284288, 284628
2469	86284387 (4937, 4938)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243480) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284582, 284692, 284555, 284556, 284557, 284558, 284559, 18108385, 284482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419882 emb CAB46424.1 - (AL096749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 28331827, 285007, 284592, 33109954, 285018, 265019, 284288, 55811957, 285020, 284693, 55811576, 56182323
2471	91013681 (4941, 4942)	Novel Protein sim. GBank gi 4539009 emb CAB39630.1 - (AL049481) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	284092, 60432049, 29331825, 60433356, 285010, 285011, 18108351, 284764, 284288, 284692, 65274620, 18108370, 18108372, 18108374, 284634, 18108385
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gi 4929747 gb AAD34134.1 AF15189 - (AF15189) CGI-139 protein [Homo sapiens]			60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 285010, 18108351, 284448, 284288, 284687, 284688, 285021, 284692, 65274620, 60431528, 65274791, 284556, 56182323, 60432113
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi 4539009 emb CAB39630.1 - (AL049481) putative protein [Arabidopsis thaliana]			65274572, 56994075, 284259, 29331826, 60170831, 285017, 265018, 265019, 284683, 284369, 265020, 284693, 284563, 284584
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]			

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gij1216486 (U48852) - HT protein (Crictetus griseus)	Contains protein domain (PF00008) - EGF-like domain	IgI	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108362, 264693, 18108370, 18108374, 18108379, 35688423, 83373044, 18108383, 18108385, 264584, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product (Homo sapiens)		UNCLASSIFIED	264259, 60424289, 86714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)			UNCLASSIFIED	263978
2478	17659185 (4955, 4956)			UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gij1644232[dbj BAA11082] - (D67056) N-WASP [Bos taurus]		Im7	56994075, 22278999, 21906754, 264682, 21908765
2480	95295605 (4959, 4960)			UNCLASSIFIED	264905, 264907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gij5689469[dbj BAA83018.1] - (AB026989) KIAA1066 protein (Homo sapiens)		collagen	85274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35688052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264768, 264686, 264768, 21908768, 55811957, 265020, 264691, 264692, 264693, 264628, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gij321249[pir S28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse		UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264683, 264631, 264632, 264636, 264638, 264639, 264583
2483	87731583 (4965, 4966)			UNCLASSIFIED	264488, 22278985, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gij728831[sp P39188 ALU1_HUMAN - IIII] ALU SUBFAMILY J WARNING ENTRY IIII		kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gij1185397 (U25281) - SH3 domain binding protein (Rattus norvegicus)		UNCLASSIFIED	22278985, 22278986, 22278987, 22278988, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264689, 35689517, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007903) KIAA0443 [Homo sapiens]			285017, 284555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 284082, 284259, 28331822, 35698052, 284106, 284905, 284907, 29331830, 284908, 285008, 284511, 265008, 265009, 80433436, 21908754, 33109954, 87168559, 265018, 264681, 264288, 284687, 21908785, 21908786, 21908787, 21908788, 21908789, 35695917, 265021, 265022, 284534, 33657023, 284692, 33657109, 283972, 18108377, 35698423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 284563, 284482, 284565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	284910, 284448, 284288, 284684, 284691, 284834
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	284686, 284693, 55811576, 22279002
2490	88068608 (4979, 4980)	Novel Protein sim. GBank gi 2586624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	284907, 285008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		Im7	284259, 28331826, 285008, 284782, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	284488, 22278998, 22278999, 28331828, 284591, 33109954, 285017, 55811150, 21908784, 21908788, 284692, 60431528, 87168518, 80432113, 22279000

2483	95422415 (4885, 4986)	Novel Protein sim. GBank gij4240307[dbj]BAAT4932.1] - (AB020718) KIAA0809 protein [Homo sapiens]	Contains protein domain (PF01424) - R3H domain	struct	19108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432048, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264508, 264906, 264907, 29331830, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21908754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 5581150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108378, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2484	30793118 (4987, 4988)			UNCLASSIFIED	264907, 264601
2485	94234551 (4989, 4990)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		collagen	263994, 22278997, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 265008, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264766, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811578, 264638, 264637, 18108385, 22278000, 264564, 264587, 264486
2486	80018765 (4981, 4982)	Novel Protein sim. GBank gij4808220[emb]CAB42832.1] - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]		struct	29147620, 264905, 265008, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108386
2487	91723554 (4983, 4994)			UNCLASSIFIED	52644507, 22278996, 22278998, 29331824, 29331828, 33657402, 21908754, 87168474, 265019, 264389, 264689, 21906765, 21908768, 21908767, 21908768, 265020, 33657023, 18108378, 18108387
2488	67724633 (4985, 4996)	Novel Protein sim. GBank gij1200503 (U47924) - B [Homo sapiens]		UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35695855
2489	94685125 (4987, 4998)	Novel Protein sim. GBank gij3510234 (AC005581) - R31237.1, partial CDS [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264909, 55812038, 264631, 264637, 264558

2500	94648324 (4898, 5000)	Novel Protein sim. GBank gi 3881275 emb CAA21725 - (AL032855) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52844507, 52845158, 22278995, 56994075, 35698286, 22278998, 264259, 52845080, 29331824, 29331825, 68714117, 60432289, 29331828, 29331827, 35698052, 29331828, 264508, 264508, 264510, 264512, 33657402, 60433438, 21906754, 52644298, 87188474, 87188559, 264603, 264681, 264448, 264683, 264288, 264389, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52844150, 33657023, 264693, 33657182, 35695763, 35698423, 35695855, 52844332, 83373044, 18108387, 87168518, 22279002
2501	94303898 (5001, 5002)	Novel Protein sim. GBank gi 4929615 gb AAD34088.1 AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_mn_bind	65274572, 56182575, 35698286, 22278998, 56994075, 22278997, 60432048, 264259, 29331822, 29331824, 29331826, 29331827, 35698052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264581, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264596, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264389, 264288, 264766, 18108357, 21906765, 21906766, 21906767, 21906768, 29148629, 35695917, 264692, 33657023, 264629, 35698423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264638, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi 3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129309) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657108, 263973, 55811576, 264835, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264583, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi 2196874 emb CAA72638 - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868706 (5007, 5008)	Novel Protein sim. GBank gi 550420 emb CAA48220 - (X88101) brg (Rattus norvegicus)			264488, 52644507, 52645156, 52646842, 22278894, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264908, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	81232326 (5011, 5012)	Novel Protein sim. GBank gi 2137562 pir j49635 - mouse Dhml protein - mouse		nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278895, 56994075, 22278896, 22278897, 22278898, 22278899, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264508, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108379, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pK1AA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 263394, 264592, 264595, 264359, 264686, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gi 4826433 emb CAB42889.1 - (AL031447) dJ128A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278895, 22278899, 60432049, 264259, 29331828, 265008, 265007, 80433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264389, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264566, 264567

2510	85421379 (5019, 5020)	Novel Protein sim. GBank gij3293537jgb/AAC25762.11] - (AF071059) zinc finger RNA binding protein [Mus musculus]			dna_rna_bind	65274572, 22278994, 22278996, 22278998, 22278999, 26432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33658970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906787, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486282, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gij4323152jgb/AAD18228.11] - (AF098863) E1b-protein Sp1-C [Mus musculus]				
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gij4502075jref/NP_001135.1pAMFR - autocrine motility factor receptor	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		transport	22278999, 264259, 29331825, 29331826, 29146498, 264907, 264909, 265006, 265008, 264591, 60432229, 21906754, 264763, 264883, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264556, 22279000
2513	95357643 (5025, 5026)	Novel Protein sim. GBank gij3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED		60424178, 52645156, 18108384, 22278994, 35696288, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264389, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108386, 33657109, 27486281, 27486282, 33657349, 18108374, 55810784, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gij2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED		264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gij375772jemb/CAA18783] - (AL022727) dJ8019.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7		
2516	87766908 (5031, 5032)			UNCLASSIFIED		264259, 29146498, 264905, 264288, 29146829, 35695917, 27486281, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gij4220527jemb/CAA23000] - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED		264091, 29331824, 29331825, 29331826, 28431828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5038)	Novel Protein sim. GBank gi 4928591 gb AAD34058.1 AF15181 - (AF151818) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284907, 284909, 264511, 265007, 60432228, 60433356, 60433436, 55812038, 265010, 265017, 264448, 264288, 264688, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 284088 264259, 68714117, 29331826, 29331827, 29331828, 264907, 68712502, 265008, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 284632, 264555, 264636, 22279002, 264584 284259, 264908, 284910, 284682, 21906769, 265020, 264563
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gi 4282722 ref NP_005085.1 pFATP - fatty acid transport protein 4	Kinase		
2520	87413235 (5038, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gi 5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family		284488, 264489, 263984, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 284907, 66712502, 264511, 265008, 265007, 284591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264784, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27488261, 18108370, 264628, 264629, 18108374, 55811578, 35696423, 35695855, 284632, 264558, 18108385, 65274727, 60432113, 264563, 264584, 264585, 264586, 264587 284489, 22278997, 20281171, 21908754, 35695917, 263967, 263976, 263981, 20281169 263969
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		
2523	95340467 (5045, 5046)	Novel Protein sim. GBank gi 1809327 (U76374) - skm- BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906769, 21908769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27488261, 35696423, 65274791, 264558, 83373044, 56526486, 87168518, 264587

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gjl2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278999, 60432049, 60432288, 29331828, 264905, 265008, 55812038, 21908754, 265019, 264369, 21908785, 21908786, 21908787, 21908789, 35695917, 265020, 265021, 33857109, 60431528, 83373044, 60432113, 22279000, 22279002, 264365
2526	85289404 (5051, 5052)	Novel Protein sim. GBank gjl459628(dbjBAA76836.1) - (ABD23209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	60424179, 264768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21906769, 21906769, 55811957, 22278994, 22278995, 35696286, 35695917, 22278998, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264680, 264691, 60432049, 264259, 264097, 33857023, 29331822, 29331824, 60432289, 29331828, 29331827, 29331828, 27486282, 264508, 264509, 264805, 264907, 18108370, 68712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810784, 55811578, 35696423, 35696555, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33857402, 56182323, 60433358, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52848317, 18108385, 33857084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264566, 264288, 264486, 264587, 264788
2527	80094580 (5053, 5054)	Novel Protein sim. GBank gjl2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264584, 264585, 264803, 264805, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gjl2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	dna_rna_bind	55812038, 265017, 264689, 35695917, 35695783, 60431528, 60432113, 22279002
2529	86670826 (5057, 5058)	Novel Protein sim. GBank gjl3785433 (AF088505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264808, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5081, 5082)			UNCLASSIFIED	28331822, 29331824, 60432288, 284508, 264509, 264908, 265011, 264769, 21908788, 33857023, 87168518, 22279000
2532	87419778 (5083, 5084)	Novel Protein sim. GBank gjl2864625(embl:CAA16972) - (AL021811) putative protein [Arabidopsis thaliana]			284593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gjl437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5087, 5088)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21908789, 265020, 265022, 33657108, 22279000
2535	81225056 (5069, 5070)	Novel Protein sim. GBank gij4468311 (embjCAB37992) - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	84218540 (5071, 5072)	Novel Protein sim. GBank gij7288361spjP39183/ALU8_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	kinase		18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264768, 264689, 21906765, 21906766, 21906767, 265021, 52845129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gij4557026 (refjNP_003913.1) pHERC - guanine nucleotide exchange factor p532	ubiquitin		65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170619, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695655, 264636, 264558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144918 (5077, 5078)			UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264766, 87168518, 22279000, 264565, 264566
2540	84218545 (5079, 5080)	Novel Protein sim. GBank gij1362647 (pirjS53876 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura))		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gij1718581spjP54797/T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gil5225320 gb AAD40850.1 AF083107 sirutin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophysial hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108384, 52846385, 52846842, 65274572, 22278994, 35898288, 22278996, 264259, 52845080, 29331822, 29331824, 29331827, 35898052, 33858970, 284907, 264909, 52844045, 264510, 265008, 264512, 265007, 265008, 265009, 264910, 60431735, 52846317, 52844288, 265010, 285011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52844228, 264789, 21908768, 21908767, 21908769, 52844150, 33857023, 33857109, 52645129, 33857182, 27486281, 27486284, 33857349, 35685763, 18108374, 35898423, 35898555, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gil5419857 emb CAB46374.1 - (AL086723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331828, 264907, 264510, 264511, 264592, 264595, 264784, 264389, 264288, 264684, 264766, 264689, 21908765, 21908767, 21908768, 60170615, 264692, 264693, 55811576, 65274791, 264636, 264558, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218549 (5087, 5088)	Novel Protein sim. GBank gil2498110 sp Q63191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00829) - MAM domain.	glycoprotein	18108397, 52846365, 22278997, 264259, 60432048, 29331822, 28331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264686, 264687, 264689, 21908765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gil3327046 gb BAA31591 - (AB014516) KIAA0816 protein [Homo sapiens]			29331825, 264908, 265008, 60170831, 265017, 264389, 21908767, 60170815, 264692, 33857109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gil2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143869 (5083, 5094)	Novel Protein sim. GBank gi 4929807 gb AAD34084.1 AF15182 - (AF15182) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56994075, 22278998, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 60432228, 29331827, 35698052, 29331828, 264104, 264508, 264805, 264806, 264808, 66712502, 264909, 56182435, 265008, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264800, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264286, 264389, 264684, 264886, 264687, 56181562, 264688, 264689, 21906765, 21906768, 21908767, 21908768, 29148627, 21908769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108382, 264692, 264693, 27488261, 18108370, 18108374, 55810764, 55811576, 35698423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 63373044, 18108385, 67168518, 22278002, 264564, 264566, 264486
2548	88179079 (5085, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278984, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432228, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87188559, 264684, 264369, 52844229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22278000, 22279002, 264563, 264567
2549	94196893 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278998, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21908764, 21908765, 21908768, 21908767, 21908769, 265020, 265021, 52644150, 264691, 18108388, 60431602, 18108376, 35698423, 56182323, 18108387, 264567, 56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638
2550	87776584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir I52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gi 4337103 gb AAD18078 - (AF128756) NG28 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21808754, 65274444, 265017, 265018, 264805, 265019, 264288, 21908766, 21908768, 21908769, 265020, 60170615, 264893, 33657109, 35698423, 264638, 56182323, 83373044, 22278900
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35698423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gi 1711858 sp P54787 T10 MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264768, 29331828, 35698052, 35698423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264768, 22278997, 29331822, 264508, 21908769, 33657023, 33657109, 56182323
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gi 728835 sp P39182 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gi 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30823_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264508, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567, 264595
2557	79437803 (5113, 5114)	Novel Protein sim. GBank gi 19110 sp P0321 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264908, 264511, 265018, 264448
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gi 4538998 emb CAB39619.1 - (AL048481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264785, 264766, 264769, 21908765, 21908768, 60432113, 264482
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gi 5051399 emb CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE protein))) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2560	87694530 (5119, 5120)	Novel Protein sim. GBank gi 5326825 gb AAD2056.1 AF044953 (NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens])		UNCLASSIFIED	22278995, 35696286, 22278998, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432228, 87168559, 265017, 265018, 265019, 264689, 21908768, 21908769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264558, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gij14106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278998, 22278997, 22278999, 284259, 29331822, 60432289, 33857402, 60433356, 21908765, 55811957, 60170615, 33857023, 284693, 35895855, 87168518, 264488, 35896286, 22278999, 264259, 29331822, 29331824, 35896052, 284508, 284907, 284908, 284909, 52844045, 284510, 284511, 285009, 284910, 264591, 284593, 33857402, 285017, 265018, 285019, 18108351, 284686, 21908767, 21906768, 55811957, 35895917, 285020, 284691, 264693, 27486262, 284628, 18108374, 35896423, 35895855, 284632, 284634, 284635, 284636, 284558, 18108384, 87168518, 22279000, 22279002, 284482, 284563, 284585, 284568, 284486, 29331822, 285007, 285010, 265019, 264769, 55811576, 56182323
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gij4886447 [emb] (CA843371.1) - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264488, 35896286, 22278999, 264259, 29331822, 29331824, 35896052, 284508, 284907, 284908, 284909, 52844045, 284510, 284511, 285009, 284910, 264591, 284593, 33857402, 285017, 265018, 285019, 18108351, 284686, 21908767, 21906768, 55811957, 35895917, 285020, 284691, 264693, 27486262, 284628, 18108374, 35896423, 35895855, 284632, 284634, 284635, 284636, 284558, 18108384, 87168518, 22279000, 22279002, 284482, 284563, 284585, 284568, 284486, 29331822, 285007, 285010, 265019, 264769, 55811576, 56182323
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gij1352844 [sp] P47179 [YJP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		sulfotransferase	29331822, 285007, 285010, 265019, 264769, 55811576, 56182323
2565	85530906 (5129, 5130)	Novel Protein sim. GBank gij628012 [pir] A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	UNCLASSIFIED	68714117, 284909, 293378, 284632, 18108370, 35895855, 284558, 284558, 18108383
2566	80224958 (5131, 5132)	Novel Protein sim. GBank gij628012 [pir] A53933 - myosin I myr 4 - rat		struct	265020, 60170615
2567	88143590 (5133, 5134)	Novel Protein sim. GBank gij468009 [sp] P34548 [YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E1.1 IN CHROMOSOME III		synthase	60424778, 18108384, 56181688, 56894075, 22278998, 284490, 284259, 29331822, 56182181, 29331824, 60424289, 29331825, 29331826, 29331828, 264509, 29331830, 285007, 285008, 285009, 33857402, 285010, 265011, 285019, 284446, 284683, 264288, 18108354, 284769, 21906766, 21906767, 35895917, 285021, 33857023, 18108362, 33857109, 33657182, 35895763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 284482

2569	95313764 (5137, 5138)	Novel Protein sim. GBank gi 2599560 gb AAB84166.1 - (AF029874) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	18108394, 56182575, 56181886, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 284905, 284908, 58182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21908754, 87168559, 265017, 265018, 265019, 264682, 264448, 264286, 21908765, 21908766, 21908767, 21908768, 29148627, 21908769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281089, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56528486, 87168518, 22278000, 22279002, 264566
2570	94136754 (5139, 5140)	Novel Protein sim. GBank gi 4758954 ref NP_004567.1 pPPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33108954, 265019, 264686, 264689, 285020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gi 732218 sp P34608 YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1088.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	97627560 (5143, 5144)	Novel Protein sim. GBank gi 4894319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21908754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	185313928 (5145, 5146)	Novel Protein sim. GBank gi 399139 sp P02745 C10A_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181886, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264806, 29331830, 264909, 264510, 285008, 264512, 265008, 265009, 264910, 264591, 264592, 60432228, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264289, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21908785, 21908788, 21908787, 29148627, 21908788, 21908789, 265020, 265021, 265022, 60170615, 264690, 52644150, 264691, 264692, 33657023, 65274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35895855, 20281071, 60431850, 264637, 264638, 264558, 264639, 56182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264565, 264566, 264567
2574	194746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 285008, 264910, 264591, 33657402, 265018, 265019, 264446, 264764, 264369, 264288, 18108357, 21908765, 21908766, 21908768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486281, 27486284, 33657349, 264636, 264555, 83373044, 18108385, 264482
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 JAF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264910, 264601, 264683, 264689, 264080
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680681 gb AAD27730.1 JAF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264906, 60433438, 264681, 18108351, 264288, 52644150, 264828, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NC28 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264768, 21908789, 264928, 264630, 264634, 264638, 264563
2579	87292879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	68168788 (5159, 5160)	Novel Protein sim. GBank gj2588628 (AC003080) - Similar to KIAA0289; 60% similarity to AB002287 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87898048 (5161, 5162)	Novel Protein sim. GBank gj4406642[gblAAD20048] - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00395) - PDZ domain (Also known as DHR or GLGF).	collagen	56994075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87188559, 21908769, 265022, 35685855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gj2739387 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264786, 264838, 264555, 264585
2583	91220950 (5165, 5166)	Novel Protein sim. GBank gj4378112[emb]CAA16521.1] - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor	56181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55610764, 264630, 264637, 264585
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264788, 264693, 18108374, 55811576, 56182323
2585	80436128 (5169, 5170)	Novel Protein sim. GBank gj2736151 (AF021935) - myofibrillar dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264908, 265007, 265009, 264591, 60433356, 33637402, 265018, 264782, 264288, 21908766, 21908767, 21908769, 265022, 264691, 83373044, 58528488, 22278002
2587	80430943 (5173, 5174)				264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264584
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gj3021598[emb]CAA71415] - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35686052, 264905, 264906, 264907, 264908, 264909, 265008, 265018, 264769, 35686423, 264638
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gj2104688 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucosylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gj15702202[gblAAD47198.1]AF12916 - (AF128166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22278002

2592	95332848 (5183, 5184)	Novel Protein sim. GBank gil3024898[sp]Q60936[YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56894075, 284259, 29331822, 29331824, 29331828, 60432289, 29331827, 29331828, 264906, 284908, 285007, 285008, 284910, 80432228, 284594, 60433358, 60433438, 55812038, 18108348, 21908754, 265011, 87188559, 265017, 265018, 284784, 264369, 284288, 284786, 265021, 60170815, 33657023, 33657109, 264629, 35698423, 35695855, 284557, 284638, 60170394, 56182323, 83373044, 56526488, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gil4929729[gb]AAD34125.1[AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		tm7	22278999, 29331825, 284758, 21906754, 52646317, 265010, 18108351, 264288, 284389, 21908768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gil4929587[gb]AAD34054.1[AF15181 - (AF151817) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	284488, 18108398, 58182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331828, 284805, 284909, 52844045, 58182435, 264510, 284512, 265007, 264757, 21908754, 87168474, 265017, 284760, 264448, 264764, 284288, 264766, 264689, 21908768, 33657109, 263975, 263977, 264634, 264556, 60170394, 58182323, 56526488, 284482, 284583, 264564, 264586, 284567
2595	79561676 (5189, 5190)	Novel Protein sim. GBank gil4309881[gb]AAD15478] - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	284692
2596	87536637 (5191, 5192)	Novel Protein sim. GBank gil4309881[gb]AAD15478] - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 285018, 284448, 265021, 60431528
2597	94784089 (5193, 5194)	Novel Protein sim. GBank gil1001351[db]BAA10838] - (D64008) hypothetical protein [Synectocystis sp.]		UNCLASSIFIED	264905, 284509, 284908, 264762, 264766, 35695917, 35695855, 284635, 264636, 83373044, 264488
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gil1001351[db]BAA10838] - (D64008) hypothetical protein [Synectocystis sp.]		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 284683, 21908768, 35695917, 264681, 33657023, 33657109, 18108370, 18108374, 264564, 264565
2599	87842889 (5197, 5198)	Novel Protein sim. GBank gil3941737 (AF109719) - BAT2 [Mus musculus]		MHC	264766, 284769, 21908768, 33657182, 35695763, 18108370, 18108374, 284635, 264636, 56526488, 22278999, 284586
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gil4263521[gb]AAD15347] - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	35696286, 264083, 264288, 21908769, 35698423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278998, 264259, 28331822, 29331824, 80432289, 29331828, 29331827, 264906, 265007, 265008, 264591, 60433356, 33857402, 60433438, 21908754, 265011, 265018, 265019, 18108351, 264448, 264389, 21908769, 265020, 60170815, 264693, 33857109, 18108376, 56182323, 18108381, 18108385, 22279002, 264563, 60433438, 21908754, 87168559, 264601, 264389, 264288, 21908767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi 406632 gb AAD200471 - (AF131801) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35988052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33857084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21908765, 21908768, 21908767, 21908768, 21908769, 55811857, 265020, 265021, 265022, 60170615, 264691, 33857023, 264693, 33857109, 27486262, 18108374, 35988423, 85274791, 35895855, 264555, 264636, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gi 5454030 ref NP_008488.1 pRRP2 - RAS-related on chromosome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33857402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264766, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi 3628745 db BAA33366 - (AB013721) mhsugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264490, 80432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264756, 21908754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21908765, 21908766, 21908768, 21908769, 264691, 264692, 264693, 85274791, 264634, 264555, 264636, 22278998, 264510, 264512, 265009, 264766, 22279002, 264566
2608	87746408 (5211, 5212)				

2807	87627742 (5213, 5214)	Novel Protein sim. GBank gi4026628[gb AAD30202.1] - (AF135022) mediator [Homo sapiens]			28331822, 28331825, 28331826, 28331827, 28331828, 284908, 284907, 284908, 66712502, 284828, 56182435, 55812038, 285010, 285017, 285018, 285019, 284768, 284689, 21908765, 55811957, 285020, 285022, 284692, 33657023, 284693, 33657109, 18108370, 284639, 56182323, 284508, 284907, 284908, 284592, 284758, 284631
2808	81734786 (5215, 5216)	Novel Protein sim. GBank gi2226005 (U48873) - ORF2: function unknown [Homo sapiens]			
2809	94843791 (5217, 5218)	Novel Protein sim. GBank gi3024889[sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)]	Contains protein domain (PF00850) - Histone deacetylase family	histone	284488, 65274572, 35696286, 22278987, 22278999, 60432049, 284259, 56182181, 28331824, 28331825, 28331826, 60432289, 28331827, 28331828, 284905, 284907, 60433356, 60433438, 55812038, 285011, 87168559, 285017, 285018, 284448, 284765, 284288, 284766, 284689, 21908765, 21908767, 21908768, 285020, 285021, 284691, 284692, 33657109, 27486261, 18108370, 65274791, 284636, 284556, 56182323, 18108385, 56528488
2810	88177654 (5219, 5220)	Novel Protein sim. GBank gi4336855[gb AA017989] - (AF108473) leucine-rich-domain inter-acting protein 1; LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcript factor	18108394, 22278994, 56994075, 60432049, 284259, 28331822, 28331825, 60432289, 28331827, 284107, 284109, 284905, 56182435, 284112, 285008, 285007, 285008, 285009, 60433356, 60433438, 285011, 87168559, 285017, 284448, 284682, 284764, 284288, 285021, 33657023, 283987, 33657182, 27486261, 18108374, 263976, 55811578, 284638, 87168518, 60432113
2811	87428890 (5221, 5222)	Novel Protein sim. GBank gi3876761[emb CAA92994] - (Z68760) predicted using GeneFinder. Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278999, 285017, 284684, 21908768, 22278000
2812	87771198 (5223, 5224)	Novel Protein sim. GBank gi5879138[gb AAD46874.1 AF16093 - (AF160934)] BcDNA LD14169 [Drosophila melanogaster]		transport	285009, 284910, 284759, 285017, 21908767, 18108385, 18108388, 60432113
2813	79481486 (5225, 5226)			UNCLASSIFIED	264685
2814	87643948 (5227, 5228)	Novel Protein sim. GBank gi5533081[gb AAD45008.1 AF16118 - (AF161181)] P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278988, 22278989, 28331825, 284508, 284908, 21908754, 284602, 284768, 284769, 52844229, 21908765, 33657109, 27486284, 18108370, 263972, 284555, 60432113
2815	87381986 (5229, 5230)			UNCLASSIFIED	284768, 18108394, 284692, 284693, 284508, 284509, 284907, 284628, 284908, 284909, 18108377, 284511, 284512, 284810, 284635, 284595, 285010, 284404, 284563, 284764, 284685, 284768

2616	87428895 (5231, 5232)	Novel Protein sim. GBank gij3876761[embjCAA92894] - (Z88760) predicted using GeneFinder. Similarity to Mouse FKBP-type peptidyl-prolyl cis-trans isomerases [elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 604322049, 60432289, 284828, 60433356, 284594, 60433438, 33109954, 87188474, 265011, 265017, 265018, 284288, 284768, 21908765, 21908787, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 284482, 284587
2617	88978888 (5233, 5234)	Novel Protein sim. GBank gij728831[spP39188]ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265018, 284369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank gij3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 284490, 284259, 29331822, 284102, 284509, 284908, 284907, 66712502, 29331830, 265008, 284910, 265009, 60433356, 60433438, 284758, 21908754, 265011, 87188559, 265017, 265018, 284369, 284288, 284768, 284788, 284889, 21908765, 21908786, 21908787, 35695917, 265020, 265022, 33657023, 264692, 33657109, 284628, 18108374, 35695955, 18108381, 83373044, 18108385, 18108388, 58528486, 284583
2619	87684000 (5237, 5238)	Novel Protein sim. GBank gij2431772 (U68411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21908754, 284369, 60432113, 284568
2620	95314841 (5239, 5240)	Novel Protein sim. GBank gij4322597[gb AAD18097] - (AF090438) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52844507, 52845156, 52846842, 65274572, 22278995, 56994075, 35696288, 22278999, 60432049, 284259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 284907, 66712502, 265008, 60433356, 33657402, 52846317, 21908754, 87188474, 265010, 265017, 265018, 284448, 264369, 284288, 284687, 284768, 52844228, 284888, 284889, 21908765, 21908786, 35695917, 52844150, 284692, 33657109, 35695763, 35696423, 284556, 52844332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002, 284594, 284638
2621	80253495 (5241, 5242)	Novel Protein sim. GBank gij4557341[ref NP_001174.1]pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			284488, 284908, 284907, 284908, 284512, 285007, 284758, 35695917, 284634, 284636, 284583, 284482
2622	81780380 (5243, 5244)	Novel Protein sim. GBank gij3880355[embj CAB05289] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 284288, 29148629

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gjj3880355[embjCAB05299] - (Z62285) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278986, 22278987, 22278988, 22278989, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35688052, 29146499, 66712502, 52644045, 265007, 265008, 60433356, 33109954, 21908754, 265010, 265011, 265018, 264448, 264288, 21908785, 21908786, 21906787, 29148629, 35695917, 265021, 265022, 27486285, 18108370, 60431528, 55811576, 35695855, 56182323, 18108365, 87168518, 222789002, 18108391
2625	88452068 (5249, 5250)	Novel Protein sim. GBank gjj2887429[dbjBAA24857] - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	264081, 264511, 263981
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gjj487418 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gjj88462[pirjA27307] - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278986, 265007, 265009, 264448, 21908787, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gjj3123552[embjCAA18609] - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	22278987, 264259, 60432048, 29331822, 29331824, 29331825, 29331827, 35698052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433436, 265010, 265017, 265018, 264369, 264288, 18108357, 21908785, 21908788, 265022, 65274791, 264638, 18108387, 87168518, 222789002
2629	87378490 (5257, 5258)	Novel Protein sim. GBank gjj4928595[gbjAAD34058.1]AF15182 - (AF151821) CGI-83 protein [Homo sapiens]		synthase	29331825, 29331826, 264102, 265006, 264786, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79188384 (5259, 5260)			UNCLASSIFIED	264638, 18108385
2631	94845909 (5261, 5262)	Novel Protein sim. GBank gjj321605[pirjJQ1161] - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - dna_ma_bind Zinc finger, CCHC class	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35698286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644286, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264768, 264768, 52644229, 21908784, 21908785, 21908786, 21908787, 21908789, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486281, 27486282, 27486285, 33657349, 35695763, 35698423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264568, 264486
2632	36730414 (5263, 5264)				264885

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gij1139548 dbj BAA10889 - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF000084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265008, 265007, 265008, 265009, 55812038, 33857084, 55811388, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148829, 33657023, 264693, 33857182, 35895763, 55811576, 264639, 56182323, 83373044, 18108385, 58528488, 87168518, 22279000, 22279002, 264585
2634	87330921 (5267, 5268)	Novel Protein sim. GBank gij544161 emb CAB46854.1 - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33857084, 265017, 265018, 264448, 264288, 21908786, 21908787, 21908788, 29148829, 18108376, 55811576, 35895855, 87168518, 22278000
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gij4680663 gb AAD27721.1 AF132946) CGI-12 protein [Homo sapiens]		264569, 29331822, 29331828, 265008, 60170831, 264681, 264765, 264685, 29148627, 21908769, 29148784, 265022, 60170815, 264635, 18108385, 56528486, 22279002, 264567
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3879146 emb CAB07846 - (Z93388) Similarity to Yeast hypothetical 52.9 KD protein (SW:P43816); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	
2637	95011299 (5273, 5274)	Novel Protein sim. GBank gij4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	264488, 264489, 52844507, 264887, 52846365, 52846842, 22278994, 22278998, 22278999, 20281171, 264259, 29331822, 52845080, 66714117, 29331825, 29331826, 29331827, 35898052, 29331828, 28146488, 264508, 264805, 264806, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33857402, 60433356, 264757, 60433438, 264596, 264758, 52846317, 21908754, 52844288, 285010, 264600, 264602, 264603, 264605, 264781, 264782, 264681, 264448, 264784, 264785, 264288, 264786, 264686, 264788, 264687, 264789, 21908765, 21908768, 21908767, 21908768, 21908769, 35895917, 265021, 80170815, 264691, 33857023, 264692, 264693, 65274820, 27486284, 18108370, 264628, 264629, 18108374, 35898423, 35895855, 264632, 264634, 264635, 264637, 264638, 52844332, 264639, 264558, 83373044, 60432113, 264584, 264585, 264586, 264488, 264567

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gi 4929888 gb AAD34105.1 AF15186 - (AF15186) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52844507, 52648842, 18108398, 58182575, 22278995, 22278996, 35686288, 22278997, 22278998, 284259, 80432049, 29331822, 80424268, 29331828, 35696052, 29148498, 284905, 52644045, 58182435, 60433356, 33857402, 55812038, 55811386, 265019, 284288, 284768, 52644228, 58181562, 29148627, 29148629, 55811957, 29148784, 35695917, 285021, 52844150, 33857023, 85274820, 33857109, 35695783, 18108374, 55810764, 35698423, 55811576, 35695655, 80431850, 58182323, 60432113, 264404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank gi 2180007 dbj BAA203551 - (AB004109) phosphatidylserine synthase II [Cricetus griseus]		synthase	284488, 29331825, 35696052, 284508, 284509, 284909, 284512, 33857402, 60433438, 284758, 85658542, 284600, 285020, 285021, 33857109, 284628, 35698423, 284555, 284639, 284583, 284584, 284585, 284586, 284488
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gi 3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.78 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 87.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 284908, 33108954, 285017, 285019, 21908788, 35695783, 284638, 284637, 18108387
2641	11689834 (5281, 5282)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	284259, 29331822, 33857402, 285019, 284389, 284691, 284634, 58528486, 22279002
2643	87843981 (5285, 5286)	Novel Protein sim. GBank gi 4490304 emb CAB38795.1 - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278997, 284259, 29148499, 58182435, 264910, 265010, 18108351, 284682, 284683, 284369, 284684, 284685, 284686, 29148627, 284690, 33857109, 18108370, 263973, 18108374, 284634, 284557, 284558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gi 3789797 gb AAC87502.1 - (AF059568) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	nuc_rept	284107, 284687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank		UNCLASSIFIED	265007
2646	84148542 (5291, 5292)	gi 1706722 sp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	284909, 284687, 284632, 83373044

2847	91212878 (5283, 5294)				UNCLASSIFIED	56182575, 22278998, 35696286, 22278998, 284259, 29331822, 56182181, 28331825, 60424288, 60432289, 35696052, 66712502, 284908, 265007, 55812038, 33109954, 21908754, 33857084, 265019, 264448, 264288, 56181562, 21908785, 21908786, 21908788, 21908789, 35695917, 265020, 265021, 52644150, 264893, 33657109, 33657348, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2848	87600587 (5295, 5286)					29148498, 56182435, 33109954, 265011, 264882, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2849	94128783 (5297, 5288)			Novel Protein sim. GBank gj3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1666171) [Homo sapiens]	UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432289, 66712502, 56182435, 60170831, 60432228, 33657402, 33109954, 21908754, 265017, 264886, 264688, 21908785, 21908786, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264563
2850	87287533 (5288, 5300)			Novel Protein sim. GBank gj5360271 [dbj BAA81908.1] - (AB0283335) HPET-3 [Haloerythra roretzi]		264685
2851	88088745 (5301, 5302)			Novel Protein sim. GBank gj424025 [dbj BAA74891.1] - (AB020875) KIAA0868 protein [Homo sapiens]		28331824, 29331826, 29331827, 265007, 55812038, 21908754, 18108366, 18108384, 22279002, 264567
2852	10343125 (5303, 5304)			Novel Protein sim. GBank gj4493956 [emb CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 187 aa. Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:...	UNCLASSIFIED	284692
2853	87798735 (5305, 5306)				UNCLASSIFIED	285018, 18108370, 18108387, 264566
2854	95103240 (5307, 5308)					60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2855	91228018 (5309, 5310)			Novel Protein sim. GBank gj3875272 [emb CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	transcript factor Zinc finger, C3HC4 type (RING finger)	56182575, 56181886, 264082, 264259, 56182181, 60432289, 264807, 33657402, 55812038, 21908754, 67168559, 265017, 264448, 264369, 264288, 21908785, 21908786, 21908787, 21908788, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526488, 264404, 60432113
2856	84562801 (5311, 5312)			Novel Protein sim. GBank gj3043718 [dbj BAA25523] - (AB011189) KIAA0597 protein [Homo sapiens]		264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gij568509[dj]BAA83038.1] - (AB029009) KIAA1086 protein [Homo sapiens]			dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gij3688089 (AC005757) - R32811_1 [Homo sapiens]		Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21906768, 35695917, 264693, 35695855, 264637, 87198518, 264486, 264567
2659	87800755 (5317, 5318)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264769, 21906769, 264693, 263972, 18108386
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gij728637[sp]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII]		Contains protein domain (PF00036) - EF hand	kinase	244488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432269, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 28148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35698423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gij4758048[ref]NP_004739.1[pcpr8 - cell cycle progression 8 protein]			glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27488262, 60431528, 18108374, 35695855, 18108388, 264482
2662	80228739 (5323, 5324)	Novel Protein sim. GBank gij3874714[emb]CAA91263] - (Z66484) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]			dehydrogenase	264555, 264556, 264558, 264486
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gij1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]		Contains protein domain (PF00008) - EGF-like domain	oncogene	264906, 264908, 264757, 264758, 264767, 264691, 33657023, 264638
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gij4884408[emb]CAB43311.1] - (AL050190) hypothetical protein [Homo sapiens]			UNCLASSIFIED	35696286, 264508, 264595, 264288, 264685, 264686
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gij5108956[gb]AAD39908.1[AF113615] FH1/FH2 domain-containing protein FHOS [Homo sapiens]			UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35698423, 35695855, 22279002, 264482, 264488
2666	87828472 (5331, 5332)	Novel Protein sim. GBank gij2500570[sp]Q17533[RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0584.1]			UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gij2500570[sp]Q17533[RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0584.1]		Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567

2668	81216716 (5335, 5336)	Novel Protein sim. GBank gi 5454186 ref NP_008327.1 pZYG - ZYG homolog		UNCLASSIFIED	56181686, 35696286, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 66712502, 58182435, 60433356, 264758, 21908754, 55811386, 285011, 87188559, 285017, 265018, 55811150, 264448, 284369, 264288, 21908765, 21908768, 21908768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35696423, 55811576, 264634, 60431850, 83373044, 18108385, 87188518, 22278000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 pr JC4889 - proline rich protein - rat			264486, 264689, 21908767, 65274572, 56182575, 21908768, 29148827, 21908769, 29148828, 35696286, 35695917, 22278998, 22278998, 285021, 285022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29148498, 29148499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265006, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433436, 264559, 264595, 55812038, 33109954, 87188559, 60432113, 265019, 264448, 264389, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10362 YD8B_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger		18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD28444.1 AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2: VLCS-H2 [Homo sapiens]		transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21908754, 264682, 264288, 285021, 33657023, 33657109, 33657182, 27486281, 27486282, 27486285, 18108376, 18108385
2672	87398123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00634 - (AC006341) Contains two PF01344 Ketch motif domains. [Arabidopsis thaliana]	Contains protein domain (PF01344) - Ketch motif	UNCLASSIFIED	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gll5457337[emb CAB41505.2 - (AJ238876) poly(ADP-ribose)] polymerase-2 [Homo sapiens]	Contains protein domain (PF00844) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331828, 35896052, 60433438, 67168474, 67168559, 265017, 265018, 265019, 264448, 21908768, 21908769, 265020, 265021, 33657109, 27486262, 35895763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gll4758824[ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3]	Contains protein domain (PF001170) - bZIP transcription factor	transcription factor	264488, 22278996, 35896266, 264091, 264259, 29331824, 29331826, 35896052, 264511, 55812038, 85658542, 264766, 21908765, 35895917, 264628, 35896423, 18108383, 67168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	94328600 (5353, 5354)	Novel Protein sim. GBank gll1079042[pir S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56984075, 22278996, 35896288, 22278997, 22278998, 264480, 264259, 52845080, 29331824, 29331825, 60432289, 29331827, 29331828, 35896052, 29146499, 29331830, 264808, 52844045, 265006, 265007, 265008, 265009, 60432228, 60433356, 60433438, 55812038, 265010, 265011, 67168559, 265017, 265018, 18108351, 264682, 264448, 264683, 264288, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 60170815, 52844150, 264691, 33857023, 263967, 33857109, 27486264, 27486265, 33857348, 35895763, 18108370, 18108374, 18108377, 55811578, 35896423, 35895855, 83373044, 18108387, 22279000, 22279002, 264564

2676	95001694 (5355, 5356)	Novel Protein sim. GBank gij68760[pri]A40465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52648942, 35696286, 22278999, 264259, 29331825, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 87188559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108384, 18108385, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264568, 264488, 264587
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gij709233[isp]PQ7514[NC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87188518, 264586
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gij4589604[jdb]BAA76824.1] - (AB023187) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	264259, 264102, 264905, 264908, 265007, 265008, 33109854, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2681	90833544 (5361, 5362)	Novel Protein sim. GBank gij728837[isp]P39194[ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264488, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gij423468[pri]JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696286, 264908, 55811368, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 56526486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gij511435[isp]AAD40286.1] - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00822) - SPRY domain	interleukinrecept	264909, 264769, 264635, 264638

2684	85787151 (5387, 5388)	Novel Protein sim. GBank gi 4886469 emb CAB43385.1 - (AL050284) hypothetical protein [Homo sapiens]				264593
2685	88054289 (5389, 5370)	Novel Protein sim. GBank gi 3342728 (AC005331) - R31341_2 [Homo sapiens]		UNCLASSIFIED		
2686	87628680 (5371, 5372)	Novel Protein sim. GBank gi 465084 dbj BAA77027.1 - (AB026180) Ketch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - Ketch motif	struct		264259, 29331822, 60432289, 29331827, 29331830, 264909, 264512, 264596, 264789, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87998183 (5373, 5374)	Novel Protein sim. GBank gi 5281314 gb AAD41475.1 AF133123 - transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor		18108394, 18108396, 22278986, 35698286, 22278987, 29331826, 29331828, 68712502, 21908754, 265011, 264760, 264761, 264763, 264889, 21908785, 35698423, 264559, 18108385, 264563
2688	79859584 (5375, 5376)					264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gi 3880023 emb CAA07339 - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat			22278987, 22278988, 22278989, 29331824, 35698052, 264908, 264908, 56182435, 264512, 264910, 265009, 80433438, 21908754, 18108351, 264882, 264683, 264767, 21908785, 21908786, 21908788, 33657023, 33657182, 27488282, 27486284, 33657349, 18108370, 18108372, 18108374, 35698423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00820) - RhoGAP domain	struct		
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gi 4107276 emb CAA67130 - (X98508) acetyl-CoA synthetase [Solanum tuberosum]		synthase		65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264389, 264684, 21908789, 60170815, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264568
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gi 3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Proyl oligopeptidase family	peptidase		
2693	20438807 (5385, 5386)			UNCLASSIFIED		264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gi 3122400 sp O35882 MUG_MOUSE - MYELOID UPREGULATED PROTEIN				264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gi 4972740 gb AAD34765.1 - (AF132177) unknown [Drosophila melanogaster]		collagen		35698286, 56994075, 22278989, 264259, 35698052, 29331830, 265011, 264288, 56181582, 264680, 264682, 33657023, 27488282, 263978, 18108376, 35698423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264568
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase		264594, 21908766, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gij5689473jdbj BAA83020.1 - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21908765, 21908768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2698	94325891 (5395, 5398)	Novel Protein sim. GBank gij841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278955, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 28331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21908765, 21908766, 21908767, 21908769, 29148629, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27488261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87780850 (5397, 5398)	Novel Protein sim. GBank gij174395jref NP_006006.1 p8120 - Brain protein 120		UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139838 (5399, 5400)	Novel Protein sim. GBank gij174395jref NP_006006.1 p8120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181582, 55811957, 264693, 33657109, 60431528, 264629, 55810784, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gij1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264768, 18108359, 21908768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57285368 (5403, 5404)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87648514 (5405, 5406)	Novel Protein sim. GBank gij5689399jdbj BAA82983.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar).		60432289, 265007, 21908765, 21908768, 265021, 264563

2704	876-9515 (5407, 5408)	Novel Protein sim. GBank gij4335694[gb AAB63294] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29148499, 264805, 264808, 264807, 52844045, 264511, 33857402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264687, 264769, 265021, 264691, 264692, 18108382, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5408, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87169474, 264604, 264286, 264687, 264769, 264638, 264566, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gij3255952[emb CAA16821.1] - (AL021728) /prediction=(method:: /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56894075, 22278997, 264259, 29331824, 29331825, 29331828, 29331828, 33856970, 264907, 264908, 264909, 52644045, 56182435, 265008, 265007, 60433438, 55812038, 21908754, 52644298, 265010, 264801, 265017, 265019, 264681, 264448, 264882, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264690, 264691, 33857023, 264692, 264693, 65274620, 27466264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394
2707	88089639 (5413, 5414)	Novel Protein sim. GBank gij3417284 (AC004381) - Unknown gene product [Homo sapiens]			83373044, 65274727, 87168518, 22278900, 22278998, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bbas]147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331828, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109854, 265010, 265011, 264369, 264288, 264785, 264693, 264585
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2710	67627979 (5419, 5420)	Novel Protein sim. GBank gij4468311[emb CAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			29331824, 264759, 264693, 18108382, 18108388

2711	94111820 (5421, 5422)	Novel Protein sim. GBank gi 3122400 sp O36882 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264789, 21908784, 21908785, 21908787, 21908788, 21908789, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264258, 264681, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27488262, 33657349, 264508, 264805, 264907, 60431528, 264908, 264909, 55810764, 35698423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33108954, 18108385, 21908754, 33657084, 87188518, 87188474, 87188559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264780, 55811150, 264681, 18108351, 264585, 264784, 264568, 264288, 264768 264488, 35698288, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264908, 66712502, 52644045, 265008, 60432229, 33657402, 60433358, 265010, 265018, 18108351, 264681, 264288, 264685, 21908785, 21908768, 21908788, 21908789, 55811857, 35695917, 265020, 265021, 80170815, 264681, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35698423, 35695855, 264555, 52644332, 58182323, 87168518, 60432113 66714117, 264908, 264583
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi 5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25985_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5428, 5430)	Novel Protein sim. GBank gi 4321968 gb AAD15897 - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264805, 264907, 264908, 264909, 264910, 264758, 265011, 264780, 264784, 264288, 264786, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25985_3 [Homo sapiens]		glycoprotein	264081, 264258, 26331822, 66714117, 264908, 264369, 264893, 264556, 264563 264593, 264558
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi 3327046 gb BAA31591 - (AB014516) KIAA0818 protein [Homo sapiens]			264693
2718	79604082 (5435, 5436)				
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gi 748495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87188559, 265018, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gij1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21906765, 21906766, 35696423, 22278997, 265020, 265022, 265008, 265008, 264092, 264638, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108368, 60424288, 29331826, 18108365, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264908, 18108351, 264681, 18108370, 29331830, 264908, 68712502, 52644045, 264909, 264828, 18108354, 22278995, 35696286, 264259, 29331822, 29331824, 68714117, 29331826, 264908, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906768, 265021, 33657109, 263969, 60431528, 264629, 55811576, 85274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gij4829663 [gb AAD34092.1 AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		22278995, 35696286, 264259, 29331822, 29331824, 68714117, 29331826, 264908, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906768, 265021, 33657109, 263969, 60431528, 264629, 55811576, 85274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gij3212997 [gb AAC23434.1 - (AC004997) match to ESTs AA667999 (NID:g2626700), AA185485 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040654 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TBC domain	oncogene	21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)			UNCLASSIFIED	264508, 264509, 264808, 264809, 264810, 55812038, 264768, 264687, 264629, 264636, 264488
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gij4680681 [gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]		ubiquitin	18108398, 22278999, 20281099, 29331824, 29331828, 60432289, 29331826, 60170831, 60432229, 60433438, 18108351, 264682, 21906768, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86880399 (5451, 5452)	Novel Protein sim. GBank gij3342738 (AC005328) - R26660_1, partial CDS [Homo sapiens]		MHC	264488, 264828, 264685

2727	81010470 (5453, 5454)	Novel Protein sim. GBank gij731287[spIP39218]RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00049) - RNA pseudouridylylate synthase	- synthase	65274572, 56182575, 22278994, 56984075, 22278998, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331828, 29331827, 35686052, 29331828, 33656970, 284509, 66712502, 284910, 33657402, 60433438, 284758, 55812038, 21908754, 33657084, 55811386, 265018, 285019, 284767, 21908765, 21908787, 21908789, 55811957, 35695917, 52644150, 33657023, 33637109, 33657182, 27486281, 27486282, 27486285, 33657349, 55811578, 35696423, 35695855, 284630, 60431850, 284636, 558182323, 87168518, 60432113, 22278000, 284564, 284585
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gij3880433[embjCAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906787, 55811957, 35695855, 265021, 284690, 284558, 284259, 284557, 29331822, 284559, 284448, 284288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gij2408095[embjCAB10300] - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 284259, 60432288, 66712502, 558182435, 284448, 284288, 284369, 55811957, 285021, 284557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gij3880433[embjCAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	284887, 29331824, 29331826, 35696052, 284107, 56182435, 285008, 285009, 284592, 60431735, 285011, 284601, 265017, 18108351, 284288, 29148827, 55811957, 265021, 284690, 18108368, 18108374, 284557, 284558, 284559, 18108387, 56528486, 284566, 284486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gij1723239[spIQ10166]YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase	-	284259, 35696052, 285008, 284758, 284762, 284448, 284288, 28148827, 21908789, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gij3880433[embjCAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	284887, 284489, 18108358, 56182435, 284889, 35696423, 55811957, 265021, 285006, 285008, 284910, 285009, 284690, 284555, 284259, 284556, 284557, 284558, 284559, 18108383, 33657109, 87168518, 285010, 284601, 60432113, 265017, 284905, 284448, 263972, 284369, 284567
2733	87363060 (5465, 5466)			UNCLASSIFIED	29331825, 284509, 284909
2734	84140286 (5467, 5468)	Novel Protein sim. GBank gij4518621[dbjBAA75670.1] - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	- transcription factor	60424179, 52644507, 56182575, 284259, 29331828, 284907, 284310, 284910, 60433356, 285019, 55811150, 284681, 284763, 284687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712338 (5468, 5470)	Novel Protein sim. GBank gij38505569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278996, 60432289, 29331827, 28148498, 284108, 284909, 284112, 33657402, 87188474, 285017, 284782, 284448, 284784, 284684, 21808765, 284693, 33657109, 263976, 284636, 284638, 284557, 22279000, 22279002, 284567
2736	80247655 (5471, 5472)			UNCLASSIFIED	284905, 284628, 284628, 263978, 264632, 284564
2737	87604528 (5473, 5474)				284680
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gij2558501[dbj BA22898] - (D63850) hepatoma-derived growth factor [Mus musculus]			284488, 285008, 284768, 284891
2739	94318834 (5477, 5478)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284684, 83373044, 284566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gij3417386[emb CAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	284488, 58182575, 22278995, 35696286, 22278987, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29148498, 29331830, 285008, 285007, 285009, 80432229, 33657402, 5812038, 87188474, 285010, 285011, 285017, 285018, 285019, 284605, 284681, 284288, 284369, 52844229, 21908765, 21908768, 21908767, 21908768, 21908769, 285020, 285022, 284691, 284692, 33657108, 18108370, 18108374, 55810764, 35695855, 284634, 80431850, 284638, 58182323, 18108382, 18108365, 65274727, 22279002, 284584
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gij3242764 (AC005154) - similar to protein U28928 (PID:g881308) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644228, 21906768, 21908769, 285020, 80170815, 284681
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gij4758412[ref NP_004472.1]pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 2 [Gallus gallus]	Contains protein domain (PF00852) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	284259, 284805, 284758, 55812038, 284369, 29148627
2743	87627891 (5485, 5486)	Novel Protein sim. GBank gij4468311[emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35698286, 284259, 284908, 284908, 285009, 80433438, 285017, 18108351, 284448, 284784, 284288, 21908765, 21908767, 284680, 284691, 284693, 283989, 283971, 35695855, 284637, 284558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gij3880433[emb CAA91399] - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL: C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 284488, 58182435, 21908765, 35698423, 35695917, 35695855, 285020, 285021, 284511, 285009, 284490, 284556, 284259, 284557, 58182323, 284558, 284559, 18108383, 29331824, 18108385, 33657109, 28331826, 21908754, 29331827, 29331828, 33657349, 87188518, 285018, 284905, 284482, 284448, 284486, 284369, 284288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gij4405795[gijAAD19826] - (AF038983) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - helicase Helicases conserved C-terminal domain	35699286, 284509, 284905, 284907, 284908, 284510, 284512, 285008, 284758, 284801, 285017, 284604, 284763, 284288, 284886, 284769, 284693, 35698423, 35695855, 284634, 284638, 284563, 284564, 284565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gij4758738[ref]NP_004680.1[pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	22278998, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 284905, 284908, 284807, 284908, 284909, 52844045, 285008, 80170831, 284598, 55812038, 285018, 284683, 284288, 21908785, 21908787, 21908788, 21908789, 265020, 284690, 33657023, 284693, 33657109, 18108368, 18108374, 284558, 18108385, 22279000, 284563
2747	94112677 (5483, 5494)	Novel Protein sim. GBank gij4557803[ref]NP_000262.1[pNPC1 - Niemann-Pick disease, type C1	glycoprotein	284589, 52844507, 18108394, 22278995, 35698286, 22278997, 22278998, 52845080, 29331824, 56182181, 29331828, 29331827, 35696052, 284907, 284908, 284909, 265009, 33109954, 55811386, 87188474, 285010, 87188559, 284603, 285019, 284760, 284688, 284788, 21908789, 35695917, 80170615, 284692, 33657023, 52845128, 27486284, 60431528, 18108374, 35698423, 35695855, 284556, 58182323, 18108385, 284482
2748	91214983 (5485, 5486)	Novel Protein sim. GBank gij4191272[emb]CAA09884] - (A012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.	63274572, 29331828, 284112, 284511, 285018, 284780, 284767, 284768, 284769, 21908788, 21908789, 265020, 27486262, 58528486, 87188518, 22279000
2749	87346307 (5487, 5498)			284258, 284908, 284510, 285008, 265009, 284760, 284389, 284768, 284563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - PIUS [Oryctolagus cuniculus]	UNCLASSIFIED	284488, 52844507, 18108396, 56994075, 284258, 29331825, 29331826, 29331827, 29331828, 284508, 265009, 284910, 284591, 284595, 33657084, 285011, 285019, 18108351, 284288, 284686, 284789, 284689, 55811957, 284693, 27486264, 18108370, 18108374, 284558, 18108385, 284482, 284563
2751	87057465 (5501, 5502)		UNCLASSIFIED	29331822, 29331824, 285017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U85067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	

2753	94138972 (5505, 5508)	Novel Protein sim. GBank gi 3851648 (AF088301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF000646) - F-box domain.	UNCLASSIFIED	56182575, 56894075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33108954, 18108351, 264288, 58181562, 21908767, 21908768, 265021, 264893, 18108374, 65274791, 264632, 58182323, 22278002, 264583, 264587
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin-like protein [Plum sativum]	Contains protein domain (PF00038) - EF hand	struct	22278998, 66714117, 29331827, 35896052, 29331828, 264806, 264808, 264809, 285011, 265017, 285018, 265019, 264288, 21908765, 21908767, 265022, 33657023, 264893, 56182323, 18108382, 22279000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gi 2896653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465808 (5511, 5512)	Novel Protein sim. GBank gi 173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	264594
2757	95361590 (5513, 5514)	Novel Protein sim. GBank gi 3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		eph	85658542, 264693
2758	79637848 (5515, 5516)	Novel Protein sim. GBank gi 3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank gi 2072200 (U94863) - p40 [Borna disease virus]			65274572, 35686286, 68714117, 29331828, 264508, 56182435, 21908754, 55811857, 264628, 264638, 56182323, 22279002
2760	76824798 (5518, 5520)	Novel Protein sim. GBank gi 4914573 (emb CABA3685.1) - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264808
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gi 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00889) - PAS domain	nuclease	22278998, 28331822, 29331830, 285010, 285019, 264288, 21908765, 21908768, 21908769, 285020, 56182323, 22279002, 264563
2762	87592699 (5523, 5524)	Novel Protein sim. GBank gi 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00889) - PAS domain	struct	18108394, 22278998, 264806, 264809, 285006, 285007, 284757, 285010, 285011, 285017, 285019, 18108351, 264448, 264883, 264886, 264768, 265020, 265021, 265022, 264891, 18108382, 264693, 18108385, 33657109, 18108388, 18108370, 18108381, 18108382, 18108394, 18108388, 87168518
2763	87539998 (5525, 5526)	Novel Protein sim. GBank gi 3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264389, 35896423
2764	84305140 (5527, 5528)	Novel Protein sim. GBank gi 2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52646842, 264258, 29331822, 29331825, 29331828, 29331828, 33656970, 284905, 264907, 29331830, 265006, 265009, 21908754, 285019, 264448, 21908769, 27486262, 58182323, 56526486, 87168518, 264487

2765	94315105 (5529, 5530)	Novel Protein sim. GBank gj4688872[embjCAA17688.2] - (AL022018) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster])			264488, 65274572, 22278995, 35898288, 22278998, 22278999, 264259, 29331822, 29331824, 35898052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55812038, 33109954, 265010, 87168559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21908764, 21908765, 21908768, 35895917, 265021, 264891, 264892, 33857023, 33857109, 264628, 18108370, 264629, 18108374, 55811576, 35896423, 35895855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168516, 22279000, 22279002, 264563, 264482
2766	94315108 (5531, 5532)	Novel Protein sim. GBank gj5441611[embjCAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264488, 65274572, 60432289, 264807, 264909, 264511, 264512, 60433356, 264288, 264685, 264689, 35895917, 265022, 264693, 264628, 65274791, 264635, 264555, 264556, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gj1078451[pirjAS5463] - tropomodulin, skeletal muscle - chicken		struct	264112, 263874, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gj5441322[embjCAB46721.1] - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35896286, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35898052, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33857402, 264594, 264595, 264757, 264598, 265011, 264604, 265018, 264760, 264881, 18108351, 264764, 264288, 264766, 264889, 264768, 18108357, 264769, 264689, 21908766, 21908768, 21908769, 35895917, 265021, 265022, 33857023, 33857109, 264628, 264629, 18108374, 35896423, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264488, 264587

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gj5419859[emb](CAB46375.1) - (AL098725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 284908, 29331830, 58182435, 264592, 33657402, 264448, 264369, 264288, 60170815, 284891, 33657023, 264892, 33657109, 18108374, 55811576, 284634, 264838, 56182323, 83373044, 60432113
2770	87730182 (5538, 5540)	Novel Protein sim. GBank gj5701965[emb](CAB52157.1) - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	18108398, 22278995, 22278996, 22278999, 264105, 265008, 265019, 18108351, 264687, 21908765, 18108384, 264628, 18108374, 264631, 18108385, 18108388
2771	88084071 (5541, 5542)	Novel Protein sim. GBank gj3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 264369
2772	95357309 (5543, 5544)	Novel Protein sim. GBank gj4885531[ref](NP_005465.1)[pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264768, 21908769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264584, 264486
2773	94138894 (5545, 5546)	Novel Protein sim. GBank gj3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 284688, 264687, 263978, 56182435, 284688, 55810764, 21908768, 35896423, 55811576, 65274791, 56181886, 55811957, 35695855, 284110, 265021, 264112, 265022, 285008, 265008, 264092, 284094, 60431850, 264637, 264891, 264259, 264692, 263981, 284594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424288, 18108385, 29331826, 29331827, 27486281, 29331828, 35696052, 55811386, 284107, 60432113, 265017, 55811150, 18108351, 264681, 264908, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 284288, 284684, 264768, 263974, 22278995, 35696288, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21908754, 87168559, 265017, 285018, 284288, 21908768, 21908767, 21908768, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263978, 35698423, 35695855, 87168518, 22279000, 264482
2774	87819908 (5547, 5548)	Novel Protein sim. GBank gj465852[sp]P34388[YL3, CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomal prot	

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4689132 gb AAD27775.1 AF077042) 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF001177) - ribosomalprot Ribosomal protein S7p/S5e	264488, 22278995, 56994075, 22278998, 35698286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35698052, 265007, 21906754, 265017, 265019, 264448, 264682, 264389, 264288, 18108354, 52844229, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 35698117, 265021, 265022, 60170615, 264691, 18108370, 35698423, 65274791, 35698555, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2778	87791557 (5551, 5552)			56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 55811366, 265017, 265019, 264448, 264288, 21906765, 21906768, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810784, 55811576, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)		UNCLASSIFIED	264907, 264768
2778	82112411 (5555, 5556)		UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87849729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297) CGI-36 protein [Homo sapiens]	UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35698052, 265006, 264512, 264448, 264288, 29148827, 18108364, 20281149, 18108370, 264629
2780	94678397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 p HGK - HPK/GCK-like kinase	Contains protein domain (PF00780) - CHK1 domain	29148499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF068502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	60424179, 29331824, 60424268, 66714117, 29331826, 56182435, 87169474, 265017, 264784, 56181562, 21906765, 21906768, 21906768, 35698117, 265020, 33657023, 35698555, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 p LRN - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	65274572, 22278998, 22278998, 60432049, 264259, 29331822, 29331824, 29331826, 60432288, 29331828, 264905, 264907, 264908, 264908, 52844045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264788, 52644228, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35698555, 264557, 56182323, 83373044, 18108385

2783	80016829 (5565, 5566)	Novel Protein sim. GBank gi 728831 sp P39189 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		Im7	264809, 264628, 263978, 263981
2784	87614360 (5587, 5588)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pf J558890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21908765, 21906768, 21906768, 265020, 264584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase: DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA1 - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21908765, 21908768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108385, 29331824, 33657109, 29331827, 35695052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88080644 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264103, 21908768, 264693
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gi 2495728 sp Q82556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (H48725)		UNCLASSIFIED	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1 - (AJ242978) p821 [Homo sapiens]		struct	22278998, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35695052, 264908, 68712502, 29331830, 264909, 60432228, 60433356, 60433438, 33108954, 265010, 265011, 265017, 265018, 265019, 264692, 264448, 264288, 264369, 264768, 52844229, 21906765, 21906768, 265020, 265021, 33657023, 263974, 18108374, 65274781, 35695856, 264636, 264558, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22279000, 264587
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]			264259, 60432288, 66712502, 265009, 264636
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi 2854163 gb AAC02581.1 - (AF045842) No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264698, 265022, 264691, 18108388, 264587
2793	87425476 (5585, 5586)			UNCLASSIFIED	264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264698, 265022, 264691, 18108388, 264587

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gi 5454146 ref NP_008348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBCA15)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35696286, 22278988, 22278989, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109854, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 58182323, 58526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2796	94848857 (5591, 5592)	Novel Protein sim. GBank gi 4680651 gb AAD27715.1 AF13294 - (AF13294) CGI-08 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278989, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264906, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265008, 264591, 264592, 60433356, 264594, 264595, 55812038, 264596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264286, 264685, 264766, 264687, 56181562, 264768, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52844150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486285, 33657349, 18108374, 35696423, 65274761, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2797	95110780 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278985, 22278986, 22278997, 29331827, 28148499, 264508, 264806, 56182435, 264757, 21906754, 265010, 265017, 265018, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 264826, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2798	86198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007180) - unknown [Homo sapiens]		UNCLASSIFIED	264486, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278986, 22278997, 22278998, 22278999, 60432049, 284259, 29331828, 35696052, 29331828, 284909, 60433358, 33657402, 33109954, 87168474, 284448, 52844229, 21908766, 21908787, 21908788, 35695917, 285020, 265021, 265022, 52844150, 35695855, 284634, 60432113, 22279000, 284488, 56994075, 284259, 20281099, 28331825, 29331827, 284905, 56182435, 285006, 265011, 87168559, 265017, 285019, 284448, 284288, 284766, 284688, 60170615, 284691, 284692, 27486265, 284628, 284629, 284636, 284557, 284558, 284559, 87168518, 284584, 284586, 284587, 265007, 284687
2800	88316481 (5589, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74928.1 - (AB020713) KIAA0808 protein [Homo sapiens]		glycoprotein	28331825, 29331827, 284905, 56182435, 285006, 265011, 87168559, 265017, 285019, 284448, 284288, 284766, 284688, 60170615, 284691, 284692, 27486265, 284628, 284629, 284636, 284557, 284558, 284559, 87168518, 284584, 284586, 284587, 265007, 284687
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		265007, 284687
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002484) - organic cation transporter; 50% similarity to JC4884 (P/D: g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	79577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC006588 - (AC006588) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	264639
2804	57111131 (5607, 5608)			peptidase	264566
2805	87398486 (5609, 5610)				264092, 284259, 29331822, 29331824, 29331827, 29331828, 284508, 285007, 285009, 21906754, 284369, 284288, 284632, 60170394, 284583, 284482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 1168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278985, 22278986, 22278987, 284259, 29331822, 29331824, 29331826, 29331827, 29146498, 285008, 285009, 60433438, 265017, 265018, 265019, 264448, 284288, 21908765, 21908787, 21908788, 28148629, 265022, 52844150, 56182323

2807	911720702 (5613, 5614)	Novel Protein sim. GBank gij4466310[emb]CAB37991] - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35698052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433356, 264594, 60433436, 52646317, 21808754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264783, 264687, 52644229, 21808765, 21808766, 21906767, 21808768, 21808769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35698423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gij5541863[emb]CAB51071.1] - (AL096857) hypothetical protein [Homo sapiens]		MHC	60432289, 284510, 265010, 265017, 265018, 264681, 264686, 265021, 264680, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gij272561 (AC004002) - similar to ciliary dynein beta heavy chain: 78% Similarity to P23098 (PID:g118965) [Homo sapiens]		ATPase_associated	18108351
2810	67259032 (5619, 5620)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29146628, 29146784, 264693
2811	91235945 (5621, 5622)			UNCLASSIFIED	264108
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1628773) [Homo sapiens]		UNCLASSIFIED	
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gij4240273[db]BAA74915.1] - (AB020699) KIAA0892 protein [Homo sapiens]		UNCLASSIFIED	
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gij3548781 (AC005620) - R33590.1 [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113, 65274572
2815	78774521 (5629, 5630)			UNCLASSIFIED	264907, 264909
2816	95358228 (5631, 5632)	Novel Protein sim. GBank gij5420389[emb]CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 35698286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21908765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264488

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi 1293946 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 28331822, 28331827, 264508, 284509, 284905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811857, 35695917, 33657109, 263978, 264634, 264636, 264639, 264584, 264565, 264566, 264486, 264587
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gi 549988 (U13149) - possible apoptosis-associated protein [Peromyscus maniculatus]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87793527 (5637, 5638)	Novel Protein sim. GBank gi 4929773 (gb AAD34147.1) AF152097 CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	264909, 264511
2820	87765744 (5638, 5640)	Novel Protein sim. GBank gi 4929773 (gb AAD34147.1) AF152097 CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264638
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi 2224671 (p JBA020820) - (AB002363) KIAA0385 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21906765, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)	Novel Protein sim. GBank gi 3856683 (emb CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]			264760
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gi 3856683 (emb CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]			52845156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656870, 52644045, 52646317, 33657084, 52644286, 265017, 265019, 265018, 264288, 21906764, 21906785, 21906768, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486285, 35695763, 35695842, 35695855, 52844332, 18108385, 87188518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 263994, 264489, 65274572, 29331822, 86714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432228, 264592, 264593, 264595, 264596, 21908754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264585, 264586, 264567, 264486, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35698052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264688, 55811957, 18108370, 18108374, 55810784, 35698423, 55811576, 56182323, 83373044, 87168518 22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 68712502, 264510, 264511, 264593, 60433438, 21908754, 265011, 264603, 18108351, 264288, 21908765, 21908788, 21908769, 26148828, 52644150, 264693, 33857109, 18108374, 264634, 18108385, 60432113, 22279000, 264585, 264488 265008, 265019, 264639, 22279002
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680689 gb AAD27734.1 AF13295 - (AF13295) CGI-25 protein [Homo sapiens]			
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi 2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21908767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5282615 emb CAB45747.1 - (AL080158) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	264259, 264112, 265010, 264762, 264784, 263974, 264555, 264558, 264559

2837	87786482 (5673, 5674)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 284908, 265006, 265007, 265018, 265019, 284682, 284288, 21908766, 21908767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775382 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 284567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gij1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]		UNCLASSIFIED	284555
2840	87774665 (5678, 5680)	Novel Protein sim. GBank gij2224605[dbj]BAA20780] - (AB002330) KIAA0332 [Homo sapiens]			264509, 264511, 265011, 264288, 264769, 285020, 284634, 284636, 284556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dbj]BAA20780] - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		56182575, 35696052, 284907, 284908, 284909, 284910, 264593, 284595, 284766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 284631, 284559, 284583, 264567
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gij5578957[emb]CAB51350.1] - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	284600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij5578957[emb]CAB51350.1] - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	284906, 284907, 284908, 284909, 284910, 284784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp]Q08878[FBL C. MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)]	Contains protein domain (PF00008) - EGF-like domain		264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		homeobox	28146498, 87168474, 284686, 35696423, 83373044, 284564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gij5306263[gb]AAD41995.1[AC008233] unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	28331830, 284909, 265008, 265011, 87168559, 284628, 284556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij3399676 (AC005390) - R31180.1 [Homo sapiens]		UNCLASSIFIED	284908, 284766, 284769, 284628, 284637, 284566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gij5262615[emb]CAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264490, 264259, 284508, 284905, 284907, 284510, 265007, 265008, 284591, 284592, 284593, 284594, 284595, 55812038, 265010, 265011, 284804, 284763, 284764, 284765, 284766, 284686, 284628, 284629, 284555, 284636, 284556, 284557, 284638, 284558, 284559, 284563, 284566, 284567
2849	86084283 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 284908, 265007, 264594, 265018, 284288, 263972, 35696423, 18108384, 56528486, 18108390
2850	87623636 (5699, 5700)			UNCLASSIFIED	35696286, 265008, 285009, 265018, 284288, 35695917, 284693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321618[gb]AAD15788.1] - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264389, 21908765, 264891, 264692, 264693, 35695855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 [U88308] - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129845) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF003397) - kinase		56182575, 55811150, 264690, 27486262, 27486285, 264632, 56182323, 56528466, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2785825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079086) [Homo sapiens]	Contains protein domain (PF01344) - dna_ma_bind Kelch motif		35696286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gij1504040[gb]BAA13219] - (D86983) similar to D.melanogaster peroxidasin(U11052) [Homo sapiens]	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264908, 264808, 265009, 33109954, 265018, 265019, 264448, 21908765, 265020, 264690, 27486285, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g1118843) and AA085546 (NID:g1628773) [Homo sapiens]			21908766, 22278997, 265022, 29331822, 29331826, 27488282, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21908765, 21908769, 265020, 18108368, 35695763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585[sp]P35227[ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)]	Contains protein domain (PF00097) - dna_ma_bind Zinc finger, C3HC4 type (RING finger)		264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 28331827, 29331828, 264508, 264905, 264908, 28331830, 264808, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 80433356, 264585, 264758, 21908754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21908766, 21908767, 265021, 264534, 60170615, 264691, 264892, 18108370, 264829, 18108374, 264631, 264636, 263981, 18108381, 264536, 18108385, 22279002, 264584, 264566, 264486, 264567
2859	90937675 (5717, 5718)	Novel Protein sim. GBank gij4325320[gb]AAD17331.1] - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	60424179, 65274572, 29331828, 264905, 284511, 264758, 265011, 21908767, 21908769, 55811957, 265021, 56182323

2860	87532569 (5719, 5720)	Novel Protein sim. GBank gij4469186jembjCAB38414.1] - (AL031588) d11633.1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridyate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 28331822, 28331824, 28331825, 28331826, 28331827, 28331828, 284510, 284511, 33109954, 18108351, 284683, 284765, 284389, 284686, 21906765, 284691, 284692, 284693, 18108388, 22279002, 284482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gij3941730 (AF108083) - BS4 [Homo sapiens]			284369, 284692
2862	87569385 (5723, 5724)	Novel Protein sim. GBank gij4505013jrefjNP_002310.1 pLRN] - leucine-rich neuronal protein		UNCLASSIFIED	284691, 284638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gij3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	56994075, 35686286, 22278998, 28331822, 28331824, 35686052, 28331828, 284108, 284511, 55812038, 33857084, 55811386, 285018, 285019, 21908765, 21906766, 21906769, 35685917, 285020, 285022, 33657023, 33657109, 33657349, 284629, 18108376, 60431650, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gij1079451 pirjA55463 - Tropomodulin, skeletal muscle - chicken		struct	284259, 284910
2865	95312181 (5729, 5730)	Novel Protein sim. GBank gij338840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2866	85105480 (5731, 5732)	Novel Protein sim. GBank gij565703 spjQ07088 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN		glycoprotein	65274572, 22278986, 22278998, 22278999, 284259, 28331824, 28331827, 29331828, 60433438, 21908754, 285018, 284448, 284764, 52844150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gij4580997 gbjAAD24571.1 AF12108 - (AF121081) cAMP Inducible 2 protein [Mus musculus]		UNCLASSIFIED	284486, 284768, 21908768, 22278998, 285022, 284259, 284508, 284905, 284907, 284511, 284910, 284635, 284638, 284637, 285011, 285017, 285018, 285019, 284583, 284088, 284566, 284784, 284369, 284587, 284486, 284288, 284766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gij1282868[emb](CAA63923) - (X94232) i-Cell activation protein [Homo sapiens]			18108392, 264488, 22278894, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284508, 52844045, 284828, 285006, 285007, 285008, 285009, 284591, 60432228, 264593, 60433358, 284595, 21908754, 285017, 285019, 284682, 264369, 21908785, 21908788, 21908787, 21908788, 285021, 285022, 284891, 33557182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35696423, 35695855, 284632, 58182323, 87168518, 264404, 22279000, 22279002, 284482, 284563, 284564, 264567, 264487
2869	88084412 (5737, 5738)			UNCLASSIFIED	284389
2870	84404574 (5739, 5740)			UNCLASSIFIED	284905, 264908, 264764, 21906789, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gij5306263[gb]/AAD41995.1(AC008233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	284259, 29331822, 60432289, 29331827, 284907, 285008, 285017, 265016, 264682, 264764, 18108354, 265021, 27486265, 284629, 18108387, 264587
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gij112203[pir](B39066 - proline-rich protein 15 - rat		kinase	263981
2873	88084252 (5745, 5746)			UNCLASSIFIED	284488, 18108374, 264768, 264687, 264688, 284689, 35696423, 35696286, 35695917, 284510, 284511, 265007, 284512, 265008, 284910, 284534, 284634, 284635, 284555, 284592, 284259, 284558, 60433438, 60432289, 35696052, 265011, 264600, 284601, 60432113, 264508, 284563, 284482, 284509, 284905, 264908, 264564, 18108351, 284763, 18108370, 284907, 284566, 284908, 284764, 284288, 264567, 264909, 264488, 264768, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gjl3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52844507, 52845156, 52846365, 58182575, 22278994, 22278995, 58994075, 35898286, 60432048, 284259, 52845080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35896052, 29331828, 33658970, 66712502, 52844045, 285007, 285008, 60433358, 284758, 55812038, 18108348, 52846317, 33109954, 33657084, 285017, 284604, 285018, 285019, 284682, 284369, 284288, 284888, 52844229, 21908786, 21908787, 21908788, 55811957, 265020, 265021, 265022, 52844150, 33657023, 52845129, 18108374, 18108376, 35696423, 58182323, 18108387, 87188518, 60432113, 22278000, 22279002, 264563, 264565
2875	88083726 (5748, 5750)	Novel Protein sim. GBank gjl2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	glycoprotein	22278996, 22278997, 22278999, 29331826, 29331828, 28148489, 66712502, 265008, 285017, 18108351, 264683, 264689, 21908787, 18108378, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gjl2979530 (AC004449) - R33863 2 [Homo sapiens]	IgI	
2877	94747029 (5753, 5754)	Novel Protein sim. GBank gjl4704208lamb(CA841646.1) - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]		52846365, 65274572, 58182575, 22278997, 22278998, 22278999, 60432048, 52845080, 60424269, 60432288, 29331827, 35896052, 29331828, 66712502, 52844045, 58182435, 60433356, 33657402, 33657084, 285018, 55811150, 284448, 284369, 21908786, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52844332, 58182323, 264558, 83373044, 18108385, 58528486, 60432113, 22278000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank gjl367675lamb(CA803067) - (Z81077) predicted using GeneFINDER. Similarity to Yeast protein 8246 (TR:G587531) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 284259, 29331822, 29331826, 264905, 284508, 284907, 264908, 284510, 285008, 284511, 264512, 33657402, 264758, 21906754, 18108351, 284681, 284682, 284288, 264684, 264685, 264768, 284689, 21908788, 284690, 33857023, 284693, 18108364, 33657109, 264629, 18108374, 284630, 284632, 284556, 284637, 284639, 264558, 18108385, 18108387, 264563, 264564, 284585, 264586, 264486, 264567

2876	87868122 (5757, 5768)	Novel Protein sim. GBank gij4895145jgb AAD32752.1 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264258, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264558, 265017, 264564, 264565, 264587, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gij4880703jgb AAD27741.1 AF13296 - (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35698286, 22278998, 22278999, 264259, 29331822, 28331824, 29331825, 29331828, 29331827, 35698052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265008, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644286, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264789, 21908788, 21908789, 35695917, 265021, 264890, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264628, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264587, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gij733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED		22278998, 28331822, 52644045, 21906765, 264639, 80432113
2882	87714387 (5763, 5764)	Novel Protein sim. GBank gij118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278998, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21908788, 21908789, 264693, 263987, 18108374, 55811578, 58182323, 22279002, 264588
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gij488008jgb AAD31087.1 AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264692
2884	87784643 (5767, 5768)	Novel Protein sim. GBank gij2224697jdbj BAA20832 - (AB002376) KIAA0378 [Homo sapiens]		UNCLASSIFIED	265018, 264634
2885	83006306 (5769, 5770)	Novel Protein sim. GBank gij1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF000084) - Sushi domain (SCR repeat)	complementrecept	264686, 264693
2886	91237823 (5771, 5772)				60432049, 264258, 29331828, 264908, 264511, 264595, 60433436, 264596, 265017, 264605, 263989, 263972, 264555, 83373044, 87168518, 264568
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gij3882323jdbj BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]	UNCLASSIFIED		18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gij4508015jref NP_003447.1 pZNF2 - zinc finger protein 205 [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcriptfactor	264488, 264259, 29331828, 264508, 264906, 264593, 264756, 264786, 264769, 18108374, 83373044, 264486

2889	87806582 (5777, 5778)				UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gij854065jembj[CA58337] - (X83413) U88 [Human herpesvirus 8]			UNCLASSIFIED	284591, 264766
2891	88094428 (5781, 5782)	Novel Protein sim. GBank gij3877750jembj[CAB01508] - (Z78084) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65885 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66028 comes from this gene; cDNA EST EMBL:D69558 comes from this gene...			UNCLASSIFIED	284591, 264595, 264389, 264685, 264693, 264628, 264563, 264566
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gij4929759jgbjAAD34140.1jAF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 285009, 60433438, 265018, 265019, 18108351, 264288, 21908765, 21908766, 21908769, 55811857, 264690, 65274620, 263987, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	284259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gij5669015jgbjAAD46135.1j - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		transcript factor	264259, 265006, 60433438, 52644296, 265011, 264389, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gij3924708jembj[CAAB4646] - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D78135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			28331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gij4885549jrefjNP_005456.1jpPKBG - protein kinase B gamma	Contains protein domain (PF00089) - Eukaryotic protein kinase domain		kinase	18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146499, 284908, 264908, 285007, 265009, 265018, 265019, 264389, 264685, 264689, 21908766, 265021, 264693, 33857182, 264639, 18108394, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gij4502877jrefjNP_001296.1jpCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424289, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811388, 265018, 18108351, 264448, 264288, 264867, 21908765, 21908766, 21908767, 21908769, 55811857, 35695917, 264534, 33857023, 33857109, 35695783, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 284555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5787, 5788)					264764, 21908784, 264692
2900	94233538 (5798, 5800)		Novel Protein sim. GBank gij4581470[emb]CAB40137.1] - (Y18483) SLCTA8 protein [Homo sapiens]		UNCLASSIFIED glycoprotein	63274572, 56182575, 35696286, 60432049, 264259, 29331824, 66714117, 29331828, 35698052, 29331828, 66712502, 56182435, 285006, 265007, 285008, 285009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21908784, 21908788, 21908789, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)		Novel Protein sim. GBank gij4759272[ref]NP_004614.1 pTTC4 - tetrairicopeptide repeat domain 4		phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35698052, 33656970, 264910, 265009, 21908754, 33657084, 87168474, 265010, 265018, 21908784, 21908785, 21908788, 21908789, 33657023, 264693, 33657109, 33657349, 35698423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)		Novel Protein sim. GBank gij2414615[emb]CAB16364] - (Z99259) hypothetical protein [Schizosaccharomyces pombe]			264683, 264691
2903	87606733 (5805, 5806)		Novel Protein sim. GBank gij1079318[pir][S52241 - XLCL2 protein - African clawed frog			264887, 22278984, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)		Novel Protein sim. GBank gij5639823[gb]AAD45885.1 AF14387 - (AF143876) multispinning nuclear envelope membrane protein nufim [Homo sapiens]		UNCLASSIFIED	52646365, 22278989, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263987, 18108374, 35695855, 264637, 264832, 18108365, 18108387
2905	84449926 (5809, 5810)		Novel Protein sim. GBank gij728637[sp]P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	265009, 264681, 264682
2906	95341051 (5811, 5812)		Novel Protein sim. GBank gij4689256[gb]AAD27831.1 AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278995, 35698286, 22278998, 264259, 60432288, 29331828, 29331830, 66712502, 265009, 60170831, 33108954, 264448, 264683, 264288, 264689, 21908788, 21908789, 21908788, 55811957, 35695917, 265022, 52644150, 264681, 33657023, 264692, 264693, 35695855, 60432113, 264568

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNAJ-like domain (PS:PS00836) [Caenorhabditis elegans]	Contains protein domain (PF00228) - DnaJ domain	eph	52844507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 58182181, 35680052, 80431735, 264595, 55812038, 21906754, 55811388, 265019, 264682, 264369, 56181582, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35686423, 35695855, 264638, 22279000
2808	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]		helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2809	87420225 (5817, 5818)			eph	264259, 87168474, 265018, 18108365, 264628
2810	86601075 (5819, 5820)	Novel Protein sim. GBank gi 4539335 emb CA837483.1 - (AL035539) putative protein [Arabidopsis thaliana]			22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2811	94216615 (5821, 5822)	Novel Protein sim. GBank gi 4459187 emb CA838415.1 - (AL031588) dJ1163J1.3 (novel protein similar to mouse B99) [Homo sapiens]		glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2812	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4928637 gb AAD34078.1 AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat		52845156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 86712502, 33109954, 264760, 264683, 264288, 264686, 265021, 264693, 18108368, 263976, 264404
2813	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854055 emb CAA583371 - (X83413) U88 [Human herpesvirus 6]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	52844507, 52645156, 52646842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264628, 52644045, 56182435, 55812038, 52646317, 21906754, 52644298, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906768, 21906767, 21906768, 35695917, 265020, 52644150, 27486281, 27486282, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2814	87797300 (5827, 5828)				264557

2915	88081972 (5829, 5830)	Novel Protein sim. GBank gjl5174485jref NP_006030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain (PF00059) - eph Lectin C-type domain	264569, 264488, 264687, 264768, 21906786, 52846842, 21908767, 21908788, 58182575, 29148629, 35695917, 22278998, 22278997, 22278998, 285021, 22278999, 52844150, 264691, 264259, 60432049, 264692, 52845129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331826, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52844045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433358, 56182323, 18108382, 55812038, 18108385, 33109954, 21908754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 285019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264369, 264288, 264768
2918	95337790 (5831, 5832)	Novel Protein sim. GBank gjl5104851 dbj BA80165.1 - (AP000081) 305aa long hypothetical dTDP-4- dehydrothamnose reductase [Aeropyrum pernix]	dehydrogenase	52845156, 65274572, 22278994, 22278995, 35696288, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33658970, 264509, 264908, 29331830, 52844045, 264909, 58182435, 60170831, 264592, 264593, 33657402, 60433356, 52846317, 21906754, 33109954, 33657084, 52844296, 85858542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52844229, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52844150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52844332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gjl3169065 emb CAA19260.1 - (AL023704) putative translocation elongation factor-Tu Ia milly [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	65690529 (5835, 5836)	Novel Protein sim. GBank gjl539216 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gjl2584955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263881

2920	87769523 (5839, 5840)				35696286, 22278987, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21908754, 52644296, 265010, 265011, 264801, 265017, 265019, 264881, 264887, 21908767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486282, 27486284, 27486285, 35696423, 35695655, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639882 (5841, 5842)	Novel Protein sim. GBank gi 4580013 gb AAD24202.1 U83194_ - (U83194) TRAF4-associated factor 2 (Homo sapiens)	Contains protein domain (PF00787) - PX domain		35696286, 22278987, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29148498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433356, 21908754, 87168474, 265017, 18108351, 264288, 21908765, 21908766, 21908767, 21908769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 56528486, 87168518, 22279000, 22279002
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gi 4589514 db BAA76779.1 - (AB023152) KIAA093S protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 36	kinase	264908, 264809, 264511, 265006, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21908765, 28148627, 35695917, 264692, 264628, 263978, 55811578, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264498
2923	95337799 (5845, 5846)	Novel Protein sim. GBank gi 4835268 emb CA42898.2 - (Z83844) dJ37E18.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00189) - PH domain	struct	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265008, 33657402, 265011, 265017, 265018, 264883, 18108354, 21908765, 21908767, 21908768, 21908769, 52644150, 264691, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264568
2924	87791987 (5847, 5848)	Novel Protein sim. GBank gi 2133095 pir J572254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomal prot	265017, 264628, 20281152, 264556
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gi 2386986 emb CAB11718 - (Z88880) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		56182575, 35696286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21908754, 264681, 264448, 264683, 264288, 264685, 52644228, 264689, 21908765, 21908766, 21908768, 21908769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 56182323

2928	95343003 (5851, 5852)	Novel Protein sim. GBank gij283032[pir][S22456 - hydroxyproline-rich glycoprotein - perennial teasalte			29331828, 285011, 284768, 284689, 284764, 284288, 284630, 284637
2927	80408018 (5853, 5854)				
2928	20452179 (5855, 5856)			UNCLASSIFIED	284559
2929	91622820 (5857, 5858)	Novel Protein sim. GBank gij3413320[emb][CAA06915] - (AJ008215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	284589, 284489, 22278994, 35686286, 22278998, 22278998, 22278999, 284094, 284259, 52845080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696032, 33856970, 284109, 29331830, 52844045, 285009, 33109954, 52844296, 87168559, 284760, 284762, 284448, 284764, 284288, 284766, 284768, 21908765, 21908768, 21908768, 21908769, 35695917, 284691, 33857023, 284693, 33857109, 18108374, 283978, 35896423, 35895855, 283981, 22279000, 22279002, 284567, 284486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278998, 284259, 29331825, 60432289, 29331828, 284905, 52844045, 58182435, 285009, 60170831, 284592, 60432228, 60433356, 87168474, 285010, 285011, 285017, 285018, 285019, 284762, 284448, 284683, 284288, 284768, 21908765, 21908769, 35695917, 60170815, 33857023, 33857109, 284628, 18108370, 18108372, 35696423, 35695855, 284556, 56182323, 60432113, 284567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gij3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52845156, 22278997, 22278998, 29331822, 52845080, 28331824, 60432289, 33856970, 60433356, 60433438, 33109954, 21908765, 21908768, 21908767, 21908768, 285020, 52844150, 33857023, 33857109, 33857182, 27488285, 35896423, 35695855, 284555, 87168518, 60432113, 284586
2932	79632623 (5863, 5864)				284906, 284907
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gij3378058 (AF017777) - helicase [Drosophila melanogaster]	helicase		284488, 18108382, 56182575, 22278998, 284091, 284259, 29331825, 60432289, 29331827, 284508, 52844045, 56182435, 285007, 285009, 284592, 60433356, 60433438, 21908754, 285017, 284682, 284288, 52844229, 21908765, 21908768, 21908768, 21908769, 285022, 52844150, 33857023, 33857109, 27488285, 284635, 284638, 60170394, 56182323, 18108385, 60432113, 284565, 284586, 284587

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 284691, 27486282, 264628, 87168518, 22278000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264756, 33109954, 21906754, 265018, 265019, 264448, 264769, 21908784, 21908765, 265021, 284692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi 4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:842735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811578, 18108387, 60432113, 284563
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gi 5174409 ref NP_008101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264759, 60432049, 29331822, 56182181, 29331827, 29331828, 284908, 264908, 264909, 56182435, 265006, 284512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644228, 21908765, 29148784, 65274791, 284556, 56182323, 60170394, 284558, 60432113, 284565, 264486, 264567
2938	95418773 (5875, 5876)	Novel Protein sim. GBank gi 3318990 emb CAA76720 - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 285008, 265009, 60432229, 33657402, 60433438, 55812038, 21908754, 85658542, 285010, 265011, 87168559, 265017, 285018, 265019, 264681, 264288, 264689, 21908765, 21908787, 21908788, 55811957, 35895917, 265020, 60170615, 264690, 264691, 284692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56326486, 60432113, 22278002
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi 3978900 emb CAA99809 - (Z75547) similar to WD domain, G-beta repeat; cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8 ...	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 284685, 264686

2940	95011103 (5879, 5880)			UNCLASSIFIED	22278986, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 68712502, 29331830, 265011, 265017, 264764, 264369, 21906768, 21906767, 33657023, 33657108, 32833966, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gi 3413872 dbj BAA32300 - (AB007924) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gi 1172845 sp P46629 RB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gi 4929653 gb AAD34087.1 AF15185 - (AF15185) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29148498, 265008, 264593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gi 4678282 emb CAB41190.1 - (AL049680) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	58984075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331828, 29331828, 264905, 264907, 52644045, 264908, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35898423, 35898655, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 58528488, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35896032, 264808, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 264887, 56181562, 21906767, 21906768, 21906769, 35895917, 265020, 265021, 264693, 60431526, 55810764, 35898423, 35895955, 264630, 60170394, 83373044, 22279000, 264566, 264567

2846	84317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	284488, 284259, 284508, 284509, 284908, 284907, 284808, 284510, 284511, 285007, 284512, 284810, 284591, 284593, 18108351, 284784, 284288, 284684, 284789, 285021, 284692, 33857109, 284628, 284637, 18108374, 284631, 284634, 284636, 284629, 18108380, 284638, 284639, 83373044, 284565, 284566, 284488, 284567
2847	87362852 (5883, 5884)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1 - (AF056118) All-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278998, 22278997, 22278999, 29148498, 284508, 29331830, 285007, 285008, 285009, 60432229, 21908754, 285010, 285017, 285019, 284788, 284685, 21908765, 21908766, 21908767, 21908768, 21908769, 285020, 284628, 18108370, 284629, 284630, 18108387, 60432113
2848	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			52846842, 22278995, 284259, 29331824, 29331825, 29331827, 29331830, 284909, 285007, 285009, 285019, 284763, 284684, 284288, 284685, 284688, 21908767, 284691, 284692, 284693, 18108374, 55811578, 18108385, 22279002, 284563, 284567
2849	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pir J587133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278998, 22278997, 60432289, 29331826, 29331827, 29331828, 35686052, 29148499, 284104, 284107, 284805, 68712502, 284808, 60433358, 60433438, 87188559, 284764, 52844229, 58181562, 21908767, 21908768, 21908769, 285022, 60170815, 33857023, 35886423, 283981, 284558, 60432113, 22279002
2850	85086870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 YQJ6 CAEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	284488, 35686286, 284259, 35686052, 284907, 285007, 284810, 285017, 285018, 284288, 284788, 35885917, 285020, 18108362, 18108370, 18108379, 35886423, 65274791, 35685855, 284558, 58528486, 284486
2851	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			284693

2952	95328952 (5903, 5904)	Novel Protein sim. GBank gij5596693[emb]CAB51405.1]- (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00850) - CRAL/TRIO domain.	transcript/factor	264887, 52845156, 21908766, 21908769, 22278998, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108385, 29331825, 60432289, 33657109, 18108388, 29331827, 35898052, 27486262, 264508, 264905, 20281149, 264908, 264907, 29331830, 264908, 264909, 35895855, 264511, 265008, 285009, 264910, 264635, 264638, 60432229, 264638, 60433358, 264639, 264738, 87188518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093375 (5905, 5906)	Novel Protein sim. GBank gij119522[sp]P10658[SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT1) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)]	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	18108398, 58994075, 22278998, 29331822, 29331824, 29331825, 29331827, 35898052, 264508, 264905, 264908, 264907, 264510, 264591, 264594, 33657402, 264595, 264586, 264758, 52846317, 21908754, 33657084, 52644286, 87168559, 264600, 264760, 264881, 18108351, 264764, 264389, 264288, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 35895917, 33657023, 18108364, 52645129, 33657109, 33657348, 18108374, 263978, 35895855, 264637, 264638, 87168518, 264482, 264563, 264565 29331822
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gij4885261[ref]NP_005251.1[pGDF9 - growth differentiation factor 9]	Contains protein domain (PF00019) - Transforming growth factor beta like domain	tgf	
2955	87898426 (5909, 5910)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331828, 35898052, 264908, 52644045, 264312, 60432229, 265018, 265019, 5581150, 264769, 21908767, 21908768, 21908769, 265021, 80170815, 55810764, 264567
2956	85789745 (5911, 5912)	Novel Protein sim. GBank gij4889254[gb]AAD27830.1[AF12185 - (AF121857) sorting nexin 7 (Homo sapiens)]	Contains protein domain (PF00787) - PX domain		22278998, 264259, 29331827, 264908, 21908768
2957	90933301 (5913, 5914)	Novel Protein sim. GBank gij4503023[ref]NP_000089.1[pCPT2 - carnitine palmitoyltransferase II precursor]		cadherin	22278998, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148629, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gij4240257[dbj]BAA74807.1]- (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264598, 264681, 264389, 264629, 264631, 264567

2859	95109420 (5817, 5916)	Novel Protein sim. GBank gj1988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - TBC domain	oncogene	263994, 22278997, 264259, 60432049, 29331826, 29331828, 35696052, 29331830, 68712502, 56182435, 265008, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264883, 264288, 264768, 264769, 21908766, 21908767, 21908769, 265020, 60170615, 264692, 27486265, 18108374, 65274791, 35695955, 83373044, 56526486, 60432113
2860	87420091 (5819, 5920)			UNCLASSIFIED	35696286, 56182435, 87169474, 265010, 60170815, 35696423, 56182323, 18108383, 87168518, 264483
2861	95413416 (5921, 5922)	Novel Protein sim. GBank gj15596646[emb] (CA805177.2) - (Z82266) predicted using Genefinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52844045, 265006, 33657402, 21908754, 87168474, 265011, 87168559, 265017, 21908768, 265020, 60170815, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264584, 264587
2862	87912700 (5923, 5924)			UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 68714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52846317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264768, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 264567, 264486
2863	95313464 (5925, 5926)	Novel Protein sim. GBank gj14240223[dbj] (BAA74890.1) - (AB020874) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21908754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486261, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2864	94324617 (5927, 5928)			UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108388, 83373044, 18108388

2865	80384762 (5929, 5930)	Novel Protein sim. GBank gi 4885447 ref NP_005452.1 pKRMML - Kreisler (mouse) maf- related leucine zipper homolog		transcriptfactor	284259, 29331826, 284508, 284509, 284905, 284907, 284908, 284909, 284511, 285008, 284910, 284591, 284593, 284594, 33657402, 285011, 284760, 284762, 284764, 284288, 284685, 284766, 284682, 33657109, 284628, 284629, 3569855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 284583, 284587, 18108391 60432289, 284682, 284448
2866	91725249 (5931, 5932)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			
2867	84656303 (5933, 5934)	Novel Protein sim. GBank gi 624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	284488, 284508, 284509, 284908, 284909, 284511, 284910, 284594, 284758, 85658542, 284782, 284784, 285021, 284556, 18108381, 284584, 284488
2868	85302776 (5935, 5936)	Novel Protein sim. GBank gi 4929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)		284687, 52645156, 21908765, 52846365, 21908767, 18108398, 35696423, 22278996, 35696286, 22278997, 285020, 22278999, 285021, 285022, 284093, 284638, 284690, 52844150, 284258, 33657023, 52845080, 284683, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52845129, 29331826, 21908754, 33657182, 29331827, 29331828, 35698052, 27486282, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 284583, 18108351, 284908, 284907, 284448, 66712502, 284588, 284389, 284288
2869	95310957 (5937, 5938)	Novel Protein sim. GBank gi 3024743 pp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	52846842, 22278996, 22278998, 22278999, 60432049, 284259, 29331824, 29331825, 29331826, 29331828, 284509, 284909, 52844045, 56182435, 285009, 60433438, 55812038, 21908754, 285011, 87168559, 285018, 285019, 284448, 284288, 284389, 52844229, 21908768, 21908769, 21908769, 29148784, 285020, 285021, 52844150, 284681, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2870	86088071 (5939, 5940)	Novel Protein sim. GBank gi 3165407 (AC004755) - fos37502.1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2971	94196830 (5941, 5942)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Im7	264488, 56182575, 35686286, 56884075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21908754, 87168559, 285018, 285019, 18108351, 264689, 21908765, 21908767, 21908768, 265020, 265021, 60170615, 18108364, 264628, 264628, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264564, 264567 265017, 35695917, 265021, 33657109, 22278002, 264563
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gi 2746788 (AF040842) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181688, 22278995, 22278996, 35686286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 68714117, 60424269, 29331826, 29331827, 29331828, 35698052, 68712502, 264808, 52644045, 265007, 284910, 285008, 60433438, 33109954, 21908754, 55811386, 52644298, 87168474, 87168559, 285017, 265018, 285019, 18108351, 264448, 264389, 264288, 52644228, 18108359, 21908765, 21908767, 21908768, 35695917, 265020, 265021, 52644150, 264891, 264892, 33657023, 27466262, 27466264, 35695783, 18108370, 18108376, 55810784, 55811576, 35686423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22279000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gi 3880812 emb CAA19508 - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 285018, 264448, 264288, 264769, 21908767, 265020, 264691, 264559, 83373044
2976	87771202 (5951, 5952)	Novel Protein sim. GBank gi 5679136 gb AAD48874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	22278998, 264806, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108365
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2878	67332059 (5955, 5956)	Novel Protein sim. GBank gj1746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 284259, 60432289, 29331827, 29146499, 56102435, 285008, 285007, 285009, 60433356, 60433438, 21906754, 285010, 285011, 285017, 285018, 285019, 284288, 284885, 284688, 21908785, 21908788, 21908787, 21908788, 21908789, 285020, 285021, 285022, 35686423, 284639, 60432113, 22279000, 22279002
2879	91725256 (5957, 5958)	Novel Protein sim. GBank gj15262751 (emb CAB45690.1 - (AJ243177) Xenopus RPA Interacting protein alpha [Xenopus laevis])	complement		284488, 65274572, 56894075, 22278998, 284093, 28331822, 29331824, 284288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2880	86286600 (5959, 5960)			UNCLASSIFIED	265009, 21908787, 263981, 22279000
2881	87376330 (5961, 5962)				264629, 284564
2882	95303675 (5963, 5964)	Novel Protein sim. GBank gj14929787 (gb AAD34144.1 AF15190 - (AF151907) CGI-149 protein [Homo sapiens])			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 28331824, 28331827, 29331828, 264905, 284591, 284592, 284594, 284595, 284596, 33657084, 284448, 21908785, 21908786, 21908787, 21908788, 21908789, 285020, 265022, 18108365, 33657182, 33657349, 35686423, 83373044, 22279000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gj15262751 (emb CAB45690.1 - (AJ243177) Xenopus RPA Interacting protein alpha [Xenopus laevis])			60424178, 52646842, 18108398, 22278997, 284093, 60432049, 284259, 29331822, 60432288, 33658970, 284905, 52844045, 285006, 60431735, 87168474, 285018, 285019, 18108351, 284448, 21908785, 21908788, 35685917, 33657023, 52845129, 18108370, 35686423, 83373044, 56528488, 60432113, 284404, 22279002
2884	94136467 (5967, 5968)	Novel Protein sim. GBank gj12393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	ATPase associated		
2885	87099072 (5969, 5970)	Novel Protein sim. GBank gj1103160 (pir S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster))	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 284828, 55810784, 284832, 284635, 60432113
2886	86284861 (5971, 5972)				55811957, 284566
2887	88455934 (5973, 5974)		UNCLASSIFIED		284369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gij4678028[gbjAAD27002.1] - (AF077207) HSPC021 [Homo sapiens]	UNCLASSIFIED	284488, 65274572, 22278995, 22278998, 22278997, 22278998, 284092, 284094, 284298, 60432049, 28331824, 28331828, 60432289, 35698052, 29331828, 284107, 284905, 284907, 284908, 66712502, 284828, 284909, 56182435, 265006, 265007, 265008, 60170831, 60432228, 284593, 80433356, 284757, 60433438, 21906754, 265010, 265011, 87168559, 285017, 265018, 264682, 264448, 284389, 284288, 284685, 52844228, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52844150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 284637, 263981, 284638, 56182323, 83373044, 60432113, 22279000, 284563, 284564, 284565, 284566, 284567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gij113671[spj23984]ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII	kinase	22278998, 22278997, 284905, 284511, 80170831, 284593, 265019, 21908785, 21906767, 21906768, 18108374
2990	87330444 (5978, 5980)	Novel Protein sim. GBank gij2829836[spj97348]RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	265007, 264512, 18108351, 264288, 264689, 265020, 284691, 33657023, 33657109
2991	94325361 (5981, 5982)		UNCLASSIFIED	284553
2992	85425184 (5983, 5984)		UNCLASSIFIED	284259, 285018, 284689, 18108365
2993	94325363 (5985, 5986)		UNCLASSIFIED	264488, 28331822, 265017, 284781, 21906769, 65274791, 263981, 284565
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gij2496549[spjQ50858]YU02_MYCTU - HYPOTHETICAL 28.7 KD PROTEIN CY339.02	transport	22278994, 22278995, 56994075, 22278997, 22278998, 284259, 28331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 285008, 284910, 33109954, 87168474, 87168559, 265018, 285019, 284448, 284288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 284693, 35695855, 83373044, 18108385, 22279000, 284565, 264568
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gij2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		284905, 264607, 265019, 18108351, 264683
2996	81013788 (5991, 5992)	Novel Protein sim. GBank gij2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	65274572, 35698286, 284259, 29331824, 35698052, 28146498, 284508, 284907, 265007, 265008, 60433438, 18108348, 265017, 284681, 284683, 284288, 284766, 284769, 284689, 35695917, 80170615, 33657023, 284692, 284634, 284555, 18108381, 18108382, 18108388, 264484

2987	87627440 (5983, 5994)	Novel Protein sim. GBank gij4589652[dj]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]	homeobox	284488, 56182575, 264259, 68714117, 29331828, 35698052, 264508, 264509, 264907, 264808, 265008, 87188474, 265019, 264446, 264882, 264885, 264766, 21908764, 21908766, 21908768, 21908769, 27486261, 18108374, 35898423, 264634, 264635, 264638, 264557, 18108385, 87188518, 52848385, 22278987, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35898423, 264636, 264639
2998	88095381 (5985, 5996)	Novel Protein sim. GBank gij3947589[emb]CAA22252] - (AL034384) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	264638, 264557, 18108385, 87188518, 52848385, 22278987, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35898423, 264636, 264639
2998	94847055 (5987, 5998)	Novel Protein sim. GBank gij115408[sp]P18835[CC]19_CAEEL - CUTICLE COLLAGEN 19	UNCLASSIFIED	56182575, 22278986, 28147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21906754, 85658542, 18108351, 29148627, 29148629, 80170815, 33657109, 27486262, 18108370, 18108374, 284558, 264557, 264558, 60170394, 18108385, 264563
3000	95098370 (5989, 6000)	Novel Protein sim. GBank gij1163174 (U32575) - similar to yeast Sec8p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]	UNCLASSIFIED	284887, 22278997, 22278999, 284259, 29331822, 29331824, 35698052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264598, 264758, 21906754, 265011, 264800, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264881, 264882, 264764, 264288, 264885, 264766, 264886, 264768, 264769, 21908765, 21908768, 35895917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486261, 264628, 264629, 18108374, 18108376, 35898423, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264638, 264639, 60170394, 83373044, 20798451, 22278902, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gij2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing.; coded for by human cDNAs AA122029 (NID:g1676048), D31562 (NID:g844442), AA158721 (NID:g1733515), R58840 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]	calthepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644298, 265017, 265019, 264268, 265020, 265021, 52644150, 264692, 35895763, 55810764, 35898423, 56182323, 18108387, 264563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gij3599478 (AF085185) - Myosin-1A [Acanthamoeba castellanii]	UNCLASSIFIED	264488, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 264510, 265009, 21908754, 264682, 264688, 33657023, 264565

3003	86848078 (6005, 6006)	Novel Protein sim. GBank gl 1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	264512, 264593, 264564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gl 2224629[db][BAA20802] - (AB002342) KIAA0344 [Homo sapiens]			29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794843 (6008, 6010)	Novel Protein sim. GBank gl 4680859[gb]/AAD27718.1[AF13294] CGI-10 protein [Homo sapiens]	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21906766, 21906767, 21906768, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3006	97422224 (6011, 6012)	Novel Protein sim. GBank gl 3930523 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	MHC	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	80936005 (6013, 6014)	Novel Protein sim. GBank gl 2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	52644507, 52845156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170616, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)				264805, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gl 3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	52846842, 56182575, 22278995, 22278998, 264259, 29331825, 29331826, 29331827, 29331828, 35686052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264737, 264758, 59612038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21906784, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486282, 20281149, 18108370, 55811578, 264637, 264558, 264557, 18108361, 264556, 56182323, 264559, 18108365, 18108368, 22278902, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gl 4927370[gb]/AAD33084.1[AF06797] DNA cytosine methyltransferase 3 alpha [Homo sapiens]	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278998, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486281, 29331828, 264508, 264909, 55811578, 35695955, 265008, 264558, 60433436, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gl 5052319[gb]/AAD38501.1[AF11883] citrin; adult-onset type II citrullinemia protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)			UNCLASSIFIED	263972

3013	91238799 (6025, 6026)	Novel Protein sim. GBank gij3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35698286, 22278997, 264259, 29331824, 60424289, 66714117, 35696052, 264905, 264906, 264907, 264908, 264909, 58182435, 264511, 264512, 264810, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21908754, 265010, 265018, 264804, 264780, 264682, 264683, 264784, 264389, 264288, 264765, 264786, 264886, 264788, 264687, 21908767, 35695917, 265020, 33657023, 264692, 264893, 33657109, 264628, 264629, 55811578, 35698423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264586, 264587
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gij3878374 (embjCAA93081) - (Z88879) Similarity to Yeast Chi12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33318 comes from...		ATPase_associated	264760
3015	86995468 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331826, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264584
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gij1168819 (sp P41733 CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656870, 52844045, 264596, 33657084, 265017, 265019, 52644229, 21908767, 35695917, 52844150, 33657023, 33657109, 27486281, 27486282, 27486284, 33657349, 27486265, 35695763, 35695855, 87188518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gij4589658 (dbj BAA78851.1 - (AB023224) KIAA1007 protein [Homo sapiens])			264488, 18108397, 22278996, 35696286, 22278998, 264259, 28331822, 60432289, 264908, 28331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52846317, 21908754, 55811388, 265010, 265011, 87188559, 265017, 265018, 265019, 264288, 264687, 21908765, 21908766, 21908767, 21908769, 265020, 265022, 65274820, 52845129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52844332, 83373044, 18108385, 18108386, 56528486, 87188518, 284404, 80432113, 22279000, 264567

3018	11073891 (6035, 6036)				264558	
3019	94148231 (6037, 6038)	Novel Protein sim. GBank gij3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264558, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278998, 264259, 29331822, 29331824, 60432289, 29331827, 284808, 56182435, 265007, 265009, 60432229, 284593, 60433356, 59812038, 21908754, 87168474, 285011, 87168559, 265017, 265018, 265018, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264688, 21908766, 21908768, 21908769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264628, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264583	
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gij3414809 (AF061529) - rjs [Mus musculus]	Contains protein domain (PF00415) - ATPase associated Regulator of chromosome condensation (RCC1)		264488, 263994, 35696288, 264259, 264508, 264905, 264508, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264638, 264639, 83373044, 18108385, 264584, 264587, 264488	
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gij3880889[emb] (CA809005) - (Z95559) cDNA EST YK2364.5 comes from this gene; cDNA EST EMBL.C13455 comes from this gene; cDNA EST YK2996.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			284769, 264628, 264482	
3022	87718500 (6043, 6044)			UNCLASSIFIED	284258, 28331826, 28331828, 264288, 264586	
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gij416592[sp]P32323JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00814) - Phospholipase D. Active site motif	UNCLASSIFIED	284488, 22278995, 35696286, 22278997, 29331826, 35696052, 264807, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21908767, 55811957, 35695917, 285021, 18108376, 263978, 264635, 264558, 22279000	
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432048, 264760, 21908768, 55811957, 35695917, 264690, 264555, 264559	
3025	85706829 (6048, 6050)	Novel Protein sim. GBank gij295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			264593, 55811578	

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gij3024052ispj97924[KARI_RAT] - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87188559, 265019, 21908765, 29148627, 263987, 20281149, 20281089, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gij4929847[gbjAAD34084.1][AF15184] CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35686286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 68714117, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264810, 33857402, 264596, 21906754, 265010, 265011, 87188559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264789, 264688, 21908765, 21908766, 21908767, 21908768, 21908769, 28148629, 35695917, 265020, 265021, 285022, 52844150, 264692, 33857023, 264693, 52845129, 33857109, 27486281, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56528486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gij3080521[embjCAA18650] - (AL022598) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87188559, 265018, 264782, 264683, 264765, 264689, 21906765, 21906768, 21908769, 28148629, 35695917, 265021, 265022, 33857109, 27486285, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87188474, 265019, 18108351, 21908768, 264534, 264690, 264893, 263989, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gij3757728[embjCAA18782] - (AL022727) dJ8019.1 (olfactory receptor-like protein [hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	-Im7	
3031	91677953 (6061, 6062)	Novel Protein sim. GBank gij4530587[gbjAAD22105.1] - (AF132000) TADA 1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21908765, 21908766, 21908767, 21908768, 265021, 263974, 18108374, 264558, 56528486, 22279000, 22279002

3032	94130124 (6063, 6084)	Novel Protein sim. GBank gi 1019951 (U37429) - similar to M. musculus MERs and other AHPCTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	synthase	22278996, 35686286, 264259, 29331824, 29331828, 284907, 29331830, 264758, 33109954, 87168474, 87168559, 265019, 264288, 21806769, 265021, 264693, 35698423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi 5031573 ref NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - Actin	struct	35698286, 284259, 29331826, 35696052, 264508, 264805, 264908, 284907, 264908, 264909, 265008, 264591, 21806754, 265010, 265019, 264681, 264369, 264768, 21806764, 21806768, 35695917, 33857023, 264628, 35695855, 264632, 264635, 264639, 264482, 264583
3034	80415373 (6067, 6088)			UNCLASSIFIED	264808, 264907, 264510, 264592, 265010, 264782, 264766, 264637, 264638, 264486
3035	91220892 (6069, 6070)	Novel Protein sim. GBank gi 3738207 emb CAA21262 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264807, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi 406590 gb AAD20040 - (AF131768) Similar to Ena-VASP like protein [Homo sapiens]			265017
3038	85421807 (6075, 6076)	Novel Protein sim. GBank gi 5360093 gb AAD42865.1 AF15509 - (AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	22278996, 22278997, 264259, 284905, 265007, 265009, 60433358, 21806754, 265016, 265019, 18108351, 264687, 21806765, 265020, 265021, 65274620, 27486262, 264638, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi 4757128 emb CAB42094.1 - (AJ238717) ZRP protein [Rattus norvegicus]		UNCLASSIFIED	35698286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35698423, 264584, 18108391, 264692, 264558, 18108382, 18108385, 264587
3040	80833517 (6079, 6080)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]			
3041	86312357 (6081, 6082)	Novel Protein sim. GBank gi 3876073 emb CAB04122.1 - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...		UNCLASSIFIED	56984075, 22278997, 22278998, 29331827, 33656970, 33108854, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi 790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]		glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264805, 66712502, 58182435, 55811386, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042276) - 6251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COO5 methyltransferase family	glycoprotein	22278998, 22278998, 22278998, 29331824, 58182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108368, 18108370, 60170394
3045	84127598 (6089, 6090)	Novel Protein sim. GBank gi 4589880 dbj BAA76859.1 - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_ma_bind	264488, 264259, 35696052, 264508, 264805, 264509, 264806, 264907, 264909, 264511, 265008, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21908765, 21908768, 55811957, 35695917, 27486282, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88088247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264806, 52846317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	85089924 (6093, 6094)			UNCLASSIFIED	264488, 22278998, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21908766, 21908768, 35695917, 52644150, 33657349, 65274781, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger, protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284102, 29148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_006286.1 pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21908766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gi 4589842 dbj BAA76843.1 - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265018, 264288, 21908766, 265020, 264693, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase	264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947613 emb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35686286, 22278998, 284259, 60432289, 265008, 265009, 60433438, 21908754, 265010, 8716859, 284603, 265018, 265019, 284783, 284784, 264288, 21908765, 21908766, 21908768, 21908769, 35695917, 18108374, 35698423, 264638, 56182323, 22279000, 284583
3054	86843510 (6107, 6108)	Novel Protein sim. GBank gi 1076211 pir IS0755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35686286, 35696052, 28331830, 264908, 284908, 264512, 284910, 265017, 264604, 284766, 265020, 33657109, 264628, 35695855, 264638, 284584, 284586, 264486, 60424179, 65274572, 56182575, 35698286, 22278998, 22278999, 60432048, 264259, 60424289, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 284594, 60433438, 21908754, 55811386, 285011, 87168559, 265018, 18108351, 264683, 264288, 264369, 264689, 21908768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810784, 55811576, 35696423, 65274791, 264638, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 284586
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	284488, 284569, 18108394, 52846842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 284905, 264906, 264907, 284908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 284596, 284758, 265010, 265011, 265017, 265018, 264780, 18108351, 264762, 284763, 264784, 284288, 284786, 264687, 18108357, 264768, 284769, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 264691, 284693, 33657109, 18108370, 284626, 264629, 18108374, 55811576, 35698423, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 18108381, 83373044, 18108385, 22279000, 22279002, 284563, 284584, 284565, 264566, 264488, 264567
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		glycoprotein	

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gi 3876119 emb CAA88860 - (Z49088) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST			264508, 264905, 264807, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264787, 18108374, 264635, 264555, 264637, 264639, 264563, 264564, 264565, 264486
3058	78646226 (6115, 6116)	Novel Protein sim. GBank		UNCLASSIFIED	264693
3059	87629425 (6117, 6118)	gi 4588034 gb AAD25982.1 AF092878 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35896052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264788, 21906765, 21906766, 21906767, 21906768, 29148628, 29148784, 265022, 52644150, 18108370, 264638, 18108365, 264583, 264587, 264587
3060	78346691 (6119, 6120)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3081	87740964 (6121, 6122)			UNCLASSIFIED	264908, 265008, 18108351, 264566
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gi 4454690 gb AAD20963 - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi 2246532 U93872 - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108358, 264558
3084	91241526 (6127, 6128)	Novel Protein sim. GBank gi 4240315 dbj BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 53274572, 56182575, 56181886, 22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644286, 265018, 264682, 264288, 264686, 264788, 264887, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264638, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3085	91639201 (6129, 6130)	Novel Protein sim. GBank gi 5656743 gb AAD45960.1 AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265018, 18108351, 264786, 264787, 21906765, 21906768, 264693, 20281089, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4884268 emb CAB43245.1 - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278998, 284905, 66712502, 285008, 284512, 284810, 284758, 60174639, 284780, 18108351, 284784, 284883, 18108359, 284892, 18108384, 18108388, 18108370, 18108377, 18108379, 60170394, 284587
3067	85422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		284488, 284489, 35698286, 22278996, 56994075, 284259, 28331822, 28331825, 35698052, 28331828, 284508, 284905, 284509, 284908, 284907, 284908, 284909, 284112, 284510, 284511, 284512, 265008, 265009, 284910, 284591, 284592, 284593, 284594, 284757, 284595, 284596, 284758, 285010, 265011, 87168559, 284801, 284802, 284603, 284604, 284605, 285019, 284780, 284782, 284448, 284783, 284784, 284288, 284369, 284786, 284788, 284687, 284789, 284688, 21908765, 21908767, 21908768, 35895917, 285020, 265021, 284534, 52844150, 284691, 33857023, 284693, 284628, 60431528, 283977, 35895855, 284630, 284631, 284634, 284635, 284636, 284637, 284638, 284639, 83373044, 56528486, 87168518, 22278900, 22279002, 284563, 284483, 284584, 284565, 284566, 284587, 284488
3068	85360851 (6135, 6136)				284112
3069	95412753 (6137, 6138)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49088) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...	Contains protein domain (PF01826) - struct GTPase of unknown function		22278998, 56994075, 22278998, 22278999, 284259, 284107, 284905, 28331830, 52844045, 284110, 60170831, 284592, 284594, 33857402, 21908754, 33109854, 87168474, 87168559, 285017, 284448, 284784, 284883, 284788, 52844229, 21908765, 21908768, 21908769, 60170815, 33857023, 18108370, 18108376, 284634, 284557, 60170394, 56182323, 18108385, 87168518, 22279000, 284482

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gi 3877788 emb CA805527 - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264486, 22278954, 22278995, 22278998, 56994075, 22278997, 22278999, 264259, 29331822, 29147820, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264756, 33108954, 21906754, 87168474, 265018, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695955, 264634, 264635, 18108381, 60170394, 56182323, 264556, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gi 4502425 ref NP_001709.1 pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Thioredoxin	lgi	264486, 65274572, 18108398, 22278996, 35698286, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60433438, 33108954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 85274791, 35695955, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22278900, 22279002, 264563, 264564, 264565, 264566, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 85274791, 264555, 56182323, 60432113, 264584
3072	95115692 (6143, 6144)	Novel Protein sim. GBank gi 1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcriptfactor	

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi134840 sp P22528 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCRNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g588461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 284693, 18108368, 18108370, 18108374, 284587
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gi14557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87619219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264891, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi3023958 sp Q00808 HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35896052, 264511, 60170831, 87168474, 284389, 35895917, 33657182, 27486284, 33657349, 35695763, 35695855, 264839
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22278002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi3875410 emb CA802876 - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906769, 265020, 265021, 264693, 18108378, 264631, 52644332, 22278002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gi5257221 gb AAD41265.1 - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278998, 22278998, 264490, 264259, 29331824, 86714117, 29331825, 29331826, 29331827, 29331828, 29148489, 264508, 284905, 264828, 52644045, 58182435, 265008, 264591, 264586, 21906754, 60174639, 265010, 264682, 264448, 264763, 264683, 264764, 264288, 264685, 284769, 264688, 284689, 21906755, 21906787, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486281, 35695783, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264585, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gi1728831 sp P39188 ALU1_HUMAN - !!! ALU SUBFAMILY J WARNING ENTRY !!!		UNCLASSIFIED	18108398, 264509, 284905, 264908, 264907, 264908, 264909, 284510, 284511, 265009, 284810, 264995, 284758, 285011, 285018, 264760, 264781, 264763, 264764, 18108354, 264685, 264768, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264583, 264585, 264588
3082	80310121 (6163, 6164)				284784, 55811957, 284555, 264564

3083	88095758 (6165, 6166)	Novel Protein sim. GBank gij868241 (U28488) - C56C10.3 gene product [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284259, 29331824, 284108, 285008, 284591, 284592, 21906754, 284288, 284767, 21908788, 21906789, 29148784, 284691, 284632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gij476774(pj)A37475 - probable structural component p38 - borna disease virus		22278995, 60432289, 35898052, 284905, 284908, 284907, 284908, 284909, 285006, 285007, 284910, 284593, 284595, 284758, 284368, 284288, 284788, 35695917, 285020, 18108374, 35898423, 284631, 284556, 284585, 284566, 284587, 284486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gij2585057 (U80741) - CAGH44 [Homo sapiens]	UNCLASSIFIED	285011, 284681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gij3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	22278998, 284092, 284259, 29331822, 29331825, 284108, 284112, 18108351, 284687, 263987, 263974, 55810764, 263981, 18108385, 284487
3087	87462988 (6173, 6174)			52848385, 56994075, 22278997, 22278998, 29331824, 29331825, 35898052, 60433438, 33109954, 21906754, 52846317, 285017, 284682, 284368, 284684, 21908787, 21908788, 285020, 284691, 33857023, 33657109, 52845128, 33657182, 27488262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3355304 (AF001549) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	284591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4889148(gb)AAD27782.1(AF077049) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - dehydrogenase 3-hydroxycyl-CoA dehydrogenase	18108397, 65274572, 56182575, 56181686, 56994075, 35898286, 22278997, 22278998, 284259, 29331824, 29331825, 29331828, 29331828, 284907, 29331830, 284809, 58182435, 284510, 285007, 60170831, 60432228, 21908754, 55811388, 285017, 285018, 285019, 284760, 55811150, 284288, 284766, 56181562, 21908765, 21908786, 21908787, 21908788, 285021, 80170615, 27488262, 18108370, 60431528, 35698423, 284558, 284559, 80432113, 284488

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gij1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	60424179, 52645156, 65274572, 56182575, 56181888, 22278995, 35698286, 56994075, 22278998, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35698052, 33656970, 264906, 264908, 52644045, 264928, 265006, 265007, 265008, 60170831, 60432229, 60433358, 33657402, 55812038, 264758, 21808754, 33109854, 52646317, 55811386, 52644286, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264881, 264448, 264288, 264389, 18108357, 264768, 52644229, 58181562, 21806784, 21806765, 21806766, 21806767, 21806768, 21806769, 35695917, 265020, 265022, 60170615, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33857109, 18108368, 33857182, 27486261, 27486265, 35695763, 18108374, 18108376, 55810784, 35698423, 55811578, 65274791, 35695855, 284557, 56182323, 83373044, 18108387, 18108388, 87188518, 22279000, 22279002, 284563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gij3873932[emb](CAB01859) - (Z79598) Similarity to Bovine aspartyl beta hydroxylase (TR:G182694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D84881 comes from this gene; cDNA EST EMBL:D88139 comes f...		UNCLASSIFIED	35698286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264693, 264685, 264766, 264768, 264769, 264693, 264628, 35698423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gij1710756jpp15860JRS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	284488, 60424179, 18108398, 22278995, 56994075, 22278998, 35698286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35698052, 29331828, 29146498, 29146499, 284508, 284509, 284905, 284906, 284907, 29331830, 284908, 284909, 284113, 284510, 284511, 265006, 284512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 284593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 284601, 284602, 265017, 284603, 284604, 265018, 264605, 265019, 264760, 264762, 284681, 18108351, 284763, 284682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21908785, 21908786, 21908787, 21908788, 21908789, 29148629, 29148784, 35695917, 285020, 285021, 264534, 60170815, 284690, 284691, 284692, 65274620, 33657109, 27488282, 264628, 264629, 18108374, 263978, 18108377, 35698423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264558, 264638, 264557, 264558, 264639, 60170394, 18108385, 284259, 29331824, 35696052, 264805, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21908787, 35698423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gj15002587jembICAB44347.1] - (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED		
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gj1400734jpp131044PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	18108398, 264259, 60432289, 29331827, 284511, 264763, 264288, 264767, 265022, 284691, 284693, 65274781, 56182323, 284584, 284585

3095	94848162 (6189, 6190)	Novel Protein sim. GBank gij487759[gb]AAD31421.1[AF12444] - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35698286, 56954075, 22278997, 22278998, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 285018, 285019, 284760, 264681, 264682, 264683, 264764, 264388, 264288, 264686, 264768, 264769, 264688, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33857023, 264693, 263972, 18108378, 55811578, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278998, 29331824, 29331825, 29331826, 29331827, 33856970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906768, 21906767, 21906768, 35695917, 265020, 60170815, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22278900, 264566, 264488, 29331822, 29331825, 60432288, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644228, 21906765, 21906767, 18108378, 35696423, 52644332, 264638, 60432113, 22278902, 264634, 264637, 264565
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gij3882221[dbj]BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gij4488288[embj]CAB37881 - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6196)				
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gij303603[dbj]BAA02145.1 - (D12621) cytochrome P-450L TBV [Homo sapiens]		510450	264488, 35698286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22278902, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gij1083784[pirj]B48013 - proline- rich proteoglycan 2 precursor, parolid - rat		UNCLASSIFIED	265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22278902, 264563
3101	79602134 (6201, 6202)			UNCLASSIFIED	265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22278902, 264563

3102	91220882 (6203, 6204)	Novel Protein sim. GBank gij5305706 gb AAD4178.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - struct SH3 domain	35696268, 22278986, 22278989, 29331827, 35696032, 264909, 264512, 265008, 60170831, 60433358, 33109954, 18108351, 264684, 264688, 21908767, 60170615, 264692, 33657023, 264638, 22279000, 264482, 264564 35695917, 264565
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gij464584 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17	UNCLASSIFIED	
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gij5032207 ref NP_005698.1 pTSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)			22278987, 264259, 28331824, 35696052, 29331828, 264508, 264509, 264905, 264908, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264768, 264768, 264687, 264769, 21908766, 21908768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gij1938374 (U97190) - B0025.2 gene product [Caenorhabditis elegans]		22278986, 22278987, 22278988, 22278989, 264092, 264093, 264094, 29331822, 264908, 264907, 264908, 52644045, 58182435, 264112, 265008, 285009, 55812038, 265017, 285018, 264683, 264688, 264687, 264768, 52644228, 21908765, 21908768, 21908769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gij3341441 emb CAA76851 - (Y17794) winged-helix transcription factor [Gallus gallus]		22278985, 22278986, 35696266, 22278987, 22278988, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265008, 60433358, 60433438, 265011, 265017, 265018, 21908765, 21908766, 21908767, 21908769, 265021, 264691, 33657108, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526486, 264482, 264487 56182435, 264288, 264890, 264564
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gij5032207 ref NP_005698.1 pTSSC - tumor-suppressing STF cDNA 6	UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gij5002587[emb CAB44347.1] - (Y17454) LSF1 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	stnd	264480, 264908, 265007, 264910, 264593, 264883, 264884, 264887, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090718 (6218, 6220)	Novel Protein sim. GBank gij1076211[prf S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii]		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29331827, 29331828, 264808, 264510, 265008, 265007, 265008, 265009, 60432229, 33857402, 60433356, 265011, 87188559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906768, 21906767, 21906768, 265020, 60170815, 264693, 65274620, 18108370, 264639, 18108384, 22278000, 264583, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gij3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108388, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33857023, 18108385, 18108388, 35698423, 52844332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gij3500848 (AC005023) - match to EST AA381117 (NID: g2013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gij2459910 (AF005856) - anon2AS [Drosophila yakuba]		lm7	18108387, 22278999, 264259, 29331824, 35698032, 264807, 264757, 60433438, 87188559, 264763, 264448, 18108354, 264288, 21906767, 21906768, 35695917, 264690, 264691, 264692, 264693, 18108385, 18108381, 18108384, 18108385, 18108388, 87188518, 22278000, 22278002
3114	78843167 (6227, 6228)	Novel Protein sim. GBank gij4888270[gib AAB5228.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase). Score=57.4, E-value=1e-13, N=1 [C...]	Contains protein domain (PF00702) - hydrolase	hydrolase	264809, 56182435, 264810, 21906754
3115	94117986 (6228, 6230)	Novel Protein sim. GBank gij5032225[ref NP_005876.1]pWBSC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 264259, 29331824, 60424289, 29331828, 66712502, 264510, 265007, 60431735, 80433356, 55812038, 55811388, 265019, 264288, 264689, 21906768, 264681, 33857023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	78842855 (6231, 6232)			UNCLASSIFIED	264805, 264758, 21906764, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264681, 18108388, 18108372, 263981, 264558, 264584

3118	84665848 (6235, 6236)	Novel Protein sim. GBank gi 3860563 emb CAB01444.1 - (278018) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST YK353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - Igf EGF-like domain	52845156, 52846842, 65274572, 56182575, 22278985, 56994075, 22278998, 35686286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35686052, 29331828, 264905, 284808, 29331830, 52844045, 56182435, 284510, 284511, 265007, 265008, 265009, 264757, 52846317, 21908754, 33657084, 52844288, 87168474, 87168559, 265017, 265018, 264605, 265018, 284782, 264448, 264682, 264684, 264288, 264786, 56181562, 21908785, 21908786, 21908788, 21908789, 265020, 265022, 264690, 52844150, 264691, 33657023, 264693, 33657109, 33657349, 284628, 18108370, 60431528, 18108374, 35686423, 65274791, 60170394, 83373044, 87168516, 22279000, 22278002, 284488
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase	265006, 264288
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284509, 264510, 264511, 264512, 264288, 264488
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACR - acrosin		52844507, 52845156, 52846365, 52846842, 22278994, 56994075, 22278998, 22278999, 264259, 29331824, 29331827, 35686052, 52844045, 285008, 52846317, 87168474, 87168559, 21908785, 52844150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)		UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gi 2439517 AC002563 - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264652, 264288, 264786, 21908784, 21908785, 21908788, 21908789, 55811957, 18108365, 18108386, 27480285, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87768899 (6247, 6248)		UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gi 4980826 gb AAD35412.1 AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	56181686, 264259, 66714117, 60432289, 29331828, 29331827, 264807, 264908, 264828, 265009, 60433358, 33657402, 60433438, 284758, 18108351, 284288, 29148827, 29148829, 33657023, 33657109, 18108392, 56528488

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 284490, 284259, 60432049, 28331822, 60432289, 29148498, 52844045, 56182435, 285009, 60433438, 285010, 87188559, 285017, 285018, 55811150, 284763, 284883, 284389, 284885, 28148629, 33857023, 284693, 33857109, 18108374, 55811578, 18108385, 60432113, 22279002, 35898286, 22278898, 22278899, 28331828, 284808, 60433438, 87188559, 284604, 21808765, 21808769, 33857023, 33857349, 284629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gj2828280[embjCAA16694.1] - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gj3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278998, 284259, 52844045, 285008, 21808754, 285017, 285018, 21808768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gj3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 284259, 29331825, 29331828, 52844045, 58182435, 60433356, 284600, 284682, 284763, 284784, 284389, 284288, 284686, 55811957, 284692, 33857023, 33857109, 60432113, 284564, 284566, 284636
3130	14993960 (6259, 6260)	Novel Protein sim. GBank gj3328465 (AF084553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gj1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 284259, 29331824, 284807, 56182435, 284594, 60433438, 55812038, 33109954, 21808754, 33857084, 87168474, 284448, 284786, 21808769, 55811957, 285020, 285021, 265022, 60170815, 33857023, 33857109, 33857182, 27488281, 33857349, 65274781, 60170394, 56182323, 83373044, 87168518, 284584

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gij4680647[gb]AAD27713.1[AF132938] CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52844507, 52846842, 52846385, 85274572, 56182575, 22278994, 22278995, 35698286, 56994075, 22278998, 22278997, 22278998, 22278999, 60432049, 52845080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35698052, 284508, 52844045, 56182435, 284910, 60170831, 60432229, 60433356, 33657402, 55812038, 52846317, 21908754, 52844296, 85658542, 87188559, 265017, 265018, 265019, 284448, 264288, 264369, 52844229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 60170615, 52844150, 264892, 33657023, 52845129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695783, 18108374, 18108376, 55811578, 35695855, 18108385, 18108387, 56528488, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gij4507613[ref]NP_003738.1[pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 285007, 87168559, 264760, 21908787, 18108374, 22279000, 22279002, 264563 264585, 264369, 264885, 264628, 264586
3134	94649518 (6267, 6268)	Novel Protein sim. GBank gij1729827[sp]P54633[ITALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	88389358 (6269, 6270)	Novel Protein sim. GBank gij3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278998, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gij827101[pri]S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264889, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257847 (6273, 6274)	Novel Protein sim. GBank gij3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21908754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 284882, 264769, 21908765, 21908766, 21908767, 21908768, 55811957, 35695917, 265020, 265021, 52844150, 18108370, 18108374, 22279000, 22279002, 284482, 284485

3138	94130188 (6275, 6276)	Novel Protein sim. GBank gij4408759[gblAAO20070] - (AC008838) hypothetical protein [Arabidopsis thaliana]			264559, 264488, 264807, 264511, 264593, 33109854, 87188558, 264681, 264884, 264685, 264688, 264687, 264768, 264688, 264689, 264691, 264892, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108386, 60432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gij228938[prfj]1814452C - Hyp-rich glycoprotein [Zea diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21906785, 265020, 264638, 264557
3140	91222692 (6278, 6280)	Novel Protein sim. GBank gij932[lemb]CAA37773] - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]	struct		22278995, 56894075, 35698286, 264808, 264909, 60433358, 21906754, 52644296, 87189474, 87188558, 264683, 264288, 264885, 264686, 265022, 264693, 27468282, 35695855, 264830, 264555, 264566
3141	87323564 (6281, 6282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE VII1a [Mus musculus]	UNCLASSIFIED		56182575, 35698286, 26331828, 264909, 265008, 265018, 18108351, 264389, 21908786, 29148627, 265020, 264628, 264628, 264631, 18108385
3142	95418028 (6283, 6284)	Novel Protein sim. GBank gij2498197[sp]Q95245[C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)]	cytochrome		52645156, 52646365, 22278995, 35698286, 22278998, 22278999, 60432048, 264259, 29331822, 29331824, 29331827, 29148488, 56182435, 265007, 60170831, 60432229, 33657402, 264585, 60433438, 264758, 21906754, 264288, 264766, 264687, 52644229, 21908785, 21906787, 21908788, 60170815, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (6285, 6286)	Novel Protein sim. GBank gij5420387[lemb]CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278998, 22278999, 29331822, 29331824, 60432289, 35698052, 29331828, 264508, 264905, 264908, 264807, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265018, 264760, 264763, 264448, 264764, 264884, 264288, 264685, 264686, 264768, 264888, 21908785, 21908786, 21908787, 21908789, 35695917, 264690, 33657023, 264693, 263987, 33657109, 264628, 264628, 18108374, 263978, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264488

3144	95338329 (6287, 6288)	Novel Protein sim. GBank gi 498446 emb CAB43322.1 - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108398, 22278896, 22278896, 35696286, 22278897, 22278899, 29331826, 29331827, 35696052, 29331828, 284106, 285008, 265007, 265009, 33657402, 85658542, 265011, 18108351, 284448, 284369, 21908765, 21908766, 21908767, 265020, 285021, 52844150, 27486281, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 284587
3145	86611857 (6289, 6290)	Novel Protein sim. GBank gi 3878709 emb CAB03330 - (Z81118) Similarly to Human endosomal protein P162 (TR-Q15075); cDNA EST EMBL-Z14487 comes from this gene; cDNA EST EMBL-Z14556 comes from this gene; cDNA EST EMBL-D27011 comes from this gene; cDNA EST EMBL-D27015 comes from 1...	UNCLASSIFIED		18108397, 29331824, 29146489, 20281100, 295006, 55812038, 265010, 21908766, 29148627, 21908769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87188518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gi 2135746 pir J568890 - mitogen inducible gene mlg-2 - human	Contains protein domain (PF00169) - PH domain	sinud	284259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 285008, 284600, 285017, 18108351, 284448, 284369, 21908766, 285021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 284584
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gi 3874270 emb CAB07315.1 - (Z92825) predicted using GeneFinder. cDNA EST yk315a12.3 comes from this gene; cDNA EST yk315a12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181866, 35696286, 60432048, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 285008, 264910, 60431735, 60433356, 60433438, 285010, 284448, 264288, 285022, 33657023, 33657109, 60431528, 65274791, 284631, 56182323, 264404, 22278002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gi 5225322 gb AA040851.1 AF08310 - (AF083108) sirIuin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87188474, 284784, 35696423, 284555, 284556, 284557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gi 4200448 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	eph	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gi 3378454 emb CAA76883 - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases.	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52846317, 284686, 35695855, 56182323, 284639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gi 172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	oncogene	29331822, 285008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21908754, 87188558, 284605, 21908768, 52844150, 27486284, 35696423, 22278000

3153	95317288 (6305, 6306)	Novel Protein sim. GBank gi4895041 gb AAD32705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct	284488, 52846365, 35698286, 22278986, 22278997, 22278998, 60432048, 264259, 29331826, 60432289, 33658870, 284508, 284908, 33657402, 284595, 60433438, 87188474, 87188558, 284601, 285019, 264448, 284682, 284764, 284288, 284369, 284788, 21908785, 21908786, 21908787, 21908788, 21908789, 28148784, 265021, 265022, 60170615, 52844150, 284690, 284691, 33857023, 65274620, 33857109, 18108370, 35695855, 284638, 60170394, 87188519, 60432113, 22279000, 22279002
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi4880861 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]	ATPase-associated	ATPase-associated	22278998, 284259, 29331824, 68712502, 285008, 265010, 285017, 18108354, 284691, 33857023, 284693, 20281149, 18108374
3155	87762394 (6309, 6310)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED	UNCLASSIFIED	29331828, 284509, 284905, 284908, 284510, 264511, 284512, 33857402, 284681, 284683, 33857023, 18108370, 284634, 284639, 18108385, 284563, 284488
3156	87737449 (6311, 6312)	Novel Protein sim. GBank gi5630078 gb AAD45921.1 AC00601 - (AC006017) N-acetylglucosaminyltransferase; similar to Q10473 (PID: g1709559) [Homo sapiens]	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 68714117, 29331825, 29331826, 29331827, 35896052, 52844045, 285007, 265008, 60170831, 60432229, 60433358, 21908754, 33109894, 87188474, 285010, 285017, 285018, 285019, 18108351, 264448, 284288, 284688, 21908786, 21908788, 21908789, 35695917, 285020, 265022, 284692, 18108370, 35698423, 56182323, 22279002
3157	88259577 (6313, 6314)				18108396, 284259, 29331826, 35698052, 28148498, 87188558, 285017, 264448, 284288, 284691, 18108388, 52845129, 35698423, 52844332
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi5306064 gb AAD41895.1 AF15877 - (AF158778) ASB-3 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	kinase	284488, 263974
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi5531272 emb CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	56182575, 22278998, 29331824, 264108, 60433356, 284758, 285011, 87188559, 264448, 18108354, 284788, 21908788, 285020, 284691, 284692, 33857109, 18108374, 35698423, 284555, 60170394, 22279000
3160	80221088 (6319, 6320)	Novel Protein sim. GBank gi3930525 (AF084447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	struct	18108351, 284555, 284556, 284557, 284558, 284559

3161	8807411 (8321, 8322)				264488, 22278995, 22278997, 22278998, 264259, 29331822, 60432289, 29331828, 5264045, 285017, 285018, 264448, 264288, 21908764, 21908787, 265020, 18108374, 264638, 264568
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalmus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalmus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalmus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U1SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberosclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberosclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3 (UtSMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema , Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura , Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis , Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura , Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UIMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-I)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIQ		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: I:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen 1		

Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

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 35 40 45
 Pro Pro Pro Ile Ser Ala Ala Arg Leu Ser Arg Met Ser Leu Val Glu
 50 55 60
 Arg Cys Ser Ala Ser Ala Ser Cys Ser Ala Val Leu Arg Asp Trp Ala
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Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
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 Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala
 65 70 75 80
 Met Cys Ser Arg Glu Gly Gly Met Asp Ile Glu Thr Leu Ala Lys Glu
 85 90 95
 Arg Pro Glu Ala Leu Ala Lys Val Pro Val Asp Pro Ile Asp Gly Val
 100 105 110
 Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
 115 120 125
 Ser Glu Gln Asp Ala Ile Val Pro Ala Val Leu Lys Leu Trp Glu Thr
 130 135 140
 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
 145 150 155 160
 Thr Gly Asp Gly Arg Ile Leu Ala Ile Asp Gly Lys Met Thr Val Asp
 165 170 175
 Asn Asn Ala Ser Phe Arg Gln Pro Asp Arg Ala Gly Leu Val Asp Arg
 180 185 190
 Ala Thr Thr Asp Pro Leu Glu Leu Arg Ala Gly Glu Leu Gly Leu Asn
 195 200 205
 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
 210 215 220
 Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
 225 230 235 240
 Pro Gly Ser Pro Ala Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala
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 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
 260 265 270
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
 275 280 285
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
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<212> DNA

<213> Homo sapiens

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 35 40 45
 Pro Ala Thr Pro Ser Leu Gln Lys Val Ile Cys Asp Leu Gln Gly Leu
 50 55 60
 Thr Ala Arg Cys Asp Val Ser Cys Cys Gln Ala Glu Arg Gly Leu Gly
 65 70 75 80
 Glu Pro Cys Arg Asp Val Met Thr Ser Tyr Val Leu Gly Asn Lys Val
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 Glu Asp Leu Asp Phe Ser Gly Thr Glu Met Gly Pro Pro Ala Cys Gly
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 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
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Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
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Val Gln Gly Glu Arg Lys Cys Leu Thr Phe Tyr Leu Pro Lys Phe Phe
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Ile Val Gly Leu Leu Trp Leu Ala Ser Val Thr Leu Gly Ile Trp Gln
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<211> 453

<212> DNA

<213> Homo sapiens

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<212> PRT

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<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

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			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
		35					40					45			
Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55					60				
Gly	Ala	Leu	Thr	Pro	Leu	Cys	Arg	Ser	Leu	Val	His	Leu	Ala	Gln	Lys
65					70					75				80	
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<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens
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429

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Leu Val Asp Ala Gly Phe Glu Thr Gly
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<210> 17
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 <212> DNA
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cactggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
540
tgttgcagag gagcttccct gggaaatgtc acacacagaa catcaatctt ccttccccac
600
tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctgggtccc
660
tgctgtctca caaatcgcaa ga
682

```

<210> 18
 <211> 110
 <212> PRT
 <213> Homo sapiens

```

<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1              5              10              15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
      20              25              30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
      35              40              45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
      50              55              60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```

```

65          70          75          80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
          85          90          95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
          100          105          110

```

<210> 19
 <211> 515
 <212> DNA
 <213> Homo sapiens

```

<400> 19
cttggctggc agacatggga cctgcttccc tcttacaccc cagtcttggc aaggatcatg
60
ccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
120
cgtctgcagt gcagtcttgg gctataagaa aactggggcc actcaatacc tcccccttt
180
tggcccttct cctcctctgg tccatgggtg ggggtggggg gagcccagtt tcagcaccag
240
cagctggagc ccataccaca ctcatTTTTc agttctggct gtgggagccc ctccacagg
300
tttcagttcc ccaagcccca ggctgagtt tttttattg caaaagctgg ttgttggtgt
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgctgt aggtgtccag tctgaaggaa tgctgggat acttctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcatgtca gatct
515

```

<210> 20
 <211> 130
 <212> PRT
 <213> Homo sapiens

```

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1          5          10          15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
          20          25          30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
          35          40          45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Leu Trp Ser Met
          50          55          60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65          70          75          80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
          85          90          95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Tyr Cys Lys Ser Trp
          100          105          110
Leu Leu Leu Trp Leu Ala Pro Arg Arg Val Arg Cys Ser Leu Leu Ser
          115          120          125
Lys Ser

```

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
 gtgcgacaaa aagagcacgt tcgcaagggg aggaagagcg tgccaccggt tctgccgagc
 60
 tagacgcggt gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg
 120
 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg
 180
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
 240
 atacaatgac tgcttgcaact gatgggttca caattgagca attggagctt acacgatctc
 300
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctgggtcaag
 360
 aattaaagca agttgtccaa ggcattccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
 1 5 10 15
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatc
 60
 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggcttc
 180
 ggggacctgg tgagcagcca gcacgccgcc taccggaacc aggggctcta ccgcctgggc
 240
 aacttcctct tcatectgct cggcgtgtgc tgcatttact cgctcttcaa cgctcatctcc
 300
 atcctcatca agcaggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg
 360
 cgctgctgcc cggctcctgg cgcgc
 385

<210> 24
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 24
 Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
 1 5 10 15
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
 20 25 30
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
 35 40 45
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
 50 55 60
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
 65 70 75 80
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
 85 90 95
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
 100 105 110
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
 115 120 125

<210> 25
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 25
 ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagtttcg
 60
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga
 120
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggaggaaag ctggtcgaat gcactgtgta tttggaggca gaaccagcag agggctctct
 240
 ggggttgagt tagggcaaaa gagaaagaag gcaccaagcc tggggctctg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgacgtcga atatccatgc agccgcgccg aggatggaga gagcgatgga gcaactcaac
 60
 cgcttgacgc gctcgctgcg ccgcgcgcgc accgtggagt tgcccagga taatgaaact
 120
 gctgtttata cattaatgcc aatggttatg gctgatcaac acaggtctgt ttctgaaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggtctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

65		70		75		80									
His	Ile	Ala	Ala	Asn	Cys	Gly	Ser	Val	Glu	Cys	Leu	Val	Leu	Leu	Leu
		85		90		95									
Lys	Lys	Gly	Ala	Asn	Pro	Asn	Tyr	Gln	Asp	Ile	Ser	Gly	Cys	Thr	
		100		105		110									

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 29
 ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
 60
 gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
 120
 tacaatatca cgatcaagcg cgctcgtgaac atgacgggca agggccgcac gccgagctgg
 180
 tactcgctcg tcgtggctgg caatggctcg ggcctcgtgg gctatggcga aggcaaagat
 240
 actaacatca gccgcgcgaa caaaaaggcg ttccacgccg cggtgaaaaa catggacttg
 300
 gtatcgggtcc accggtcgaa gagtggcgcc aacacgctcg agccccccgt cgagggccgc
 360
 tggggcgcta cgcgt
 375

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30
 Xaa Pro Ser Val Leu Ala Ile Met Thr Ala Gly Ser Asp Gln Gly Glu
 1 5 10 15
 Glu Val Asn Ser Glu Ser Tyr Leu Ser Ala Val Thr Pro Leu Ser Pro
 20 25 30
 Lys Glu Ile Arg Gln Leu Pro Arg Tyr Asn Ile Thr Ile Lys Arg Val
 35 40 45
 Val Asn Met Thr Gly Lys Gly Arg Thr Pro Ser Trp Tyr Ser Leu Val
 50 55 60
 Val Ala Gly Asn Gly Arg Gly Leu Val Gly Tyr Gly Glu Gly Lys Asp
 65 70 75 80
 Thr Asn Ile Ser Arg Ala Asn Lys Lys Ala Phe His Ala Ala Val Lys
 85 90 95
 Asn Met Asp Leu Val Ser Val His Arg Ser Lys Ser Gly Ala Asn Thr
 100 105 110
 Leu Glu Pro Pro Val Glu Gly Arg Trp Gly Ala Thr Arg
 115 120 125

<210> 31
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 31

accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
60
gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctggggcccct gagagtgcag
120
agattcctgg atccagagct gcggtggggc ggctgcagct gcgcctggga gtgcagggct
180
cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttgccc
240
ctgcagagtgc cacaaacctc gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
300
cactcccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
360
tggcctgcat tgttt
375

<210> 32

<211> 118

<212> PRT

<213> Homo sapiens

<400> 32

Met	Gln	Ala	Met	Ser	Leu	Lys	Leu	His	Thr	Leu	Trp	Ser	His	Arg	Trp
1				5					10					15	
Gln	Trp	Gln	Pro	Ile	Gly	Ser	Gly	Cys	Cys	Lys	Asp	Val	Ser	Cys	Ser
			20					25					30		
Gly	Gly	Ser	Ala	Ala	Arg	Phe	Val	His	Ser	Ala	Gly	Pro	Thr	Gly	Ala
		35				40					45				
Arg	Asn	Arg	Gln	Glu	Pro	Pro	Phe	Pro	Phe	Glu	Leu	Ala	Gly	Arg	Glu
	50					55				60					
Pro	Cys	Thr	Pro	Arg	Arg	Ser	Cys	Ser	Arg	Pro	Ala	Ala	Ala	Leu	Asp
65				70					75					80	
Pro	Gly	Ile	Ser	Ala	Leu	Ser	Gly	Ala	Gln	Glu	Ala	Ser	Leu	Thr	Arg
			85					90					95		
Arg	Leu	Val	Ser	Ala	Cys	Ser	Arg	Ser	Ser	Pro	Leu	Leu	Ala	Pro	Thr
			100					105					110		
Ser	Ile	Ser	Glu	Gln	Ser										
			115												

<210> 33

<211> 351

<212> DNA

<213> Homo sapiens

<400> 33

ccatgcagcc caaccgttgg cgataaagtc cgtttaggcg ataccaattht atgggcaacc
60
attgaacaag atttattaac caaaggtgat gagtgtaaat ttggtggcgg taaaagtgtg
120
cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
180
gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggg
240

attcgcgatg gtcgtattgt cggatcggga caagcaggta accctgacac catggatgac
 300
 gtcacgccaa acatgattat cggtgctagc acagaagtac ataacgggtgc a
 351

<210> 34
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
 1 5 10 15
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
 20 25 30
 Lys Phe Gly Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
 35 40 45
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
 50 55 60
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
 65 70 75 80
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
 85 90 95
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
 100 105 110
 Val His Asn Gly Ala
 115

<210> 35
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 35
 nngctagctg caccaccacc tgttcatgca ggcagagcgg ccaccctca tggaagaaga
 60
 ggaatccact gtattgggca caggcttcct gctggacctt ggcaagcagg tgcttggtctg
 120
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct
 180
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcggcga
 240
 gagtgctctg cacacagtcc tccactggct caggctccat ggctcggcgc cgggcccgtg
 300
 ccgacgcttg gtcggggcgg cggggccggg cgcgccaccg cctcccttca cgcgt
 355

<210> 36
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 36
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1             5             10             15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20             25             30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35             40             45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50             55             60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65             70             75             80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85             90             95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100             105             110
Thr Ala Ser Leu His Ala
      115

```

<210> 37
 <211> 492
 <212> DNA
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggacccgcc
60
gcaaccatga caagggcgat gttgtgatct ggggtggattc cttctccgac atgctcgagg
120
gatcggatct ctccggcgta gtcacggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc ggggtgacgt ggatcactac cggtcagctc gacggtgctc
240
ggcgtcggct gcgcgctggt ctgcagctgc tggcaccctt gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcgtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca cctcgtctag caggccacac cctcgtcgct cagccccatt
480
gtcatcccgcc gg
492

```

<210> 38
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
      1             5             10             15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20             25             30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35             40             45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

```

      50              55              60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu
65              70              75              80
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met
      85              90              95
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser
      100             105             110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala
      115             120             125

```

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

```

<400> 39
aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgttaaag agcggtccga tcgccgggaa
60
gtgatgngca ccgcaaaaat gcaggtgggtc gaagccgcga gttcaggcaa gattgtcttt
120
gaaatggaag acgtttatta cagcattgcc ggaaaacaac tggtagagcaa cttctctgcg
180
caagtcatgc gtggtgataa aattgcgctg attggcccga acggttgttg taaaacgacg
240
ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
300
aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacgggtg
360
atggataacc tggccgaagg taagcaggaa gtgatggtaa atggccgtgt an
412

```

<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

```

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1              5              10              15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
      20              25              30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
      35              40              45
Ile Ala Gly Lys Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
      50              55              60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65              70              75              80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
      85              90              95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
      100             105             110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
      115             120             125
Gln Glu Val Met Val Asn Gly Arg Val

```

130

135

<210> 41
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 41
 gaattcaagt ggacacaggc tccacgcccg cgtctcaccg ataagagcta caagcacaac
 60
 tactatgacg agcgggtttc gctcgaagag cgtcttgagc gcactgtggc taaggatttc
 120
 gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgcggat gggtaaggat
 180
 ctcttcatcc agcacggtct gacgacaaat cggaaagtcaa tggagtgggt taagcggttac
 240
 taccctgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatc
 300
 gacgcgacct ttgtgccgct tcgtccgggg ctcacatca acaaccgaa tcgtccactg
 360
 ccgcaggagc agaggaagat cttcgaggcc aatgactggc agatcggtga tgcgtgctcag
 420
 ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
 480
 ttggtacttg atccgaagac ggtcatctgc gaggttcgga aagttcatca gatggagcag
 540
 atggacaagc tgggtatgaa cgtcatcccc gtcgccttcc gtgacgcgta cccattcggg
 600
 ggaggtctcc actgcgccac agctgatgta tatcggaag gtacctgtga ggactacttc
 660
 ccgaatcagg tcgacgaccc gaccttggtg tgagaaaacc ccgtgggtcat gtcatgactg
 720
 acggatctcg gtggctcggg acggaactta cgttgctcgt taccgggccc ccgggtctga
 780
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
 840
 aacgtcaaac aggaagttcc aggcgtcggg acgatgaacc agaaagtggg attcgtgtcc
 900
 atgcttcttt ctgcaacggg tatggggttg gtgggtactt tcgggcgtct cagcactcct
 960
 gtggatccca cgacgggcag taagtacatc atcggtgatt ttttggccac tggtaggatg
 1020
 atagtcgggg tcctgggatt tctgcttatt atcgtcatatc ttggaaaatg gtctgagctc
 1080

<210> 42
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 42
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
 1 5 10 15
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu

```
<210> 43
<211> 358
<212> DNA
<213> Homo sapiens
```

```
<210> 44
<211> 105
<212> PRT
<213> Homo sapiens
```

441

1	5	10	15
Leu Gly His Arg Gly Cys Leu Pro Ala Ala Pro Gly Arg Ala Val Asp			
	20	25	30
Thr Thr Ala Trp Ser Ala Val Pro Gly His Cys His Ala His Arg Cys			
	35	40	45
Pro Leu Arg Met Asp Leu Gly Phe Arg Ile Arg Val Ala Tyr Gln Arg			
	50	55	60
Glu Ser Gln Ile Leu Lys Glu Val Gln Ser Pro Glu Gly Met Ile Ser			
65	70	75	80
Leu Arg Asp Thr Ala Ala Ser Leu Arg Leu Glu Arg Asp Thr Arg Gln			
	85	90	95
Leu Pro Leu Leu Thr Ser Ala Leu His			
	100	105	

<210> 45
 <211> 905
 <212> DNA
 <213> Homo sapiens

<400> 45
 gtcgacgata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcggggtttc
 60
 gcggctcctg gaatcccaga gcagtatggg ggcgacgggt cggatgcgat tgcgtccgca
 120
 ataatcatgg aagaggctcg tcgagtcctgt gcgtcgtcgt ccaccgtcat atcgtccaat
 180
 gagcttggtta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
 240
 tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga
 300
 tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
 360
 ggcgttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt
 420
 actgacccag acgatccgcg ccacagaatc agcgcgttga tggccatgc agatgacccg
 480
 ggcattagct acggggctcc ggagcacaaa atggggatac gcgggtcagt taccagggaa
 540
 gtggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgtcg agggcacggt
 600
 ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg
 660
 ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
 720
 ggccagccac tgtccaattt tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
 780
 ttggaggcgg cgcgagcgct gacatactct gcagctgatc gtagtgggcg ccagactgac
 840
 gatgtgagtt acttcggcgc ggcggccaaa tgtttcgctt ccgacacagc gatggcagtg
 900
 tgcac
 905

<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46
 Val Asp Asp Lys Gly Val Phe Ala Gln Gln Gln Tyr Asp Ala Leu Val
 1 5 10 15
 Glu Ala Gly Phe Ala Ala Pro Gly Ile Pro Glu Gln Tyr Gly Gly Asp
 20 25 30
 Gly Ala Asp Ala Ile Ala Ser Ala Ile Ile Met Glu Glu Val Ala Arg
 35 40 45
 Val Cys Ala Ser Ser Ser Thr Val Ile Ser Ser Asn Glu Leu Gly Thr
 50 55 60
 Val Pro Leu Leu Lys Tyr Gly Ser Glu Glu Gln Arg Lys Arg Tyr Leu
 65 70 75 80
 Ser Glu Val Ala Ser Gly Lys Ala Leu Phe Gly Tyr Ala Leu Ser Glu
 85 90 95
 Ala Asp Ala Gly Ser Asp Pro Ala Ala Leu Lys Cys Arg Ala Asp Glu
 100 105 110
 Asp Gly Asp Ser Phe Val Leu Asn Gly Val Lys Ala Trp Val Thr Glu
 115 120 125
 Ala Gly Glu Ala Lys Tyr Leu Val Ile Phe Ala Val Thr Asp Pro Asp
 130 135 140
 Asp Pro Arg His Arg Ile Ser Ala Leu Met Val His Ala Asp Asp Pro
 145 150 155 160
 Gly Ile Ser Tyr Gly Ala Pro Glu His Lys Met Gly Ile Arg Gly Ser
 165 170 175
 Val Thr Arg Glu Val Val Phe Lys Asn Thr Arg Ile Pro Lys Glu Arg
 180 185 190
 Val Ile Gly Arg Arg Gly His Gly Leu Ser Val Ala Leu Gly Thr Leu
 195 200 205
 Asp Asn Ser Arg Val Ser Ile Ala Ala Gln Ala Val Gly Ile Ala Gln
 210 215 220
 Gly Ala Leu Asp Ile Ala Thr Asp Tyr Val Gln Lys Arg Lys Gln Phe
 225 230 235 240
 Gly Gln Pro Leu Ser Asn Phe Glu Gly Ile Gln Phe Met Leu Ala Asp
 245 250 255
 Met Ala Met Arg Leu Glu Ala Ala Arg Ala Leu Thr Tyr Ser Ala Ala
 260 265 270
 Asp Arg Ser Gly Arg Gln Thr Asp Asp Val Ser Tyr Phe Gly Ala Ala
 275 280 285
 Ala Lys Cys Phe Ala Ser Asp Thr Ala Met Ala Val Cys
 290 295 300

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47
 aagctttag agctagtccg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcatttta ccgctgcgta tgccgtagct acggaagctg ggtgcatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgtcg actgcgttta
 240
 gatttcgaaa aaggactcac caaatcccag ggtcgacgag aagagttcat acccgctggc
 300
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His
 1 5 10 15
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg
 20 25 30
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala
 35 40 45
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys
 50 55 60
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly
 65 70 75 80
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg
 85 90 95
 His Asp Val Ile Lys Ser Gly Lys Leu Ala
 100 105

<210> 49
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 49
 tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc
 120
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc cccttgtctg
 180
 cacattaccc tctgccagct ggctcatttt tctgctcccc ttacagggga aactcttcaa
 240
 aaagttatct ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctctttttg
 309

<210> 50
 <211> 101
 <212> PRT

<213> Homo sapiens

<400> 50

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Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1           5           10           15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
          20           25           30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
          35           40           45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
          50           55           60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65           70           75           80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
          85           90           95
Val Leu Pro Pro Phe
          100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

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agatctttga agaattgccca cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagtctgt cttgtacttc atgtgcccct
300
caaaatcttc tgttgctgag ggagaagagg ccagccggtg ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggcctctgt ttcatttatg tgacctccca
480
tcagggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1           5           10           15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
          20           25           30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

          35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
          50          55          60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
          85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
          100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
          115          120          125

```

<210> 53
 <211> 474
 <212> DNA
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcatcgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcgggtt acgtaaccgt
300
gaccaagtcg acgggcgctc ccgcggttac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474

```

<210> 54
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 55
 ccatggccca ggacagccgg catatcggtt acgactacgg tacaccggtg gcgccacagt
 60
 tcggcgccagc caagcccgcg gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
 120
 tgggtgttcga ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc
 180
 agcccgatgc caccgcgcag caggtcaatg ccgacaaccc gcactacgtc gggcggtttca
 240
 gccgcacggg catgggcctg gtggatgaca agggccggtg cattaccagc ggcgtatcgc
 300
 gcgcgttgaa tgcggcgccg agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
 360
 agttatcggt gaggcgta
 378

<210> 56
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
 1 5 10 15
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
 20 25 30
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
 35 40 45
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
 50 55 60
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
 65 70 75 80
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
 85 90 95
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
 100 105 110
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
 115 120 125

<210> 57
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 57
 agacccaccc gacacagatc aggagtcgtc atgtccagaa agaagaaggc cggcatcctc
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
 120
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
 240
 atcctgggaa ctagccgtga caaggtcaat cacatgatta tcgacggcga ggaacgggat
 300
 atgggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcgggtg gcaccgcca gaacgcgt
 388

<210> 58
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 58
 Arg Pro Thr Arg His Arg Ser Gly Val Val Met Ser Arg Lys Lys Lys
 1 5 10 15
 Val Gly Ile Leu Thr Ala Gly Gly Asp Cys Pro Gly Leu Asn Ala Ala
 20 25 30
 Ile Arg Gly Phe Gly Lys Ala Ala Ile Arg Gln His Asp Met Glu Leu
 35 40 45
 Ile Gly Ile Gln Asp Gly Phe Leu Gly Leu Ala Gly Asn Arg Thr Ile
 50 55 60
 Ser Leu Gly Pro Arg Ala Leu Ser Gly Ile Leu Thr Val Gly Gly Thr
 65 70 75 80
 Ile Leu Gly Thr Ser Arg Asp Lys Val Asn His Met Ile Ile Asp Gly
 85 90 95
 Glu Glu Arg Asp Met Val Pro Thr Thr Val Glu Asn Tyr Glu Lys Leu
 100 105 110
 Gly Leu Asp Ala Leu Val Thr Leu Gly Gly Gly Gly Thr Ala Lys Asn
 115 120 125
 Ala

<210> 59
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 59
 ggtaccatcg gagctcgaca agaaatgggt ggggtgaagtc gtggcttctg ctccaccag
 60
 tgcctcatg ggtcagccca cctgaatata ttcatgcctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaacct
 240
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaagggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacgggtga
 360
 tgcttttcaga agccccgggag agcgtcttgg gggcagtgct gaaggttggtg ctgtaca
 417

<210> 60
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 60
 Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
 1 5 10 15
 Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
 20 25 30
 Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
 35 40 45
 Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
 50 55 60
 Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
 65 70 75 80
 Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
 85 90 95
 Lys Val Val Leu Tyr
 100

<210> 61
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 61
 agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccttatcc
 60
 gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
 120
 tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
 180
 ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
 240
 tcccctagac cgggcccattg gccaggcctg accacagagc tcccattgcc tttcctgcac
 300
 gcgt
 304

<210> 62
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 62
 Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
 1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
 20 25 30
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
 35 40 45
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
 50 55 60
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
 65 70 75 80
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
 85 90

<210> 63
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 63
 cgcgtcaagg gggctctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
 60
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
 120
 accgtgggtcg ggctggccca aaccctcggc cctccgtgc gagcactggg cgtcgacacc
 180
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
 240
 ccggcagcct ggcagatcca ccccgacgac ggtgcccgc caacaccggg tgatggcccg
 300
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg
 360
 ggtatcatgg cgcctcaatc ggtctgtgac gccttgccg aggcgataga ccacggctcc
 420
 gagaccgtct tgaatggggg tcccgcagc cgcctcaacc ctgcccacg gcgtcgctctg
 480
 gtgctgggtg ctccccgctc ccccgaaactg ttcgacgata ctgccgtgc gaacatcggtg
 540
 cttgacagcc agacgactgt cgccaggctg aatgcat
 577

<210> 64
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 64
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1 5 10 15
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
 20 25 30
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
 35 40 45
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
 50 55 60
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                    105                    110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                    120                    125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                    135                    140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
      145                    150                    155                    160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                    170                    175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                    185                    190

```

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<210> 65
<211> 339
<212> DNA
<213> Homo sapiens

```

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<400> 65
gtcgaccgcg ccttgggatc gctcgaaggg gccagcctgg accaggtagc ggaagaagtc
60
aagaaggccg ctttcaagat caccgcgcgc gggcaactag tgggcacccat ggcctccgag
120
cgccttggcg tacccttcgg catcatcgac ctttcgcttg ccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggctgcccc
300
cgcgtcggcg gtttgtcttg ctcttcate ccgggctcc
339

```

```

<210> 66
<211> 113
<212> PRT
<213> Homo sapiens

```

```

<400> 66
Val Asp Arg Ala Leu Gly Ser Leu Glu Gly Ala Ser Leu Asp Gln Val
1      5      10      15
Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
      20      25      30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
      35      40      45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
      50      55      60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
      65      70      75      80
Thr Ala Ala Leu Ala Leu Leu Asn Asp Ala Val Lys Lys Gly Gly Met
      85      90      95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
      100     105     110

```

Ser

<210> 67

<211> 446

<212> DNA

<213> Homo sapiens

<400> 67

tgatcataaa ccacgcgtca ccgaggggat gtggcacacc tacctgcgcg tcgcagatgc
 60
 cgcacaggca cgggtcaggg gcgttcgcgg cgccagctgg cacaacttcg cgaccggtga
 120
 caaggggtcc ttcgacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca
 180
 gggagtcggg cccgccctag ccctcctcga ttcagcgtgg ggacgccaga tccacgtgga
 240
 gacaacaggg tgtcccagtg ccgtggtctg gaatccacgc tcctcgtcga cacatgccga
 300
 taaccgcgaca gcccaggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga
 360
 caatgcggtc attgttgccc cacacagcga cctcaccatg tccacacgga ttagcgtcga
 420
 aacgttgtga tcgctgcatg gatatt
 446

<210> 68

<211> 133

<212> PRT

<213> Homo sapiens

<400> 68

Met	Trp	His	Thr	Tyr	Leu	Arg	Val	Ala	Asp	Ala	Ala	Gln	Ala	Arg	Val
1				5					10					15	
Arg	Gly	Val	Arg	Gly	Ala	Ser	Trp	His	Asn	Phe	Ala	Thr	Gly	Asp	Lys
			20					25					30		
Gly	Ser	Phe	Asp	Ala	Asn	Glu	Leu	Ala	Val	Thr	Pro	Asp	Thr	Asp	Thr
		35					40					45			
Val	Ile	Gln	Gly	Val	Gly	Pro	Ala	Leu	Ala	Leu	Leu	Asp	Ser	Ala	Trp
	50					55					60				
Gly	Arg	Gln	Ile	His	Val	Glu	Thr	Thr	Gly	Cys	Pro	Ser	Ala	Val	Val
65					70				75					80	
Trp	Asn	Pro	Arg	Ser	Ser	Ser	Thr	His	Ala	Asp	Asn	Pro	Thr	Ala	Gln
			85						90					95	
Ala	Trp	Arg	Asp	Phe	Val	Cys	Val	Glu	Thr	Gly	Ala	Cys	Lys	Asp	Asn
			100					105					110		
Ala	Val	Ile	Val	Ala	Pro	His	Ser	Asp	Leu	Thr	Met	Ser	Thr	Arg	Ile
		115					120					125			
Ser	Val	Glu	Thr	Leu											

<210> 69

<211> 552

<212> DNA

<213> Homo sapiens

<400> 69

nnaagggttaa ggagaaaagc aaggaccttg caaagagagc ctctgtgccg gagaggctgg
60
ccctcaagga ggagcaaaaa gaagacccca gtggagcagc tgtgcccgag atgccaaaaa
120
agtcctccaa gattgccagc ttcattccca aaggggggaa gctcaacagt gccaagaagg
180
agcnccatgg ccccttcctt cagtgggaata ccaaaaccag gaatgaaaag catgcccggg
240
aaatccccaa gtgccccagc gccttccaag gaagggggagc ggagccggag tgggaagctg
300
agctcaggac tccccagca gaagccccag ctggacggca gacactccag ttcctcttcc
360
agcctggcgt cctcagaagg aaaaggccca ggagggacca ccctgaacca cagcatcagc
420
agccagactg tcagtgggtc tgtcgggacc acccagacca caggaagcaa tnnaccgtca
480
gtgttcagct acctcagccc cagcagcaat acaaccatcc caacactgcc acggttgca
540
ctttcctgta ca
552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

Xaa	Arg	Val	Arg	Arg	Lys	Ala	Arg	Thr	Leu	Gln	Arg	Glu	Pro	Leu	Cys
1				5					10					15	
Arg	Arg	Gly	Trp	Pro	Ser	Arg	Arg	Ser	Gln	Lys	Lys	Thr	Pro	Val	Glu
		20						25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35					40					45			
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
	50					55					60				
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
65					70					75					80
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
			85						90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
			100					105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys	
	115						120					125			
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
	130					135					140				
Ser	Gly	Ser	Val	Gly	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser	
145					150					155				160	
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
				165					170					175	
Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
															180

<210> 71
 <211> 316
 <212> DNA
 <213> Homo sapiens

<400> 71
 cgcgttgaaa tggcgttcga acttaaactg ttacatattg actccgtgcc attaaacatt
 60
 ttgaatcctg ttaaaggagc tccatttgaa agcaacgaag ctttacgtcc tttaaataac
 120
 ttacgtacct tcgccgtatt ccgtttcatc ttgccaaacg cattgatacg aactgcaggt
 180
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtg cctaaacggt
 240
 atcatgggtg gtggctactt aactactggc ggctggtcac ctcaagacga tctccaaatg
 300
 attcaagact tggagt
 316

<210> 72
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 72
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 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
 50 55 60
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
 65 70 75 80
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
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 Asp Leu Gln Met Ile Gln Asp Leu Glu
 100 105

<210> 73
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 73
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<210> 74
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 <213> Homo sapiens

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 35 40 45
 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala
 50 55 60
 Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg
 65 70 75 80
 His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro
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 His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly
 115 120 125

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 <211> 405
 <212> DNA
 <213> Homo sapiens

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<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 76
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 35 40 45
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
 50 55 60
 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
 85 90 95
 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
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<210> 77
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 <213> Homo sapiens

<400> 77
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 420
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 5816

<210> 78
 <211> 799
 <212> PRT
 <213> Homo sapiens

<400> 78
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 20 25 30
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 35 40 45
 Asn Asn Leu Leu Arg Leu Pro Phe Gly Cys Gly Glu Gln Asn Met Ile
 50 55 60
 His Phe Ala Pro Asn Val Phe Val Leu Lys Tyr Leu Gln Lys Thr Gln
 65 70 75 80
 Gln Leu Ser Pro Glu Val Glu Arg Glu Thr Thr Asp Tyr Leu Val Gln
 85 90 95
 Gly Tyr Gln Arg Gln Leu Thr Tyr Lys Arg Gln Asp Gly Ser Tyr Ser
 100 105 110
 Ala Phe Gly Glu Arg Asp Ala Ser Gly Ser Met Trp Leu Thr Ala Phe
 115 120 125
 Val Leu Lys Ser Phe Ala Gln Ala Arg Ser Phe Ile Phe Val Asp Pro
 130 135 140
 Arg Glu Leu Ala Ala Ala Lys Ser Trp Ile Ile Gln Gln Gln Gln Ala
 145 150 155 160
 Asp Gly Ser Phe Leu Ala Val Gly Arg Val Leu Asn Lys Asp Ile Gln
 165 170 175
 Gly Gly Ile His Gly Ile Val Pro Leu Thr Ala Tyr Val Val Val Ala
 180 185 190
 Leu Leu Glu Thr Gly Thr Ala Ser Glu Glu Glu Arg Gly Ser Thr Asp
 195 200 205
 Lys Ala Arg His Phe Leu Glu Ser Ala Ala Pro Leu Ala Met Asp Pro
 210 215 220
 Tyr Ser Cys Ala Leu Thr Thr Tyr Ala Leu Thr Leu Leu Arg Ser Pro
 225 230 235 240
 Ala Ala Pro Glu Ala Leu Arg Lys Leu Arg Ser Leu Ala Ile Met Arg
 245 250 255
 Asp Gly Val Thr His Trp Ser Leu Ser Asn Ser Trp Asp Val Asp Lys
 260 265 270
 Gly Thr Phe Leu Ser Phe Ser Asp Arg Val Ser Gln Ser Val Val Ser
 275 280 285
 Ala Glu Val Glu Met Thr Ala Tyr Ala Leu Leu Thr Tyr Thr Leu Leu
 290 295 300
 Gly Asp Val Ala Ala Ala Leu Pro Val Val Lys Trp Leu Ser Gln Gln

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305          310          315          320
Arg Asn Ala Leu Gly Gly Phe Ser Ser Thr Gln Asp Thr Cys Val Ala
          325          330          335
Leu Gln Ala Leu Ala Glu Tyr Ala Ile Leu Ser Tyr Ala Gly Gly Ile
          340          345          350
Asn Leu Thr Val Ser Leu Ala Ser Thr Asn Leu Asp Tyr Gln Glu Thr
          355          360          365
Phe Glu Leu His Arg Thr Asn Gln Lys Val Leu Gln Thr Ala Ala Ile
          370          375          380
Pro Ser Leu Pro Thr Gly Leu Phe Val Ser Ala Lys Gly Asp Gly Cys
385          390          395          400
Cys Leu Met Gln Ile Asp Val Thr Tyr Asn Val Pro Asp Pro Val Ala
          405          410          415
Lys Pro Ala Phe Gln Leu Leu Val Ser Leu Gln Glu Pro Glu Ala Gln
          420          425          430
Gly Arg Pro Pro Met Pro Ala Ser Ala Ala Glu Gly Ser Arg Gly
          435          440          445
Asp Trp Pro Pro Ala Asp Asp Asp Asp Pro Ala Ala Asp Gln His His
          450          455          460
Gln Glu Tyr Lys Val Met Leu Glu Val Cys Thr Arg Trp Leu His Ala
465          470          475          480
Gly Ser Ser Asn Met Ala Val Leu Glu Val Pro Leu Leu Ser Gly Phe
          485          490          495
Arg Ala Asp Ile Glu Ser Leu Glu Gln Leu Leu Leu Asp Lys His Met
          500          505          510
Gly Met Lys Arg Tyr Glu Val Ala Gly Arg Arg Val Leu Phe Tyr Phe
          515          520          525
Asp Glu Ile Pro Ser Arg Cys Leu Thr Cys Val Arg Phe Arg Ala Leu
          530          535          540
Arg Glu Cys Val Val Gly Arg Thr Ser Ala Leu Pro Val Ser Val Tyr
545          550          555          560
Asp Tyr Tyr Glu Pro Ala Phe Glu Ala Thr Arg Phe Tyr Asn Val Ser
          565          570          575
Thr His Ser Pro Leu Ala Arg Glu Leu Cys Ala Gly Pro Ala Cys Asn
          580          585          590
Glu Val Glu Arg Ala Pro Ala Arg Gly Pro Gly Trp Phe Pro Gly Glu
          595          600          605
Ser Gly Pro Ala Val Ala Pro Glu Glu Gly Ala Ala Ile Ala Arg Cys
          610          615          620
Gly Cys Asp His Asp Cys Gly Ala Gln Gly Asn Pro Val Cys Gly Ser
625          630          635          640
Asp Gly Val Val Tyr Ala Ser Ala Cys Arg Leu Arg Glu Ala Ala Cys
          645          650          655
Arg Gln Ala Ala Pro Leu Glu Pro Ala Pro Pro Ser Cys Cys Ala Leu
          660          665          670
Glu Gln Arg Leu Pro Ala Ser Ser Ser Ser Thr Tyr Gly Asp Asp Leu
          675          680          685
Ala Ser Val Ala Pro Gly Pro Leu Gln Gln Asp Val Lys Leu Asn Gly
          690          695          700
Ala Gly Leu Glu Val Glu Asp Ser Asp Pro Glu Pro Glu Gly Glu Ala
705          710          715          720
Glu Asp Arg Val Thr Ala Gly Pro Arg Pro Pro Val Ser Ser Gly Asn
          725          730          735
Leu Glu Ser Ser Thr Gln Ser Ala Ser Pro Phe His Arg Trp Gly Gln

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740							745					750			
Thr	Pro	Ala	Pro	Gln	Arg	His	Ser	Gly	Arg	Val	Val	Gly	Ala	His	Arg
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Pro	Gly	Leu	Leu	Ser	Pro	Val	Phe	Val	Tyr	Ser	Pro	Ala	Phe	Gln	Ser
770							775					780			
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785							790					795			

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<210> 79
<211> 346
<212> DNA
<213> Homo sapiens
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<210> 80
<211> 101
<212> PRT
<213> Homo sapiens
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Lys Ala Glu Tyr Leu Ala Ala Thr Ser Tyr Arg Asp Phe Leu Leu Lys
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Asp Val Gly Leu Ser Glu Gly Ala Val Lys Tyr Phe Gln Ser Arg Thr
 35                    40                    45
Asn Asp Phe Met Ala Leu Ser Ile Asp Ala Val Ala Ser Ala Asp Ala
 50                    55                    60
Tyr Ser Val Gly Phe Pro Gly Phe Gly Gly Met Asn Leu Ala Pro Ile
 65                    70                    75                    80
Ser Glu Glu Ala Ala Glu Met Glu Glu Pro Tyr Ile Tyr His Phe
 85                    90                    95
Pro Asp Gly Asn Ala
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<210> 81
<211> 429
<212> DNA
<213> Homo sapiens
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<400> 81

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 cctctatgag tggaatccag tctcatggcc ccccccattg ctctgttac cctggaggag
 180
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 420
 tgcacgcgt
 429

<210> 82
 <211> 79
 <212> PRT
 <213> Homo sapiens

<400> 82
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 20 25 30
 Met Cys Pro Cys Ala Cys Leu Cys Cys Val Cys Ala Cys Met Cys Ala
 35 40 45
 Cys Leu Cys Val Xaa Val Cys Val Arg Ala Cys Val Cys Thr Cys Val
 50 55 60
 His Val His Val Cys Ala Pro Val Cys Met Ser Val Cys Thr Arg
 65 70 75

<210> 83
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 83
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 411

<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
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 20 25 30
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile
 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
 85 90 95
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
 100 105 110
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His
 115 120 125

<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 85
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 atcctcgacg cggtgaaact gctgagttcg ctcggttca aggtgatcgc cacctcgggc
 120
 acccagcgtt tcctggtgga gaacggagta ccggcggaaa agatcaacaa ggtgctggaa
 180
 ggccgccccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc
 240
 accgaggggc cacaggcgtt ggctgacagc cgctcgttgc gacgcgctgc cctcttgcac
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 aaagtgccat attacaccac tctttcaggt gca
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<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr
 1 5 10 15
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly
 20 25 30
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

ATTORNEY DOCKET NO.: 15966-543

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      35          40          45
Gly Val Pro Ala Glu Lys Ile Asn Lys Val Leu Glu Gly Arg Pro His
  50          55          60
Ile Val Asp Ala Ile Thr Asn Gly Glu Val Gln Leu Val Phe Asn Thr
  65          70          75          80
Thr Glu Gly Pro Gln Ala Leu Ala Asp Ser Arg Ser Leu Arg Arg Ala
      85          90          95
Ala Leu Leu His Lys Val Pro Tyr Tyr Thr Thr Leu Ser Gly Ala
      100          105          110

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<210> 87
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 87
acgcgtgagg aaatgggggc cgcaggcctg gatcgcaagg tatggcagtg cccggtcgtc
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ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
  120
attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
  180
tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
  240
gtgggtactcg atatcacatc taaaccgccg gccaccatcg agtgggaatg agccccgtct
  300
caccgtgaac atgacatggc cgcacacctt cttggggcgg gccatgccgt gttag
  355

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<210> 88
 <211> 96
 <212> PRT
 <213> Homo sapiens

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<400> 88
Thr Arg Glu Glu Met Gly Ala Ala Gly Leu Asp Arg Lys Val Trp Gln
  1          5          10          15
Cys Pro Val Val Leu Leu Ser Asp Val His Ser Val Gly Val Gln Gly
      20          25          30
Asp Gly Arg Thr Tyr Gly Ser Pro Ile Val Leu Arg Pro Val Thr Ser
      35          40          45
Glu Asp Ala Met Thr Ala Asp Trp Ala Arg Ile Pro Tyr Asp Val Leu
      50          55          60
Glu Lys Ile Ser Thr Arg Ile Thr Asn Ala Cys Pro Gln Ile Asn Arg
  65          70          75          80
Val Val Leu Asp Ile Thr Ser Lys Pro Pro Ala Thr Ile Glu Trp Glu
      85          90          95

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<210> 89
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 89

ATTORNEY DOCKET NO.: 15966-543

nacgcgtcaa caccaggcta cggtgggtat gatcatgata agggctggga cccgcaggag
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 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca
 120
 ggtgattgga taaggccaga gggttgggag gggttctgcc cctgctgaag cctgggtggg
 180
 cccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg
 240
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc
 300
 caggtcctc gcagccggcc agaactcaca actcgagcgg tccatcagat c
 351

<210> 90
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 90
 Ser Leu Val Gly Pro Arg Ser Val Ile Trp Asp Arg Asn Asn Thr Ser
 1 5 10 15
 Ala Leu Gly Leu Leu Asp Val Ala Gln Ala Leu Glu Gln Asn His Ser
 20 25 30
 Leu Lys Ser Met Pro Leu Pro Leu Asn Asp Val Thr Gln Ala His Arg
 35 40 45
 Ser Arg Pro Glu Leu Thr Thr Arg Ala Val His Gln Ile
 50 55 60

<210> 91
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 91
 nggtgggtcc tctcgcagga caggtaatcc tgagacctac gcagctccct ggagctctgc
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 acgtcgaagc ccagcagggc ctctctgcagg tccctggggc agccagcaca cacaagtc
 120
 cggaaggggc tgtagactcc ctgccagcgg ctttcccgga gaaggcacc acgccagct
 180
 gcctcttgca ggtactgctc gggctctggtg ggagggcagc cgtgtccagc acaccctgtg
 240
 tgtgcagtcc tctccctgcc cactgccga acgagccctc cacggtgaag ccattgggga
 300
 acgtgacctt gcccttcccc atgaggt
 327

<210> 92
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 92
 Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

ATTORNEY DOCKET NO.: 15966-543

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      1             5             10             15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20             25             30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35             40             45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50             55             60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
      65             70             75             80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85             90             95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100             105

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<210> 93
 <211> 394
 <212> DNA
 <213> Homo sapiens

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<400> 93
nccgcgtacg acaagcagta cctcgagggg cgttacggtg cggacccata cctgagcaac
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atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaagggc
120
ggcgcgctct gcggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
ttttgtaccg ataaatcccc ggcgccacct gatcgtgacc gaggggtacga aaacggaacc
240
gctctatttc gaggetatca ggttgctgt caacaaccgt tatcacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcactct
360
ggcgggaagaa agtgccacag gattcactca cgta
394

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<210> 94
 <211> 109
 <212> PRT
 <213> Homo sapiens

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<400> 94
Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
  1             5             10             15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20             25             30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35             40             45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
      50             55             60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
      65             70             75             80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85             90             95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

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100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95
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 tgcttggatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc
 120
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa ggaagaaat
 180
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggcctc
 240
 tggggctctg cttggccata ggactgcac attgtgccac ctgctcatca cctcctctag
 300
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag
 360
 gctgagcatg gagctcacc catgccatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttct
 480
 aatctctgtt cccaccacat ttcataggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
 1 5 10 15
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
 100 105 110
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
 115 120

<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97

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 tcgcggtgcc ttgcgcgcgg gctggtaggt ggagaagccg cgcgagtacg cgcgctagag
 120
 cgacatcgtg tctgagacgt cgaagctcag gccagctttt ggcgctccagg cgcgctcggt
 180
 cggtcgcgcc tcttgccgca attgattcag cgcaatcccg gccatcacat gccagcgctt
 240
 gtccaggggc atgaaatcct gggcataggc gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98

<211> 122

<212> PRT

<213> Homo sapiens

<400> 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
1				5					10					15	
Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35					40				45				
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50					55					60				
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65					70					75				80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
				85				90						95	
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
			100					105						110	
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
			115					120							

<210> 99

<211> 545

<212> DNA

<213> Homo sapiens

<400> 99

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 tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg
 120
 tcgatcccat cactcgggat ttgctggaat ccctgggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcggtcgca tcgattgggt ctccccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggaggtac tcgatgatga ctgaacgttc
 300
 ccattccacg atcagggttaa ggtggccggc ggtgggtggt ctcgtcctcg ttccgctgct
 360
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccgggtg ggccgggtga
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 aagcggccgt cgtcaacgag gacaaggccg tcaagggtcg tggacaactg gttccgatgg
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 tcgac
 545

<210> 100
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 100
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 1 5 10 15
 Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
 20 25 30
 Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
 35 40 45
 Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
 50 55 60
 Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
 65 70 75 80
 Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
 85 90 95
 Ser Gly Ala Asp Ala
 100

<210> 101
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 101
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 tcatgcacga tccggacttc gatccgatcc ccatgggtgaa caaggagctt gacgccttcg
 120
 aagctgccgg ggggtgactat ctcatcctcg ccacggattc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatgggtccag
 300
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
 360
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
 420

gtcgacattg tccacgccaa agatgtccat aaggagatgg ccgacaagct ttgcctggc
 480
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacgggtgat
 540
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 600
 ctagagcagg acatcatga
 619

<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
 Thr Arg Ser Leu Thr Pro Ser Lys Leu Pro Gly Val Thr Ile Ser Ser
 1 5 10 15
 Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 103
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 gccattgggg ggagaccctt gccgtgggga aagacccttg ccatggggca gaccctgccc
 120
 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgccc
 180
 atggggaaag acccctgcca ttgggggaga ntacctgcca ttgggggaga tccctgccc
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 tggggggaga tccctgctgt tggggggaga ntccctcctg taggggaaga cccctgcagg
 300

agtgggttggg gcgaagaccc c
321

<210> 104
<211> 107
<212> PRT
<213> Homo sapiens

<400> 104
Xaa His Gly Gly Arg Gln Gln Pro Cys Gly Gly Asp Pro Ser His Trp
1 5 10 15
Gly Glu Thr Pro Ala Ile Gly Gly Arg Pro Leu Pro Trp Gly Lys Thr
20 25 30
Pro Ala Met Gly Gln Thr Pro Ala Thr Gly Gly Arg Pro Leu Pro Leu
35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
65 70 75 80
Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
85 90 95
Asp Pro Cys Arg Ser Gly Trp Gly Glu Asp Pro
100 105

<210> 105
<211> 344
<212> DNA
<213> Homo sapiens

<400> 105
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ccgggtcaac gaggggttgg cgcacgggtcc actccgtggc gcccggggtg atgtgcaaca
120
gggcggggccc gcgcgcggcc gggcctgatt ccagcctctc gtgctcgtcc cagtacccat
180
ccagcgcacg cccccagcgg tcggcatccc agccgtggtc gccgtcgagc gccccaggg
240
cctcaatgtc gtcacgcggc gccagttcca cccggcgga catctcgttg cggaccatga
300
cccgaaggc gcgggaattc tcggtcagtt tcggcggtgc cggc
344

<210> 106
<211> 62
<212> PRT
<213> Homo sapiens

<400> 106
Cys Ala Thr Gly Arg Ala Arg Ala Arg Pro Gly Leu Ile Pro Ala Ser
1 5 10 15
Arg Ala Arg Pro Ser Thr His Pro Ala His Arg Pro Ser Gly Arg His
20 25 30
Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

	35		40		45
Arg	Arg	Pro	Val	Pro	Pro
	50		55		60

<210> 107
 <211> 549
 <212> DNA
 <213> Homo sapiens

<400> 107
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 60
 gccgcttaat aaccgaccaa catgaaactc aagggtgccc ccttcctagc ggggacctg
 120
 cacagaccg aaaataagg gttttgctct gccctcctca gttcacgtgg gcaccttgga
 180
 aactgaaga aggcattttc cgaactcact gtcctacgga cttattctcc gactgtttt
 240
 cgctccttc gccctgttct cgtgactgac aggagcagg gtcacaagca ggcagcccga
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 gagctctgct cacctggaaa agcatttttg ttagcttaa atgtgaagg ctcaggcagt
 360
 ggctgttgt cctcctccac atgcgcccat cttcactctt tcatgtgact ggctgtttt
 420
 tgaaggcaag gccctgtca cccttggeta ggccaggat gttctgcacc gaaaatggc
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 ctgccctctg cattggatgg ctagctctta ggttggttta ttttagcaaa taagcgttac
 540
 agggtaggc
 549

<210> 108
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 108
 Met Lys Leu Lys Gly Cys Pro Phe Leu Ala Gly Thr Leu His Arg Pro
 1 5 10 15
 Glu Asn Lys Gly Phe Cys Ser Ala Leu Ser Ser Arg Gly His Leu
 20 25 30
 Gly Thr Leu Lys Lys Ala Phe Ser Glu Leu Thr Val Leu Arg Thr Tyr
 35 40 45
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
 50 55 60
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
 65 70 75 80
 Ala Phe Leu Cys Ser Leu Asn Val Lys Ala Ser Gly Ser Gly Leu Leu
 85 90 95
 Ser Ser Ser Thr Cys Ala His Leu His Ser Phe Met
 100 105

<210> 109
 <211> 748

<212> DNA

<213> Homo sapiens

<400> 109

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nngaattcag atttactttt tgcatttcct tgaatataaa ataggcagta aactaaccta
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aagtcagaag acttatttgt tctggtacct attctgctgt taataaattg ataaatgagt
120
gatattgggg taagttacca atttacttta cagcccttaa gtaaataatc tgctttcctc
180
agcatcatag acttttgaag aggattaatt aagcgcttaa aaaacctgta gactctatta
240
cagtcagtga aaggaataat tctctttaca aagtaaatgc agttgtttta ttttagacaa
300
gagtgttcta aacttcgtga agagttaagg cttcaacatg aagaggataa gaagtcagca
360
atgtctcaac ttttgcagtt gaaagatcga gagaaaaatg cagcaagaga ttcattggcag
420
aagaaagtag aagatctctt aaaccagatt tccttgctga aacagaatct ggagatacac
480
ctttcccagt ctcagacttc tttgcaacaa ctgcaagccc agtttacgca agaacgacag
540
cggcttacgc aagagcttga agaattagag gagcaacatc agcaaagaca caaatcatta
600
aaagaagcac atgtccttgc atttcaaact atggaagagg aaaaggaaaa ggagcaaaga
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cacagagagt caatggaggg cttccgga
748

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<210> 110

<211> 157

<212> PRT

<213> Homo sapiens

<400> 110

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Met Gln Leu Phe Tyr Phe Arg Gln Glu Cys Ser Lys Leu Arg Glu Glu
1           5           10           15
Leu Arg Leu Gln His Glu Glu Asp Lys Lys Ser Ala Met Ser Gln Leu
20           25           30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35           40           45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50           55           60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65           70           75           80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85           90           95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100          105          110
Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Glu Gln Arg
115          120          125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

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130	135	140
Leu Lys Asp Ala His Arg Glu Ser Met Glu Gly Phe Arg		
145	150	155

<210> 111
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 111
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 120
 tcgggttatn nacgccacca gcatncgact ttggctgaga tcatcgcacc gttcgggacat
 180
 ctgggtcatga tcgacggaac cgactcattc gatctcatgg ccttcaagtc aaagtcgtta
 240
 acggtgacca gcgagtcgat gttcagccgt ccacagttcg cgacgcccga cgtcgccgaa
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 420
 ggtccggc
 429

<210> 112
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 112
 Ala Arg Pro Glu Ser Ala Gln Trp Cys Gln Asp Met Gly Ala Thr Gly
 1 5 10 15
 Ile Ile Asn His Arg Glu Pro Leu Ala Pro Gln Val Asn Asp Phe Gly
 20 25 30
 Ile Thr Gly Phe Asp Gly Ile Leu Ser Ala Tyr Xaa Arg His Gln His
 35 40 45
 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
 50 55 60
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
 65 70 75 80
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
 100 105 110
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
 115 120 125
 Thr Thr Gln His Val Arg Glu Ala Thr Ala Ala Val Glu Ser Gly
 130 135 140

<210> 113
 <211> 382

<212> DNA

<213> Homo sapiens

<400> 113

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 120
 gtccacagcc ccaccttctg ccagctggcg tgcggccagg atgggcagct gaagggttc
 180
 gcggtgctgg agtatgagac ggctgagatg gcggaggagg cacagcagca ggcggacggc
 240
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<210> 114

<211> 125

<212> PRT

<213> Homo sapiens

<400> 114

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Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
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Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
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Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
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Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
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<210> 115

<211> 4798

<212> DNA

<213> Homo sapiens

<400> 115

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<210> 116
<211> 1062
<212> PRT
<213> Homo sapiens

<400> 116
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Cys His Leu Ser Pro Ser Ser Leu Ser Pro Phe Ser Val Ala Glu Arg			
35	40	45	
Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile			
50	55	60	
Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr			
65	70	75	80
Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg			
85	90	95	
Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg			
100	105	110	
Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val			
115	120	125	
Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe			
130	135	140	
Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu			
145	150	155	160
Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu			
165	170	175	
Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser			
180	185	190	
Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu			
195	200	205	
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg			
210	215	220	
Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser			
225	230	235	240
Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro			
245	250	255	
Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro			
260	265	270	
Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg			
275	280	285	
Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg			
290	295	300	
Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser			
305	310	315	320
Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu			
325	330	335	
Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln			
340	345	350	
Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys			
355	360	365	
Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala			
370	375	380	
Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys			
385	390	395	400
Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu			
405	410	415	
Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro			
420	425	430	
Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln			

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Tyr	Phe	Glu	Leu	Gln	Cys	Arg	Gln	Tyr	Lys	Arg	Lys	Met	Leu	Leu	Ala		
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Arg	His	Ser	Leu	Asp	Gln	Asp	Leu	Leu	Arg	Glu	Asp	Leu	Asn	Lys	Lys		
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Gln	Thr	Gln	Lys	Asp	Leu	Glu	Cys	Ala	Leu	Leu	Leu	Arg	Gln	His	Glu		
500						505						510					
Ala	Thr	Arg	Glu	Leu	Glu	Leu	Arg	Gln	Leu	Gln	Ala	Val	Gln	Arg	Thr		
515						520						525					
Arg	Ala	Glu	Leu	Thr	Arg	Leu	Gln	His	Gln	Thr	Glu	Leu	Gly	Asn	Gln		
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Ala	Gln	Val	Arg	Gln	Gln	Pro	Lys	Ser	Leu	Lys	Val	Arg	Ala	Gly	Gln		
565						570						575					
Arg	Pro	Pro	Gly	Leu	Pro	Leu	Pro	Ile	Pro	Gly	Ala	Leu	Gly	Pro	Pro		
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Asn	Thr	Gly	Thr	Pro	Ile	Glu	Gln	Gln	Pro	Cys	Ser	Pro	Gly	Gln	Glu		
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Ala	Val	Leu	Asp	Gln	Arg	Met	Leu	Gly	Glu	Glu	Glu	Glu	Ala	Val	Gly		
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Glu	Arg	Arg	Ile	Leu	Gly	Lys	Glu	Gly	Ala	Thr	Leu	Glu	Pro	Lys	Gln		
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Gln	Arg	Ile	Leu	Gly	Glu	Glu	Ser	Gly	Ala	Pro	Ser	Pro	Ser	Pro	Gln		
645						650						655					
Lys	His	Gly	Ser	Leu	Val	Asp	Glu	Glu	Val	Trp	Gly	Leu	Pro	Glu	Glu		
660						665						670					
Ile	Glu	Glu	Leu	Arg	Val	Pro	Ser	Leu	Val	Pro	Gln	Glu	Arg	Ser	Ile		
675						680						685					
Val	Gly	Gln	Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp		
690						695						700					
Glu	Ser	Leu	Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro		
705						710						715					
Ala	Leu	Thr	Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala		
725						730						735					
Pro	Ile	Gly	Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp		
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Ile	Pro	Pro	Glu	Pro	Pro	Pro	Thr	His	Leu	Arg	Pro	Cys	Pro	Ala	Ser		
755						760						765					
Gln	Leu	Pro	Gly	Leu	Leu	Ser	His	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Phe		
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Ala	Val	Gly	Ser	Ser	Ser	Gly	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu		
785						790						795					
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805						810						815					
Leu	Ala	Leu	Glu	Val	Gly	Leu	Val	Gly	Leu	Gly	Ala	Ser	Tyr	Leu	Leu		
820						825						830					
Leu	Cys	Thr	Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala		
835						840						845					
Gln	Gly	Thr	Ala	Leu	Gly	Ala	Val	Leu	Gly	Leu	Ser	Trp	Arg	Arg	Gly		
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865 870 875 880
 Pro Gly Leu Ala Leu Pro Leu Val Ala Met Ala Ala Gly Gly Arg Trp
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 Val Arg Gln Gln Gly Pro Arg Val Arg Arg Gly Ile Ser Arg Leu Trp
 900 905 910
 Leu Arg Val Leu Leu Arg Leu Ser Pro Met Ala Phe Arg Ala Leu Gln
 915 920 925
 Gly Cys Gly Ala Val Gly Asp Arg Gly Leu Phe Ala Leu Tyr Pro Lys
 930 935 940
 Thr Asn Lys Asp Gly Phe Arg Ser Arg Leu Pro Val Pro Gly Pro Arg
 945 950 955 960
 Arg Arg Asn Pro Arg Thr Thr Gln His Pro Leu Ala Leu Leu Ala Arg
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 Val Trp Val Leu Cys Lys Gly Trp Asn Trp Arg Leu Ala Arg Ala Ser
 980 985 990
 Gln Gly Leu Ala Ser His Leu Pro Pro Trp Ala Ile His Thr Leu Ala
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 Ser Trp Gly Leu Leu Arg Gly Glu Arg Pro Thr Arg Ile Pro Arg Leu
 1010 1015 1020
 Leu Pro Arg Ser Gln Arg Gln Leu Gly Pro Pro Ala Ser Arg Gln Pro
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<210> 117

<211> 471

<212> DNA

<213> Homo sapiens

<400> 117

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<210> 118

<211> 157

<212> PRT

<213> Homo sapiens

<400> 118

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 20 25 30
 Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
 35 40 45
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
 50 55 60
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
 65 70 75 80
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
 85 90 95
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
 100 105 110
 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
 115 120 125
 Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
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 Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu Leu
 145 150 155

<210> 119

<211> 302

<212> DNA

<213> Homo sapiens

<400> 119

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 180
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<210> 120

<211> 98

<212> PRT

<213> Homo sapiens

<400> 120

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 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
 35 40 45
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

50 55 60
 Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr
 65 70 75 80
 Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys
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 Ala Arg

<210> 121
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 121
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<210> 122
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 122
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 35 40 45
 Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
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 Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Phe Cys Leu Glu Thr
 65 70 75 80
 Glu Ser Xaa Ser Val Ala Arg Leu Glu
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<210> 123
 <211> 338
 <212> DNA
 <213> Homo sapiens

<400> 123
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 240
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 338

<210> 124
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 124
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 Pro Val Glu Gln Arg Ala Pro Ala Pro Gln Leu Ile Pro Leu Cys His
 35 40 45
 Ile Arg Ala Ser Ser His Ala Val Pro Ser Ala Trp Val Ala Phe Ser
 50 55 60
 Pro Ser Ala Trp Val Thr Val His Thr Thr Gly His Phe Pro Gln Gly
 65 70 75 80
 Arg Ala Leu Thr Ala His Thr Pro Lys His Ala Pro Cys Ser Ser Ile
 85 90 95

<210> 125
 <211> 280
 <212> DNA
 <213> Homo sapiens

<400> 125
 ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc
 60
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca cttttctgca
 180
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
 240
 gcttctgctg tcctggccca ttctggatag gcctgatcta
 280

<210> 126
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 126
 Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

      1             5             10             15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
      20             25             30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
      35             40             45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
      50             55             60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
65             70             75             80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
      85             90

```

<210> 127
 <211> 444
 <212> DNA
 <213> Homo sapiens

```

<400> 127
cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcatca ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgcca tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggctg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccg ccgatctgga tgcctgatc gccaggatgg ccactgtgcg caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caacgtggca
420
cgcgacatgc tcaagcactg gtgc
444

```

<210> 128
 <211> 148
 <212> PRT
 <213> Homo sapiens

```

<400> 128
Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
      1             5             10             15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
      20             25             30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
      35             40             45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
      50             55             60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
65             70             75             80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
      85             90             95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

	100		105		110										
Met	Ala	Thr	Val	Arg	Thr	Ala	Arg	Ala	Trp	Val	Tyr	Lys	Glu	Gln	Leu
	115		120		125										
Arg	Glu	Ile	Leu	Ala	Arg	Lys	Gln	Ile	Asn	Val	Ala	Arg	Asp	Met	Leu
	130		135		140										
Lys	His	Trp	Cys												
145															

<210> 129
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 129
 gaggagggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac
 60
 ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgtc
 120
 gagtgtccgc tcgaggaagt tccgctgac caaaagcaga tcatcgagaa ggctcgttta
 180
 caggctaagc ccgtcattgt ggccaccag atgcttgagt cgatgatcca cgctccccgt
 240
 ccgaccgcg ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
 291

<210> 130
 <211> 97
 <212> PRT
 <213> Homo sapiens

Glu	Glu	Gly	Arg	Thr	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro	Gln	
1				5				10					15			
Ala	Ile	Glu	Asn	Leu	Asp	Glu	Ile	Ile	Asp	Val	Phe	Asp	Ala	Val	Met	
			20					25					30			
Val	Ala	Arg	Gly	Asp	Met	Ala	Val	Glu	Cys	Pro	Leu	Glu	Glu	Val	Pro	
		35				40					45					
Leu	Ile	Gln	Lys	Gln	Ile	Ile	Glu	Lys	Ala	Arg	Leu	Gln	Ala	Lys	Pro	
	50				55					60						
Val	Ile	Val	Ala	Thr	Gln	Met	Leu	Glu	Ser	Met	Ile	His	Ala	Pro	Arg	
65				70				75					80			
Pro	Thr	Arg	Ala	Glu	Ala	Ala	Asp	Val	Ala	Asn	Ala	Ile	Leu	Asp	Gly	
			85					90					95			
Ala																

<210> 131
 <211> 416
 <212> DNA
 <213> Homo sapiens

<400> 131
 tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag
 60

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcggtgtct tccgctacgc cgaacgtctg gtaggccacg acctgggtct gcggatgcag
 180
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
 240
 cgccgggggtg acctgctggt acgggttact gccgacgtcg acgcggtgtt ggacatggtc
 300
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggtcctt
 360
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggg
 416

<210> 132
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 132
 Ser Gly Ala Ser Val Ala Leu Met Gly Val Ser Ala Trp Leu Leu Ser
 1 5 10 15
 Arg Ala Ala Glu Ile Pro Pro Val Leu Tyr Leu Glu Ala Ala Val
 20 25 30
 Gly Val Arg Phe Phe Gly Ile Ser Arg Gly Val Phe Arg Tyr Ala Glu
 35 40 45
 Arg Leu Val Gly His Asp Leu Ala Leu Arg Met Gln Gly Ala Leu Arg
 50 55 60
 Met Arg Val Tyr Asp Arg Leu Ser Arg Thr Xaa Pro Ala Gly Xaa Arg
 65 70 75 80
 Arg Arg Gly Asp Leu Leu Val Arg Val Thr Ala Asp Val Asp Ala Val
 85 90 95
 Leu Asp Met Val Val Arg Val Ile Val Pro Ala Cys Ala Ser Ser Leu
 100 105 110
 Val Ile Ile Gly Thr Thr Val Leu Leu Cys Pro Arg Glu Gly
 115 120 125

<210> 133
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 133
 gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatatcgct
 60
 gcggtgaaga gactcgccga catctaccag ggtcgtgttc acacagtagt atccaccgc
 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttggtga tcggttctgt ccttattccg
 180
 ggtagtctta ccccgaagct tgttactacc gatatgggtg ctcacatgca gcctgggtct
 240
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca cccaccact
 300
 tacgatgacc ccactttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
 1 5 10 15
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat
 60
 ttacactcag ggctacagcc acggggggct gaggcccaag gctgcaatct cgggggaagg
 120
 ggaagtggc ttttctggt ggattggaaa catcctcttg gaggcaaaga ctttctctgg
 180
 atcttacaga cttcccggga tttttagatt agaattattgg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
 300
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccattggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
 420
 atgacatctt gtcttcacgc tcgagagaga attacttcac tggtccact tggagtgcc
 480
 gtgttcagac accaagcctg actgggaggg ttccgttttc ttaacacctt cccaccgccg
 540
 acttccaagt cccacgcgt
 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

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Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
           20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
           35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
 50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
           85           90           95
Ile Ser Ser Gly
           100

```

<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

```

accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaca gctggtcgcy cacctgcttg aggtccaccg attgcgcata gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggctgcaac gcgcataatc ggcagcgccct ggctggcgcc ctggctgagc
240
cagcgctcgc gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggt catgcagaat gtttcgcccc agccgggata acggcaagtg
360
ccggcgctcg aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

```

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
           20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
           35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
 50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

65		70		75		80									
Gln	Ser	Gly	Phe	Val	Glu	Asp	Leu	Phe	Arg	Ser	Gln	Val	Ala	Asp	Lys
		85							90					95	
Thr	Asn	Trp	Arg	Ala	Leu	Leu	Lys	Gly	Asp	Ala	Gln	Ser	Val	Asp	Leu
		100						105					110		
Lys	Gln	Val	Arg	Asp	Gln	Leu	Phe	Ala	Ser	Cys	Ala	Glu	Gly	Leu	Leu
		115					120					125			
Ser	Leu	Gln	Glu	Arg	Phe	Gly	Leu	Gln	Ala	Ile	Gln	Pro			
	130					135					140				

<210> 139

<211> 341

<212> DNA

<213> Homo sapiens

<400> 139

acgcgctcggtt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
60
ttgtgaacag cagaatcaag ccgctggtaa atcttcctgg gagcttcata ggcgggggatg
120
ctacacgagc tggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatgggaccg
240
acggccactt caccgatctc ttcatagccc tggcggttct agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

<210> 140

<211> 113

<212> PRT

<213> Homo sapiens

<400> 140

Met	Thr	Arg	Thr	His	Gln	Ala	Ser	Cys	Ser	Thr	Leu	Ala	Ile	Arg	Ala
1				5					10					15	
Thr	Trp	Ile	Ser	Thr	Asn	Ala	Arg	Ala	Met	Lys	Arg	Ser	Val	Lys	Trp
		20						25					30		
Pro	Ser	Val	Pro	Ser	Trp	Ser	Met	Cys	Phe	Ser	Ile	Arg	Thr	Leu	Ser
		35					40					45			
Arg	Tyr	Arg	Leu	Gln	Arg	Phe	Glu	Thr	Glu	Leu	Phe	Arg	Gln	Phe	Arg
	50					55					60				
Val	Gln	Ser	Val	Ser	Pro	Ala	Arg	Val	Ala	Ser	Pro	Pro	Met	Lys	Leu
65					70				75					80	
Pro	Gly	Arg	Phe	Thr	Ser	Gly	Leu	Ile	Leu	Leu	Phe	Thr	Ser	Cys	Gly
			85						90					95	
Ala	Leu	Ala	Gln	Ser	Glu	Leu	Asp	Val	Arg	Ile	Lys	Pro	Ser	Asn	Asp
		100						105					110		

Ala

<210> 141

<211> 324

<212> DNA

<213> Homo sapiens

<400> 141

gaattcctct tggatagctt cgggtaaattg ggtacagcaa atatcaggag cgcaaccgca
 60
 acctttactt actggtacat gaacaccatt tacattacag ctatcgctact caccacacgt
 120
 catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
 180
 gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcatagaact cctttgacca
 240
 tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
 300
 gcagttatca ccgccatac gcgt
 324

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

Met	Gly	Gly	Asp	Asn	Cys	Cys	Arg	Ser	Phe	Cys	Phe	Ala	Pro	Ser	Gly
1				5					10					15	
Val	Thr	Asn	Asp	Gly	Arg	Ile	Tyr	Tyr	Ala	Trp	Ser	Lys	Glu	Phe	Met
		20					25					30			
Gln	Ala	Pro	Ala	Gly	Tyr	Tyr	Leu	Ala	Val	Phe	Thr	Val	Asp	Gly	His
		35				40					45				
Thr	Tyr	Arg	Glu	Thr	Val	Val	Tyr	Lys	Pro	Phe	Ser	Tyr	Val	Ser	Val
	50				55					60					
His	Met	Thr	Trp	Gly	Glu	Tyr	Asp	Ser	Cys	Asn	Val	Asn	Gly	Val	His
65				70					75				80		
Val	Pro	Val	Ser	Lys	Gly	Cys	Gly	Cys	Ala	Pro	Asp	Ile	Cys	Cys	Thr
			85				90					95			
His	Leu	Pro	Glu	Ala	Ile	Gln	Glu	Glu	Phe						
			100				105								

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

nacgcgtgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
 60
 gcaccccagg agaagaactt cctgtacaaa tgcataggca ccaccctggg tgctgcttca
 120
 agtaaggagg tgggtaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
 180
 gaggcagaac gcgagggcct cgctgctgc ttcgggatct gtgccatctc ccacctcgag
 240
 gagacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
 300

attctcaaca tttttaagga tcgaagtga aacgaagtgg agaagtgaa gagtgctctg
 360
 atcctgtgct atgggcacgt ggcgccccgg gccccccggg agctgggtgct ggccaaggta
 420
 gagtcagaca tcctccggaa catcntgcca gcacttcagc acnnaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgag ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaaagca gagctgggtg cacagatgat ggagttcatc
 600
 agggcagagc ccccgactc cttgaggaca cctattcgga agaaagccat gctcacctgc
 660
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggaggga tgtgatccat
 720
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
 cagaagtccc tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg
 840
 cagcggaaca tgacccccca aggcctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtcaccaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc
 960
 tacttcctgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
 1020
 cccaggatcc tgtgcaatgg ccctggtgcc cttccacaac ctgggccttc tcatcgccct
 1080
 cttctcccca cgggtgtgagg acctgtggcc tgccacccgc caggaggccg tggactgtgt
 1140
 ctactccctg ctgtacctcc agctcggcta tgagggtctc tcccgggact accgcgatga
 1200
 cgtggcggag cggctcctca gcctcaagga cggcctcgtg caccctgacc ccgccattct
 1260
 cttccacacc tgccacagtg taggccagat tattgccaag cgctccccc cagcccttca
 1320
 cgcgt
 1325

<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Xaa	Ala	Trp	Ile	Cys	Gln	Leu	Ser	Leu	Glu	Leu	Cys	Arg	Gln	Leu	Pro
1				5					10					15	
Cys	Tyr	Asp	Glu	Ala	Pro	Gln	Glu	Lys	Asn	Phe	Leu	Tyr	Lys	Cys	Ile
			20					25					30		
Gly	Thr	Thr	Leu	Gly	Ala	Ala	Ser	Ser	Lys	Glu	Val	Val	Arg	Lys	His
			35				40						45		
Leu	Gln	Glu	Leu	Leu	Glu	Thr	Ala	Arg	Tyr	Gln	Glu	Glu	Ala	Glu	Arg
			50				55				60				
Glu	Gly	Leu	Ala	Cys	Cys	Phe	Gly	Ile	Cys	Ala	Ile	Ser	His	Leu	Glu
65				70					75					80	
Asp	Thr	Leu	Ala	Gln	Leu	Glu	Asp	Phe	Val	Arg	Ser	Glu	Val	Phe	Arg

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<210> 145
<211> 802
<212> DNA
<213> Homo sapiens
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<400> 145
cgcccgctcta ggtccggctc agtgcgctgt tgctcgccgt agaacacgag gctgcgcaag
60
cataagcaga cgtagagagt ggtcacatcc atgtcgatgg tgtgcgcgta atgaaggtct
120
acatcaccct ggtgaaggcc tgcaccacta gcgtcggcac catttccccg cgtcggacaa
180
gacatcatgc cccatatctt gacagaatgt ctgacatgag tatgccacgc cgagcagcac
240
```

cagaggacga caccgatctg gcggaagccg cccgttcacg gcgcagatac ctcatcctcg
 300
 tcatttggtg cgttatcgtc gctgtcctcg gactaggcat ttctgggtat cttgcgtggt
 360
 ggtcattgtg cgatcaagct gccgggggtct gtcagcgtgg tgaaccggtt atgtactggt
 420
 gttcgggtgt ctctctggcc attctcggac tcattatcgg ggtcttgacg cagatctggc
 480
 tggagaagcg ctggtggcac atgcttgcca tcgtcatccc ggctgttttc atcgtcgccg
 540
 gtatcttttt ctggctcgcc gtctaagaag gggcgtcaca gattccacaa acgacacagg
 600
 tattgatctc cgttttatcg gctcctagca gccgtggtca acgtatcgct atcaagcgat
 660
 acaggactcg tcgttcgcat cgttgttggt ctgctgggaa acaatcccag cgatctactc
 720
 ggctaccgcc agacagttca ctcacaaccc ctcacgccgg cgcagacatc aaatcccatt
 780
 ctcgatagac ggcccacacc ac
 802

<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

Met	Lys	Val	Tyr	Ile	Thr	Leu	Val	Lys	Ala	Cys	Thr	Thr	Ser	Val	Gly
1				5					10					15	
Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
			20					25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35					40					45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65					70				75					80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
			85					90					95		
Gly	Glu	Pro	Val	Met	Tyr	Trp	Cys	Ser	Val	Val	Ser	Leu	Ala	Ile	Leu
			100					105					110		
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
		115					120					125			
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
		130				135					140				
Ile	Phe	Phe	Trp	Leu	Ala	Val									
145						150									

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147

acgcgtgaaa acggtatgac tcttctggcc ttagtagatc tgtctaaaaa acccgatgag
 60
 ttacacagc gggcattagt agcccgcat gttcatgaca ttcttggtct acgaaaagtt
 120
 attggtcaga aagtaccttg tgttcagtg acggggtcgg aaaagggtgct tcataaaaag
 180
 gattactggg atctagcaac acctatgcc aattgcgtggg gtacaacgga ccgaacagtt
 240
 attgctgatg cagcagctac aatccccacc acggagtggg atatccttgc aagactacgt
 300
 ccacgcctag aagaggttcg caagcaacgt aatgatgtat tgctcctcaa cgaggaggat
 360
 ccccccta
 368

<210> 148
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 148
 Met Thr Leu Leu Ala Leu Val Asp Leu Ser Lys Lys Pro Asp Glu Phe
 1 5 10 15
 Thr Gln Trp Ala Leu Val Ala Arg Asp Val His Asp Ile Pro Gly Leu
 20 25 30
 Arg Lys Val Ile Gly Gln Lys Val Pro Cys Val Ala Val Thr Gly Ser
 35 40 45
 Glu Lys Val Leu His Lys Lys Asp Tyr Trp Asp Leu Ala Thr Pro Met
 50 55 60
 Pro Ile Ala Trp Gly Thr Thr Asp Arg Thr Val Ile Ala Asp Ala Arg
 65 70 75 80
 Arg Thr Ile Pro Thr Thr Glu Trp Asp Ile Leu Ala Arg Leu Arg Pro
 85 90 95
 Arg Leu Glu Glu Val Arg Lys Gln Arg Asn Asp Val Leu Leu Leu Asn
 100 105 110
 Glu Glu Asp Pro Pro
 115

<210> 149
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 149
 nngctagcat ggaccctagt cacacaggca gccatacccg aggtcaaagt gaccatttt
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 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
 50 55 60
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
 65 70 75 80
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
 85 90 95
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
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 65 70 75 80
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 85 90 95
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
 100 105 110
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<400> 154

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<211> 344

<212> DNA

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 35 40 45
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln
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<210> 157

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<211> 1572

<212> PRT

<213> Homo sapiens

<400> 158

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Val	Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys
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His	Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro
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Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg		
		805
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly		
	820	825
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp		
	835	840
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu		
	850	855
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe		
	865	870
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys		
		885
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr		
	900	905
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe		
	915	920
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys		
	930	935
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr		
	945	950
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr		
		965
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser		
	980	985
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe		
	995	1000
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu		
	1010	1015
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg		
	1025	1030
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn		
		1045
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr		
	1060	1065
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg		
	1075	1080
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val		
	1090	1095
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val		
	1105	1110
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg		
		1115
		1120

507

1555
Ser Ser Val Val
1570

1560

1565

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<400> 159
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tccgctcatc tgcagaatgg gtgatgctgt cggctacttcg tggcatacag gaaagtgtccc
120
agcatggtca gcctcagtga gaggtggcca gtggggagtgt gtggccactg tacacctggc
180
acagcccaga gatgcatgtg cactctgtt gtgtgcttca accaaggggc gctctggcag
240
ggcttgggtg ggacttccca aagggcatgg aaaagttccc agtcaatgag atccatggag
300
acccatggga gtgggggtca gccccagcct aagaggaccc ccagccctgc cctgtgtcccc
360
aggacacacc aggcaactgtc ccttgctgcc ttcccagaca acctgtaccc tccaggccac
420
cagttctcgt ccatgacaaa gaaaggagcc ttctaaataa gtgcccgcga gaggtgtcac
480
gcttccctgc cccttccggg tggacctggg tttcaaagag aagctgccag tgcaacgcgt
540

<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys
1 5 10 15
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
20 25 30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala
35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65 70 75 80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
85 90 95
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
100 105 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

<400> 161
 nnacgcgtac gtctttcggc cgaagaagga acgtgggcag gggcctcctt cgctggccgc
 60
 cgcgcttggc tcgcagcgac gatgaagggc gacgacagca gcaagatcac ccacaagatc
 120
 gcccgggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg
 180
 ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag
 240
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc
 300
 aagacggtgc atgcgtactt tgggtgctgag acgtgcatgc atctgacgtg c
 351

<210> 162
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 162
 Xaa Arg Val Arg Leu Ser Ala Glu Glu Gly Thr Trp Ala Gly Ala Ser
 1 5 10 15
 Phe Ala Gly Arg Arg Ala Trp Leu Ala Ala Thr Met Lys Gly Asp Asp
 20 25 30
 Ser Ser Lys Ile Thr His Lys Ile Ala Arg Ala Lys Arg Glu Gly Arg
 35 40 45
 Val Trp Trp Ser Phe Glu Tyr Phe Pro Pro Arg Thr Pro Gln Gly Met
 50 55 60
 Gln Asn Leu Tyr Asp Arg Ile Glu Arg Met Ser Gln Leu Gly Pro Glu
 65 70 75 80
 Phe Val Asp Ile Thr Trp Asn Ala Gly Gly Arg Thr Ser Asp Met Thr
 85 90 95
 Thr Gln Leu Val Lys Thr Val His Ala Tyr Phe Gly Val Glu Thr Cys
 100 105 110
 Met His Leu Thr Cys
 115

<210> 163
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 163
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 60
 gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcatcactcc gttcaacttc
 120
 ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg
 180
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa
 240
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg
 300

ctgtgcaccc ataaagatat caaggcagtt tctttcgtcg gttcgaccgc cgttggtacc
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

Ala	Cys	Ser	Ile	Gly	Thr	Leu	Gln	Met	Gly	Glu	Phe	Ala	Glu	Asn	Val
1				5					10					15	
Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35				40						45			
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55				60					
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65					70					75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
				85				90						95	
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
			100					105					110		
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
			115				120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

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60
tcccagcgag ggacgcccgg ggctgggggt gccggtcgag cccggggcaa cagcttcacc
120
aagtttgga accgcaacgt cttcatgaag gacaacagct cttcttcag cacagactcc
180
cgctcccgct cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca
240
gactccgaca gctcctactc aggggaatgag tgtcaccctg tgggccgcag gaaccgcgcc
300
cctaagggcc ggggaggctg agggggccat atggatcggg gccgaggcag ggcgcagcgt
360
gggaagaggc acgatctggc gccaccaag cgcagtcgaa agaagatggc ggcgctggag
420
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgtt ccagcacgga
480
cactcccgcc gcctgcgect cgagcccctg gtgctgcaga tgagcagcct ggagagcagt
540
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag
600
cactacctgc gcctcacctg tgccccgac cgtccaccg tgcgccctgt ggcattccct
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga
 720
 ctacgcgt
 728

<210> 166
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 166
 Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly
 1 5 10 15
 Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly
 20 25 30
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
 35 40 45
 Met Lys Asp Asn Ser Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
 50 55 60
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
 65 70 75 80
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
 85 90 95
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
 100 105 110
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
 115 120 125
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
 130 135 140
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
 145 150 155 160
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
 165 170 175
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
 180 185 190
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
 195 200 205
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
 210 215 220
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly
 225 230 235 240
 Leu Arg

<210> 167
 <211> 510
 <212> DNA
 <213> Homo sapiens

<400> 167
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 gcaacacaga attgtcaggt cctgtgccgt gaccaccaac cctcggggcca tgccaggtgc
 120

tgggtgagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgccacag
 180
 gtcctcatgg ggcctctccg gctgggcttc gtgtccgcct acctctcaca gccactgctc
 240
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg
 300
 ggctgcgga tcccgcggca ccaggggccc ggcatggtgg tctcacatg gctgagcctg
 360
 ctgcgcggcg ccgggcaggc caacgtgtgc gacgtggtca ccagcacggt gtgcctggcg
 420
 gtgctgctag ccgcgaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg
 480
 cccacggagc tgctggtcat cgtggtggcc
 510

<210> 168
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 168
 Gly Ala Gly Gly Ser Arg Gln Ala Pro Ala Gly Leu Thr Ala Leu Arg
 1 5 10 15
 Pro Gln Val Leu Met Gly Val Leu Arg Leu Gly Phe Val Ser Ala Tyr
 20 25 30
 Leu Ser Gln Pro Leu Leu Asp Gly Phe Ala Met Gly Ala Ser Val Thr
 35 40 45
 Ile Leu Thr Ser Gln Leu Lys His Leu Leu Gly Val Arg Ile Pro Arg
 50 55 60
 His Gln Gly Pro Gly Met Val Val Leu Thr Trp Leu Ser Leu Leu Arg
 65 70 75 80
 Gly Ala Gly Gln Ala Asn Val Cys Asp Val Val Thr Ser Thr Val Cys
 85 90 95
 Leu Ala Val Leu Leu Ala Ala Lys Glu Leu Ser Asp Arg Tyr Arg His
 100 105 110
 Arg Leu Arg Val Pro Leu Pro Thr Glu Leu Leu Val Ile Val Val Ala
 115 120 125

<210> 169
 <211> 537
 <212> DNA
 <213> Homo sapiens

<400> 169
 gaattccacc gcatgtcgtg tctggacgta ttaggtcgc ggtagtgtgc gaccgccggt
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 gccttaaagg agagcgggca tcggcgttgc agtacgagag ggaaggtgt gcggatactt
 120
 attgtcgggtg cggcatcgtc catccacacc gttcgatggg tcaatggact ggtcaagcgg
 180
 ggtcacgagg ttcacctggc atcagtccat ccggcggggc gtcactccat tgatccccga
 240
 gttcggatcc acctggcccc acacggcggg aaggcaaaat acgtcgtcaa tgccggctgg
 300

ctgcgatcag tggcggctgg ggtgcaacct gacatcgta acgtccacta tgcgaccggt
 360
 tatggctctgc tcgctcgtct tgcccatatt gacgccccga cgctgctgtc ggtgtgggga
 420
 agtgacgttt acgattcccc ccgggcaaat cccctcatgc gtcacatggt ccgatccaac
 480
 ttggtctcag ctactcggat cgcacgcaca agccactgca tggcgcgtgt caccgct
 537

<210> 170
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 170
 Cys Ala Thr Ala Gly Ala Leu Lys Glu Ser Gly His Arg Arg Cys Ser
 1 5 10 15
 Thr Arg Gly Glu Gly Val Arg Ile Leu Ile Val Gly Ala Ala Ser Ser
 20 25 30
 Ile His Thr Val Arg Trp Val Asn Gly Leu Val Lys Arg Gly His Glu
 35 40 45
 Val His Leu Ala Ser Val His Pro Ala Gly Arg His Ser Ile Asp Pro
 50 55 60
 Arg Val Arg Ile His Leu Ala Pro His Gly Gly Lys Ala Lys Tyr Val
 65 70 75 80
 Val Asn Ala Gly Trp Leu Arg Ser Val Ala Ala Gly Val Gln Pro Asp
 85 90 95
 Ile Val Asn Val His Tyr Ala Thr Gly Tyr Gly Leu Leu Ala Arg Leu
 100 105 110
 Ala His Ile Asp Ala Pro Thr Leu Leu Ser Val Trp Gly Ser Asp Val
 115 120 125
 Tyr Asp Ser Pro Arg Ala Asn Pro Leu Met Arg His Met Val Arg Ser
 130 135 140
 Asn Leu Val Ser Ala Thr Arg Ile Ala Ser Thr Ser His Cys Met Ala
 145 150 155 160
 Arg Val Thr Arg

<210> 171
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 171
 ctagacaagc tcgcgcgggt gggcttcgac actcttggtc tacagacctt cctaactgcg
 60
 ggggagaagg agtcccgcgc atggacgatt cacaagggcg acaccgcccc tgaggctgct
 120
 ggcgtcatcc ataccgactt ccagaagggg ttcacaaagg cccaggtggt gtccttcggc
 180
 gaccttggtg aatttggcgg cgaaaaggag gccaggtg ctgggaagct gcgggtggag
 240
 ggcaaggagt acgttatgca ggacggtgac gtagtggaat tccgatttaa cgtgtagctc
 300

tggtttgata cttacttggc ttaaccgcat ctgagatccg tcatatcttt ggcgtagcct
 360
 tattggtatg aataacatgc cgtagccaaa g
 391

<210> 172
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 172
 Leu Asp Lys Leu Ala Arg Val Gly Phe Asp Thr Leu Gly Leu Gln Thr
 1 5 10 15
 Phe Leu Thr Ala Gly Glu Lys Glu Ser Arg Ala Trp Thr Ile His Lys
 20 25 30
 Gly Asp Thr Ala Pro Glu Ala Ala Gly Val Ile His Thr Asp Phe Gln
 35 40 45
 Lys Gly Phe Ile Lys Ala Gln Val Val Ser Phe Gly Asp Leu Val Glu
 50 55 60
 Phe Gly Gly Glu Lys Glu Ala Gln Ala Ala Gly Lys Leu Arg Leu Glu
 65 70 75 80
 Gly Lys Glu Tyr Val Met Gln Asp Gly Asp Val Val Glu Phe Arg Phe
 85 90 95
 Asn Val

<210> 173
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 173
 ccatggagtg tcccttgtgc gagcattttg agagctatac caacacccat ccctgcaggt
 60
 cccagagccg agccatttct caggagagca ggaagggagc aggccgaggg gtgctcccag
 120
 ccagccccgg aaccgaggt ctggggacgc agccgaccag ccctccttgt ctgggcctct
 180
 gtttcctctt cgacacaggg aagcagggag gggccgatca gcgacttagg cctgttggct
 240
 gtggtggggg cccctgcgtt tctgggaagc cacggaccct gggatgtacc tgggtttcat
 300
 tcgcagtga
 309

<210> 174
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 174
 Met Glu Cys Pro Leu Cys Glu His Phe Glu Ser Tyr Thr Asn Thr His
 1 5 10 15
 Pro Cys Arg Ser Gln Ser Arg Ala Ile Ser Gln Glu Ser Arg Lys Gly

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<210> 175
<211> 8484
<212> DNA
<213> Homo sapiens
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515

tccttgggga gccatactca tgtcggggca agcggcatat cttgggcatc acctctatca
1140
gtgttttcac atactggaga atggttcctt ggagcaagct cttcacaatc tttagcagtt
1200
cctccatgac cacagcgatg ccctgataac ccaggagtct gcagatagtc ttgaaagtgt
1260
ggaggtccca cgaagtcccg gtagctgccg taaatgctgg agtaggccaa gttcaaagcc
1320
ttggatccat gcagatactg aggctgtgca ttaggctgct tatctctttg aaattcctga
1380
gaaaaaggta acactgtccg aacaaaccgg ttggtagagc cgttgtagca gtagttgggc
1440
aggaagtcac agttgagctc ccagaagacg tgcaggggtga tcctcccgta gggcgctgac
1500
acgttggtgt tggcctcccg gaacatggcg tcgaagccgt ccagcgtcag gtaccggctc
1560
agcagcttgt gggcatgacg gttgatttcc aacaggccat ccagctcaac tatggaggtc
1620
aaatcttcac tttcaaactg tccaatcgcc agttctaggg acttatacat ggctgctgag
1680
acgcgctggg tgatcagacg attgaggtct attgatctgc cgaggagctg cacatgcctc
1740
tgcttcagca gcgtctcgta gcggttagac ggcgggaggt ggatcgctggc tcctgatcc
1800
ttgcattctg atcgtaaccg tttatcaaga agcaaacttc ctgccataac cttataatag
1860
gcaaatatct ggtctgccag cttgtagaca aactgatcaa aacacagggt cacctcagct
1920
tctatctcat cgtacaggaa ctgcttttta aacttggtca gagcatagta ggcgctgtca
1980
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2040
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2100
atggctcagct ccaggaagaa ctctcggaac cacagctgag aaaggtcaca gcactgctgc
2160
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2220
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2280
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2340
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2400
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2460
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2580
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2640
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2700

gcgggtgccag gacagtcctt gttgcagaac ttgtctgtgg gatgaaccag cttccaagag
 2760
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 2940
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 3240
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 3300
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 3600
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 3660
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 3720
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 3780
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 3840
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 4200
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 4260
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 4320

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4380
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4440
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4500
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4620
aaattcatca acatgttcgc tgtgctggac gagctgaaga acatgaagtg cagtgtgaag
4680
aacgaccact cagcgtacaa gagggccgct cagtttttac gtaaaatggc agatccacag
4740
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4800
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4980
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5040
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5100
gcccactacg aggaaaataa atctcgatgg acgtgcacat cctccggcag cagccctcag
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<210> 176

<211> 1393

<212> PRT

<213> Homo sapiens

<400> 176

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			20					25					30		
Ser	Met	Tyr	Leu	Ala	Met	Pro	Val	Thr	Asn	Ala	Phe	Leu	Ser	Ser	Lys
		35					40					45			
Phe	Val	Ser	Lys	Leu	Ala	Trp	Tyr	Met	Met	Glu	Glu	Gly	Gly	Gly	Ser
	50					55				60					
Met	His	Gly	Cys	Trp	Ser	Gly	Arg	Gly	Ser	Ser	Ser	Ser	Arg	Ser	Thr
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Leu	Asp	Arg	Ala	Ser	Ser	Arg	Val	Thr	Cys	Val	Val	Met	Ala	Ala	Val
			85						90					95	
Ser	Val	Phe	Cys	Thr	Gly	Ser	Ala	Ala	Gly	Pro	Gly	Glu	Gly	Pro	Glu
			100					105					110		
Ala	Thr	Ala	Gly	Pro	Arg	Ala	Gly	Ala	Gln	Asp	Ala	Leu	Pro	Arg	Ser

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130					135					140						
Val	Thr	Leu	Glu	Asp	Ala	Leu	Ser	Asn	Val	Asp	Leu	Leu	Glu	Glu	Leu	
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Pro	Leu	Pro	Asp	Gln	Gln	Pro	Cys	Ile	Glu	Pro	Pro	Pro	Ser	Ser	Ile	
165					170					175						
Met	Tyr	Gln	Ala	Asn	Phe	Asp	Thr	Asn	Phe	Glu	Asp	Arg	Asn	Ala	Phe	
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Val	Thr	Gly	Ile	Ala	Arg	Tyr	Ile	Glu	Gln	Ala	Thr	Val	His	Ser	Ser	
195					200					205						
Met	Asn	Glu	Met	Leu	Glu	Glu	Gly	His	Glu	Tyr	Ala	Val	Met	Leu	Tyr	
210					215					220						
Thr	Trp	Arg	Ser	Cys	Ser	Arg	Ala	Ile	Pro	Gln	Val	Lys	Cys	Asn	Glu	
225					230					235					240	
Gln	Pro	Asn	Arg	Val	Glu	Ile	Tyr	Glu	Lys	Thr	Val	Glu	Val	Leu	Glu	
245					250					255						
Pro	Glu	Val	Thr	Lys	Leu	Met	Asn	Phe	Met	Tyr	Phe	Gln	Arg	Asn	Ala	
260					265					270						
Ile	Glu	Arg	Phe	Cys	Gly	Glu	Val	Arg	Arg	Leu	Cys	His	Ala	Glu	Arg	
275					280					285						
Arg	Lys	Asp	Phe	Val	Ser	Glu	Ala	Tyr	Leu	Ile	Thr	Leu	Gly	Lys	Phe	
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Ile	Asn	Met	Phe	Ala	Val	Leu	Asp	Glu	Leu	Lys	Asn	Met	Lys	Cys	Ser	
305					310					315					320	
Val	Lys	Asn	Asp	His	Ser	Ala	Tyr	Lys	Arg	Ala	Ala	Gln	Phe	Leu	Arg	
325					330					335						
Lys	Met	Ala	Asp	Pro	Gln	Ser	Ile	Gln	Glu	Ser	Gln	Asn	Leu	Ser	Met	
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Phe	Leu	Ala	Asn	His	Asn	Lys	Ile	Thr	Gln	Ser	Leu	Gln	Gln	Gln	Leu	
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Glu	Val	Ile	Ser	Gly	Tyr	Glu	Glu	Leu	Leu	Ala	Asp	Ile	Val	Asn	Leu	
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Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Arg	Met	Tyr	Leu	Thr	Pro	Ser	Glu	Lys	
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His	Met	Leu	Leu	Lys	Val	Met	Gly	Phe	Gly	Leu	Tyr	Leu	Met	Asp	Gly	
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Ser	Lys	Ile	Asp	Lys	Tyr	Phe	Lys	Gln	Leu	Gln	Val	Val	Pro	Leu	Phe	
435					440					445						
Gly	Asp	Met	Gln	Ile	Glu	Leu	Ala	Arg	Tyr	Ile	Lys	Thr	Ser	Ala	His	
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Tyr	Glu	Glu	Asn	Lys	Ser	Arg	Trp	Thr	Cys	Thr	Ser	Ser	Gly	Ser	Ser	
465					470					475					480	
Pro	Gln	Tyr	Asn	Ile	Cys	Glu	Gln	Met	Ile	Gln	Ile	Arg	Glu	Asp	His	
485					490					495						
Met	Arg	Phe	Ile	Ser	Glu	Leu	Ala	Arg	Tyr	Ser	Asn	Ser	Glu	Val	Val	
500					505					510						
Thr	Gly	Ser	Gly	Arg	Gln	Glu	Ala	Gln	Lys	Thr	Asp	Ala	Glu	Tyr	Arg	
515					520					525						
Lys	Leu	Phe	Asp	Leu	Ala	Leu	Gln	Gly	Leu	Gln	Leu	Leu	Ser	Gln	Trp	
530					535					540						
Ser	Ala	His	Val	Met	Glu	Val	Tyr	Ser	Trp	Lys	Leu	Val	His	Pro	Thr	

522

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 995 1000 1005
 Leu Pro Phe Ser Gln Glu Phe Gln Arg Asp Lys Gln Pro Asn Ala Gln
 1010 1015 1020
 Pro Gln Tyr Leu His Gly Ser Lys Ala Leu Asn Leu Ala Tyr Ser Ser
 1025 1030 1035 1040
 Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val
 1045 1050 1055
 Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu
 1060 1065 1070
 Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr
 1075 1080 1085
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 1090 1095 1100
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 1105 1110 1115 1120
 Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn
 1125 1130 1135
 Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln
 1140 1145 1150
 Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe
 1155 1160 1165
 Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp
 1170 1175 1180
 Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val
 1185 1190 1195 1200
 Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg
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 Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met
 1220 1225 1230
 Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile
 1235 1240 1245
 Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys
 1250 1255 1260
 Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile
 1265 1270 1275 1280
 Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly
 1285 1290 1295
 Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg
 1300 1305 1310
 Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys
 1315 1320 1325
 His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met
 1330 1335 1340
 Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr
 1345 1350 1355 1360
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<210> 177
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 177
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 120
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 180
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 240
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 300
 gacgatatac acctgggcga aaaaccccgcg gatgaaaacg gggaatctat tgcacttccc
 360
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<210> 178
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 178
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 Arg Thr Met Ala Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser
 20 25 30
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Ala Val Lys Pro Pro Lys Asn
 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
 85 90 95
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
 100 105 110
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys
 115 120 125
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
 130 135

<210> 179
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 179
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aggtgattgc ccgtgggttg atggtggaag atcccccatc cccaagaatc cggaattcg
 120
 ccattgggcc gggcagcccg aatccaaaat gtcggggcac gcccagtggg agtatggtaa
 180
 ggggccggca ccgatgttg nggcagcata cggatggaag tgctgggcga ggcctgggt
 240
 ttgccggcag agcaactggg gcagctcaag gcggcgggg tgatcgagca gttggattga
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 360
 aa
 362

<210> 180
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 180
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 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg
 20 25 30
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala
 35 40 45
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
 50 55 60
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
 65 70 75 80
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg
 85 90 95
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg
 100 105

<210> 181
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 181
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 120
 cagcaaggta tctgccgggt aatcctgtcg cggaattgt cactggaaga aatcggcgaa
 180
 atccgccaac aggtgccggc catggagctg gaagtgttg tgacgggtgc cctgtacatg
 240
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 297

<210> 182
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 182

Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
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 Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
 20 25 30
 Trp Ala Ser Val Glu Phe Trp Gln Gln Gln Gly Ile Cys Arg Val Ile
 35 40 45
 Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
 50 55 60
 Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
 65 70 75 80
 Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
 85 90 95
 Ala Asn Gln

<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

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 120
 aagcgcacat ctttggcgac cgacgggctc ggccaccagg tcctgctcaa gggctaccag
 180
 gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca ccgtagccggc
 240
 gggatgaagg atctcgagaa gctcaccgag tcgggcaggc agtggaacac cgatttcggc
 300
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<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
 1 5 10 15
 Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
 20 25 30
 Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
 35 40 45
 Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
 50 55 60
 Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
 65 70 75 80
 Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

	85		90		95
Thr Asp Phe Gly	Ile His Val Asn Leu Val Glu Ser Tyr Pro Glu Ala				
	100		105		110
Asn His Phe Gly Asp					
	115				

<210> 185
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 185
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 gctgtgtgtgg gcattgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
 120
 gggccacgggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
 180
 gtcattgttc tggtcataat gtgcttaact ggcgcagtag gtcattggaat ctggctgagc
 240
 aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca
 300
 ctggtggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
 360
 atttctctct atgtttccat cgaaattgtg aagctt
 396

<210> 186
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 186
 Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Arg Gly Cys Thr Ile
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 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
 20 25 30
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
 35 40 45
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
 50 55 60
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
 65 70 75 80
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
 85 90 95
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
 100 105 110
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
 115 120 125
 Ile Val Lys Leu
 130

<210> 187
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 187

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120
gatgagcatc gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggctgctcgc
180
cgcgagatc gcagtattgc tgacgcgggtg gaaactaacg gcacccctcac ggcgcggacc
240
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300
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360
tcacgagctc gcgacgaggc aggagagggg tctgtcatgt ccttgagaa caccggaaag
420
ctt
423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
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		20						25				30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
	35					40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50				55				60						
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70					75				80		
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90				95			
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105				110			
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
		115				120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

ngatggttta ccaacatatg cacgggttcga gcggcaatag ctctcgggg gctggcagtg
60

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<210> 190
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 190
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 35 40 45
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala
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 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg
 65 70 75 80
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly
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<210> 191
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 <212> DNA
 <213> Homo sapiens

<400> 191
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<210> 192

<211> 428

<212> PRT

<213> Homo sapiens

<400> 192

Pro Pro Gly Ala Met Ala Thr Leu Ser Phe Val Phe Leu Leu Leu Gly
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 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
 20 25 30
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

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<210> 193
<211> 350
<212> DNA
<213> Homo sapiens
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<400> 193

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 240
 ccgttaaggg catacgccgc agtttcgagg gctcgtcgct ggagaccatc aagcacatcg
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<210> 194

<211> 116

<212> PRT

<213> Homo sapiens

<400> 194

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Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25						30	
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50					55					60				
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70					75				80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85						90					95	
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105						110	
Val	Arg	Ala	Ala												
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<210> 195

<211> 495

<212> DNA

<213> Homo sapiens

<400> 195

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 240
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<210> 196
 <211> 165
 <212> PRT
 <213> Homo sapiens

<400> 196
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 Glu Trp Ala Val Glu Met Val Arg Phe Asp Glu Ser Glu Thr Leu Asp
 20 25 30
 Arg Leu Ala Ser Gly Val Leu Glu Pro Glu Leu Gly Asp Asp Leu Ala
 35 40 45
 Ala Val Leu Leu Asp Ser His Arg Val Ala Val Ile Ser Glu Gly Ser
 50 55 60
 Asn Trp Leu Ala Ser Leu Pro Val Ile Val Gly Arg Asn Thr Glu Gln
 65 70 75 80
 Phe Arg Ser Ile Pro Asp Leu Ala Arg Asp Arg Ile Asp Lys Leu His
 85 90 95
 Gln Leu Ser His Arg Glu Ile Ala Arg Asn Arg Glu Leu Leu Arg Ala
 100 105 110
 Arg Ala Ala Ser Gly Gln Val Arg His Cys His Gly Asp Ala His Leu
 115 120 125
 Gly Asn Ile Val Met Ile Asp Gly Lys Pro Val Leu Phe Asp Ala Ile
 130 135 140
 Glu Phe Asp Pro Asp Ile Ala Thr Thr Asp Val Leu Tyr Asp Phe Ala
 145 150 155 160
 Phe Pro Leu Met Asp
 165

<210> 197
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 197
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 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttcctg
 180
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
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cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
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 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
 402

<210> 198
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 198
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 20 25 30
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala
 35 40 45
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly
 50 55 60
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg
 65 70 75 80
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu
 85 90 95
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys
 100 105 110
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile
 115 120 125
 Leu Glu Arg Met Glu Phe
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<210> 199
 <211> 507
 <212> DNA
 <213> Homo sapiens

<400> 199
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<210> 200
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 200
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 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
 20 25 30
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35 40 45
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50 55 60
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65 70 75 80
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85 90 95
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100 105 110
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115 120 125
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130 135 140
 His Arg Ser Met His Asp Phe Thr Arg
 145 150

<210> 201
 <211> 527
 <212> DNA
 <213> Homo sapiens

<400> 201
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 180
 ccttttccat ctctttggct agctgcaagt tctggagctg ctcggtgagg tctgtgatct
 240
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 300
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 360
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 420
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<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202
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 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
 20 25 30
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
 35 40 45
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
 50 55 60
 Ser Cys Pro Leu Ser Ser
 65 70

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203
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 cgtcgattcc acgcagatca cactctcga accctgcact tcgccacccc cagcttcgac
 180
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 accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
 300
 gcgt
 304

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204
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 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
 20 25 30
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
 35 40 45
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
 50 55 60
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
 65 70 75 80
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
 85 90 95
 His Val Thr His Ala

100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
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 240
 atcattcaaa gatttggacg gattgatcga attggttcga agaataaatg tgtacaatta
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<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
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 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
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<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
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 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcatg
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
 240
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 300
 gtatgcatgg taatgtgcac gtgt
 324

<210> 208
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 208
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 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 209
 nnctccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggetaccat
 60
 attcaagggt ccacgactcg cacctgcctt gccaatataa catggagtgg gatacagacc
 120
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg caccgcg
 168

<210> 210
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 210
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45
Gln Pro Glu Thr Pro Ala His Ala
50 55

<210> 211
<211> 354
<212> DNA
<213> Homo sapiens

<400> 211
tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgttgg aggcaatgtc
60
cagctggcag ctcagaccct tgcacaccat ggaggaagcc tcccaccga cctgcagttc
120
tcaggagagg actcctcccc cacaccgtcc acatccccat ctgactctgc agggacctct
180
agtgcctcga cagatgaaga catggagacg gaggtgtgca acgaaatcct ggaggacatt
240
ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
300
gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
354

<210> 212
<211> 118
<212> PRT
<213> Homo sapiens

<400> 212
Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
1 5 10 15
Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
20 25 30
Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
35 40 45
Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
50 55 60
Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
65 70 75 80
Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
85 90 95
Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
100 105 110
Xaa Lys Glu Gln Leu Ile
115

<210> 213
<211> 669
<212> DNA
<213> Homo sapiens

<400> 213
attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tggtgcagtc tattggggaa
60

gttgaacaaa acctggaagg gaaacagggtg tcatactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccacccgtg agatgggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta cccaggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttga aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214

<211> 223

<212> PRT

<213> Homo sapiens

<400> 214

Ile	Ala	Gln	Ser	Gln	Ser	Val	Gln	Glu	Ser	Leu	Glu	Ser	Leu	Leu	Gln
1				5					10					15	
Ser	Ile	Gly	Glu	Val	Glu	Gln	Asn	Leu	Glu	Gly	Lys	Gln	Val	Ser	Ser
		20					25					30			
Leu	Ser	Ser	Gly	Val	Ile	Gln	Glu	Ala	Leu	Ala	Thr	Asn	Met	Lys	Leu
		35				40					45				
Lys	Gln	Asp	Ile	Ala	Arg	Gln	Lys	Ser	Ser	Leu	Glu	Ala	Thr	Arg	Glu
	50					55				60					
Met	Val	Thr	Arg	Phe	Met	Glu	Thr	Ala	Asp	Ser	Thr	Thr	Ala	Ala	Val
65				70					75					80	
Leu	Gln	Gly	Lys	Leu	Ala	Glu	Val	Ser	Gln	Arg	Phe	Glu	Gln	Leu	Cys
			85					90					95		
Leu	Gln	Gln	Gln	Glu	Lys	Glu	Ser	Ser	Leu	Lys	Lys	Leu	Leu	Pro	Gln
		100					105					110			
Ala	Glu	Met	Phe	Glu	His	Leu	Ser	Gly	Lys	Leu	Gln	Gln	Phe	Met	Glu
	115					120					125				
Asn	Lys	Ser	Arg	Met	Leu	Ala	Ser	Gly	Asn	Gln	Pro	Asp	Gln	Asp	Ile
	130				135				140						
Thr	His	Phe	Phe	Gln	Gln	Ile	Gln	Glu	Leu	Asn	Leu	Glu	Met	Glu	Asp
145				150				155						160	
Gln	Gln	Glu	Asn	Leu	Asp	Thr	Leu	Glu	His	Leu	Val	Thr	Glu	Leu	Ser
			165				170						175		
Ser	Cys	Gly	Phe	Ala	Leu	Asp	Leu	Cys	Gln	His	Gln	Asp	Arg	Val	Gln
			180				185					190			
Asn	Leu	Arg	Lys	Asp	Phe	Thr	Glu	Leu	Gln	Lys	Thr	Val	Lys	Glu	Arg

195 200 205
 Glu Lys Asp Ala Ser Ser Cys Gln Glu Gln Leu Asp Glu Phe Arg
 210 215 220

<210> 215
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 215
 aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag
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 agagggttcca tctcagccgt tategggcac tccggagccg gcaaateccac cctgggttcgc
 120
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
 180
 tcgcagctct cggacaaagc gatgcgcccgc ctacgcgcag acatcgggat gatcttccaa
 240
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
 300
 gctcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
 360
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcggggt
 420
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg
 480
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
 540
 ctaggggtga cggtcgtcgt catcacccac gagatggagg tcgtccgctc gattgccag
 600
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcgcg ccaggtcttc
 660
 gctcateccac agtcagagac caccacgcgt ttcctggcga cgattatcgg ccagcacccg
 720
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc
 780
 agttcggtgg ccagtcactc gttcgggtgac gcgt
 814

<210> 216
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 216
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1 5 10 15
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
 20 25 30
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
 35 40 45
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
 50 55 60
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

65					70					75				80
Gln	Phe	Asn	Leu	Phe	Gly	Ser	Arg	Thr	Ile	Tyr	Asp	Asn	Val	Ala
				85					90					95
Pro	Leu	Lys	Leu	Ala	His	Trp	Lys	Lys	Ala	Asp	Glu	Lys	Lys	Arg
			100					105					110	
Thr	Glu	Leu	Leu	Ser	Phe	Val	Gly	Leu	Thr	Ser	Lys	Ala	Trp	Asp
	115						120				125			His
Pro	Asp	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Gly	Ile	Ala
	130						135				140			Arg
Ala	Leu	Ala	Thr	Lys	Pro	Ser	Ile	Leu	Leu	Ala	Asp	Glu	Ser	Thr
145					150					155				160
Ala	Leu	Asp	Pro	Glu	Thr	Thr	Ala	Asp	Val	Leu	Ser	Leu	Leu	Lys
			165						170					175
Val	Asn	Ala	Glu	Leu	Gly	Val	Thr	Val	Val	Val	Ile	Thr	His	Glu
			180					185					190	Met
Glu	Val	Val	Arg	Ser	Ile	Ala	Gln	Gln	Val	Ser	Val	Leu	Ala	Ala
	195						200					205		Gly
His	Leu	Val	Glu	Ser	Gly	Ser	Ala	Arg	Gln	Val	Phe	Ala	His	Pro
	210					215					220			Gln
Ser	Glu	Thr	Thr	Gln	Arg	Phe	Leu	Ala	Thr	Ile	Ile	Gly	Gln	His
225					230					235				240
Ser	Gly	Glu	Glu	Gln	Ala	Arg	Leu	Gln	Ser	Glu	Asn	Pro	Asp	Ala
			245						250					255
Leu	Val	Asp	Val	Ser	Ser	Val	Ala	Ser	His	Ser	Phe	Gly	Asp	Ala
			260					265					270	

<210> 217
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 217
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 60
 agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
 120
 tttcctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
 180
 ctgttcacta tccaaggctc ggaccccagc ttgcagccct acctgctgat ggctcacttt
 240
 gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctcttg gttggagcgt
 300
 gatggcgtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
 360
 caggccttgg agctcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
 420
 ctgggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
 480
 tcaaggggcg tccagctagc
 500

<210> 218
 <211> 166
 <212> PRT

<213> Homo sapiens

<400> 218

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Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
      65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
      145          150          155          160
Ser Arg Gly Val Gln Leu
                        165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccatata
60
caaggctccgc acgtcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgctcg agattgcgcc tgatatcaag cgcatacagg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgata ggccgcgata cgctggcatt gatcgatccc
240
ggtcgcgttg acgaggccca tcacgcggcg ctgctgcgtg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
g
361

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<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

```

Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

      1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
      20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
      35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
      50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
      65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
      85           90           95
Ile Pro Val Ser Thr Arg
      100

```

<210> 221

<211> 401

<212> DNA

<213> Homo sapiens

<400> 221

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agatctctgt gtcgtcggct gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcgggt ccagtgacca cccccccagg gcataccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagga cgctgtgta accagcatcc aggcctggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

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<210> 222

<211> 124

<212> PRT

<213> Homo sapiens

<400> 222

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Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
  1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
      20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
      35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
      50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
      65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
      85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
 115 120

<210> 223
 <211> 331
 <212> DNA
 <213> Homo sapiens

<400> 223
 tcatgaaatc tgtgggcagt gaccagagg ggtatgggca ggcccaacca ggttggtgtg
 60
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
 120
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
 180
 cgtggtgcct ggcagatagt gttcgacccc cnaggacctt cttgctgggc agcccagtcc
 240
 aaaagctggt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa
 300
 gcaagggcat ttcccggggc ttctgttcc c
 331

<210> 224
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 224
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
 1 5 10 15
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val
 20 25 30
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
 35 40 45
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
 50 55 60
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
 65 70 75 80
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
 85 90 95
 Ser Leu Pro Thr Asp Phe Met
 100

<210> 225
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 225
 tgatcacggg cgtgagccac cagcccagca tcccttgctt ttcattcgca cctccacctc
 60
 cagaatgacc ctcattccct cctgcacaga cggtgacagc agtaactcct acaaacacca
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
 180
 caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
 240
 cctcagccag ccgggtccaa accaactccc agcctggcct caccatccca ccgccaaacc
 300
 ttgctcaca ctggccctc ttcctggaac atgggcctn
 339

<210> 226
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Thr Leu Ile Pro Ser Cys Thr Asp Gly Asp Ser Ser Asn Ser Tyr
 1 5 10 15
 Lys His His Gln Thr Asp Leu Gln Glu Gln Arg Asn Ser Gln Ser Arg
 20 25 30
 Phe His Pro Arg Arg Ala Leu Lys Ser Ser Arg Ala Ala Cys Tyr Gly
 35 40 45
 Gly Gly Arg His Thr Leu Leu Gly Ser Gln Gly Leu Ser Gln Pro Gly
 50 55 60
 Pro Asn Gln Leu Pro Ala Trp Pro His His Pro Thr Ala Lys Pro Leu
 65 70 75 80
 Leu Thr Leu Ala Pro Leu Pro Gly Thr Trp Ala
 85 90

<210> 227
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 227
 gtcgaccct tcgattgtgg cgaactccat ggctgctgcg ggcctgcgta ggctctcgag
 60
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc
 120
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccgga
 180
 ggccaggccg acaagtgctg cctcctgccca cccgctgagc gacgctgccca tggtgagtac
 240
 ggcgtcttca ctggtcaggg cgagcgcggg atcgaccagg ttggcgcca gcccgagaga
 300
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
 353

<210> 228
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 228
 Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

```

      1           5           10           15
Leu Thr Ser Glu Asp Ala Val Leu Asn Met Ala Ala Ser Leu Ser Gly
      20           25           30
Trp Gln Glu Ala Ala Leu Val Gly Leu Ala Ser Gly Met Thr Pro Glu
      35           40           45
Gln Val Arg Gln Glu Leu Leu Glu Ser Pro Glu Glu Leu Pro Glu Pro
      50           55           60
Ser Lys Lys Gln His Gly His Ala Ala Ser Pro Arg Glu Pro Asp Val
      65           70           75           80
Glu Leu Leu Glu Ser Leu Arg Arg Pro Ala Ala Ala Met Glu Phe Ala
      85           90           95
Thr Ile Glu Gly Val Asp
      100

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<210> 229

<211> 743

<212> DNA

<213> Homo sapiens

<400> 229

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nnggctaggg acacggcctc ctcctcaaca ggcagtgcct gtgcaggctc aggggcatca
60
tcaaagataa cacagggctg gtcaggggct gctggctgct cctgccccag gactggctcc
120
aggatgggca aggctgcctc cctggtagcc agggggagag gggaaggag caccaggag
180
tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
240
agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttgg aaagccagcc
300
cagcttggca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
360
gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
420
agagattcac tgggtaccta cagtagtcga gatgtaagcc ttggggactg ggaatttggg
480
aagagagatt ctctgggtgc ttatgccagc caagatgcca acgagcaggg ccaagatttg
540
gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
600
tttcagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
660
caggagtgtg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
720
cttgacgccc aggacagaag ctt
743

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<210> 230

<211> 247

<212> PRT

<213> Homo sapiens

<400> 230

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Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

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      1           5           10           15
Ser Gly Ala Ser Ser Lys Ile Thr Gln Gly Trp Ser Gly Ala Ala Gly
      20           25           30
Cys Ser Cys Pro Arg Thr Gly Ser Arg Met Gly Lys Ala Ala Ser Leu
      35           40           45
Val Ala Arg Gly Arg Gly Glu Gly Ser Thr Arg Glu Trp Ala Ser Arg
      50           55           60
Cys Gly Ile Gly Gln Glu Glu Met Glu Ala Ser Ser Ser Gln Asp Gln
      65           70           75           80
Ser Lys Val Ser Ala Pro Gly Val Leu Thr Ala Gln Asp Arg Val Val
      85           90           95
Gly Lys Pro Ala Gln Leu Gly Thr Gln Arg Ser Gln Glu Ala Asp Val
      100          105          110
Gln Asp Trp Glu Phe Arg Lys Arg Asp Ser Gln Gly Thr Tyr Ser Ser
      115          120          125
Arg Asp Ala Glu Leu Gln Asp Gln Glu Phe Gly Lys Arg Asp Ser Leu
      130          135          140
Gly Thr Tyr Ser Ser Arg Asp Val Ser Leu Gly Asp Trp Glu Phe Gly
      145          150          155          160
Lys Arg Asp Ser Leu Gly Ala Tyr Ala Ser Gln Asp Ala Asn Glu Gln
      165          170          175
Gly Gln Asp Leu Gly Lys Arg Asp His His Gly Arg Tyr Ser Ser Gln
      180          185          190
Asp Ala Asp Glu Gln Asp Trp Glu Phe Gln Lys Arg Asp Val Ser Leu
      195          200          205
Gly Thr Tyr Gly Ser Arg Ala Ala Glu Pro Gln Glu Gln Glu Phe Gly
      210          215          220
Lys Ser Ala Trp Ile Arg Asp Tyr Ser Ser Gly Gly Ser Ser Arg Thr
      225          230          235          240
Leu Asp Ala Gln Asp Arg Ser
      245

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<210> 231

<211> 431

<212> DNA

<213> Homo sapiens

<400> 231

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acgcgttgcc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcagggtcc
60
cagggtgcag cctgcgcagc agctcctcca tcaccttgcg gatgaactgt cttcccacgg
120
ccaccaggac gccactcgcc gcctgctgcc agtcccagac caggctcctc gtcttggtca
180
tctcgctgga ggccaggagg atgatggtgc tggtgtgtgc cttgtccagc tcaactggcg
240
gactgctcag gacctctccc atggccctca ggaccgctgc tcggtatggg tgtgccagct
300
tgtcatgctg ccgcagatac tcctcgcagg cacggagcgt ctccaccctg ctggacgcca
360
tcaccgataa ggacccccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg
420
aggtgcggcc g
431

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<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga
 60
 aaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt cccagcttct
 120
 gtgctggaat gcacccccat cggaaaggct cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaa atcaaacttc
 240
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 300
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tcccagttga
 360
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 420
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 480
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<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
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 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
 20 25 30
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
 35 40 45
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
 50 55 60
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
 65 70 75 80
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
 85 90 95
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
 100 105

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235
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 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga
 120
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atgggtcaag
 180
 aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
 240
 acatttctca aggagataga ataagtgaaa gaaaattgga tttattgagc ctcaaaaata
 300
 tgagtgaagc acaatcaaag aatgaatt
 328

<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1 5 10 15
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
 20 25 30
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
 35 40 45
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
 50 55 60
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65 70 75 80
 Leu Asp Leu Leu Ser Leu Lys Asn Met Ser Glu Ala Gln Ser Lys Asn
 85 90 95
 Glu

<210> 237

<211> 2059

<212> DNA

<213> Homo sapiens

<400> 237

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 cccgaacagc acccgctggg cgccgatcag cgtgaggag tgccccacca gtggcacttt
 240
 tcttagatag cggaacccat ccaccacatc ccagtcacc gttctcatcg tccgggaacg
 300
 atccaccagt ggcggcccaa gctcccgacg tgaaaactgc agcccctagg cgaccgagac
 360
 tgcgaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtgggtgca caggaatatg
 420
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 480
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 540
 aaccacgca ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaaccca
 600
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 660
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 780
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 840
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 1260

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 1800
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 1920
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 2040
 agacttgaaa tgttctaga
 2059

<210> 238
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 238
 Ala Glu Gln Lys Phe Cys Ala Arg Leu Pro Pro Ser Pro Pro Gly His
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 Val Leu Asp Gly Pro Cys Ser Cys Gly Ser Trp Val Ser Ser Glu Leu
 20 25 30
 Asp Ile Asn Ala Trp Ile Leu Gln Pro Ala Leu Pro Ser Phe Arg Arg
 35 40 45
 Gln Glu Ser Pro Gly His Ser Pro Pro Gly Pro Pro Gln Glu Gly Met
 50 55 60
 Lys Gly Met Pro Ser Ser Leu Val Pro Arg Ala Gln Pro Ser Pro Ser
 65 70 75 80
 Pro Pro Gly Gln Gly Gln Cys Gly Ile Phe Arg Phe Arg Pro Leu Trp
 85 90 95
 Ala Glu Pro Pro Cys Glu Cys Ser Tyr Cys Leu Cys Val Ala Val Thr
 100 105 110
 Ser Ile Cys Leu Leu Leu Ile Cys Gln Pro Ile Ala Ala Gly Ser Thr
 115 120 125
 Phe

<210> 239
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 239
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 300
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 360
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 388

<210> 240
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 240
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
 1 5 10 15
 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
 20 25 30
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
 35 40 45
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
 50 55 60
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
 65 70 75 80
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
 85 90 95
 Arg Val Tyr Lys Ala Lys Glu Leu
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<210> 241
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 241
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 tcccatctgg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttcctt
 240
 ggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat
 300
 gggaaacggg ttgacttgca caaccagcac
 330

<210> 242
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr
 1 5 10 15
 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val
 20 25 30
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp
 35 40 45
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly
 50 55 60
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile
 65 70 75 80
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn
 85 90 95
 Ser Ala Pro Arg
 100

<210> 243
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 243
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 120
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatggtg
 180
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cgggtgtcccc
 240
 agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc
 300
 ttctggccgg ctcccaatgt tgattctggn
 330

<210> 244
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 244
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

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1           5           10           15
Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
35           40           45
Ile Leu Pro Ser Leu Arg Thr Thr Val Val Met Val Gln Ala Glu Val
50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
65           70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
100           105           110

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<210> 245
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 245
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120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtcccagg catccatctc gagttgacga cgaaaatctt tccagtccac gccgtagggg
240
ganttggcaa ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggattg
300
ccccattcaa tacgcgcac tccccggaag cgcgcctcta ttgcggccaa cgcgt
355

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<210> 246
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 246
Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
65           70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
85           90           95
Lys Leu Gly Gly Gly
100

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<210> 247
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 247
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 gcctgggaca ccagcgtcgt gtccgagatc aagatgggag acaggtacga gacggtcagg
 120
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 180
 gagagggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac
 240
 agggacaacc agctgcggtt cagcctgcta tgccaggcag cacttgaagc tccaaggatc
 300
 ctgagcctca acaacaaccc atacttctcc gga
 333

<210> 248
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 248
 Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp
 1 5 10 15
 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met
 20 25 30
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly
 35 40 45
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
 50 55 60
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu
 85 90 95
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
 100 105 110

<210> 249
 <211> 5503
 <212> DNA
 <213> Homo sapiens

<400> 249
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 120
 tcgccacgca ccgcatgcc cctgaacccc agccccgatg gtgaggccta cacactggct
 180
 tcgagaccac ccgtccgcct caatgatgtc atgctcaggc tggtgacgga gctgcgctgg
 240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg
300
gaccaggcct cgcggtctggg ccttgacgtc tctttacaaa aggtggacaa gaacattagc
360
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420
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480
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720
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1140
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2760
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2820
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2880
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 ggttctgctt agaattgagtg tcaaggagga aagagagggga gatggaggat gtgtttgtgc
 5100

gectgtgtgt gtgtgtttgt gtgtgtgtgt gtgtgtgaga gagagagaga gagagagaga
 5160
 gaccagcatc ttcaagagaa gtattctgct tatacaaaat ccttaacacc tcatgggtgtt
 5220
 attcttcacc atgtttatat atatatatat atattttttt ttttttttag aattttctac
 5280
 ccttggtcatg aggggaaatg attgatattc aagcaagttc tctaggaaaa aaaaaaaact
 5340
 tcccaactca gattttctgtg tcagctcaga atgtatcttt ttttcatgct ttgtctcttg
 5400
 gatttataac tctgtttaga ctattccata catttttaggt atattttgtg ccttcagaca
 5460
 ctgcaataaa taatcagcat ttggattaaa gttgtttaat aat
 5503

<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

Met	Thr	Gln	Gly	Ile	Leu	Ala	Leu	Val	Thr	Ser	Thr	Gly	Cys	Ala	Ser
1			5					10					15		
Ala	Asn	Ala	Leu	Gln	Ser	Leu	Thr	Asp	Ala	Met	His	Ile	Pro	His	Leu
		20						25				30			
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
	35					40					45				
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
	50				55					60					
Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
65				70					75					80	
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
			85					90					95		
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
		100						105					110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
		115					120					125			
Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
	130					135					140				
Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
145					150					155				160	
Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
			165					170					175		
Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
		180						185					190		
Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
	195						200					205			
Asn	Gln	Lys	Cys	Thr	Arg	Asn	Asn	His	Arg	Ile	Ser	Ser	Leu	Leu	Cys
	210					215				220					
Asp	Pro	Gln	Glu	Gly	Tyr	Leu	Gln	Met	Leu	Gln	Ile	Ser	Asn	Leu	Tyr
225				230						235				240	
Leu	Tyr	Asp	Ser	Val	Leu	Met	Leu	Ala	Asn	Ala	Phe	His	Arg	Lys	Leu
			245					250					255		
Glu	Asp	Arg	Lys	Trp	His	Ser	Met	Ala	Ser	Leu	Asn	Cys	Ile	Arg	Lys

[illegible]

690		695		700
Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln				
705		710		715
Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser				
	725		730	735
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val				
	740		745	750
Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala				
	755		760	765
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys				
	770		775	780
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser				
785		790		795
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile				
	805		810	815
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu				
	820		825	830
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe				
	835		840	845
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly				
	850		855	860
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro				
865		870		875
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln				
	885		890	895
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly				
	900		905	910
Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile				
	915		920	925

<210> 251

<211> 291

<212> DNA

<213> Homo sapiens

<400> 251

nngatcagcc gcgggggtccg cgccctcgat tcggcgggtgg agaccgagag tctgcgtgag
60

gacgtcaacg cgctcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catcctcatc
120

gagtaccacc attcgggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
180

gaggccctcg aggcccgccg ccgtatcgat gcgaaggttc ccgctctcgt cgagagcgcc
240

atcgccgagg gtggtctgcg ctcggatttc actcccgggc tcatcacgcg t
291

<210> 252

<211> 97

<212> PRT

<213> Homo sapiens

<400> 252

Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

```

1           5           10           15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
           20           25           30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
           35           40           45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
           50           55           60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
65           70           75           80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
           85           90           95
Arg

```

<210> 253
 <211> 327
 <212> DNA
 <213> Homo sapiens

```

<400> 253
gtgcacggat gggagcgcgc gcgcgcgtgc tggcgccttc acagcccggc gagcggcgctg
60
cgctcacggg cctgtaccga cgcgtctcgc aaccttcgcg agaccgatcc accaaccgcg
120
cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacgggc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gctcactcgt cgcggtgtcc tccgcggtct ccatcacctg ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

```

<210> 254
 <211> 106
 <212> PRT
 <213> Homo sapiens

```

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
1           5           10           15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
           20           25           30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
           35           40           45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
           50           55           60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
65           70           75           80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
           85           90           95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
           100           105

```

<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 255
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt
 60
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
 120
 atcgagctaa ctgcgcgctt aaagaaagac agcacgacag cagaaatccc tggtatttta
 180
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
 240
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
 300
 cgagcgactc cacaaggat tgatgatcct attgaaattg atggtttaac gcttgatccc
 360
 attagccaac gc
 372

<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1 5 10 15
 Ala His Glu Ile Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
 85 90 95
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
 115 120

<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
 nnacgcgtag cggtcgaggt tgccgacacc atgcccgaac ccggcctgct cgccatcgag
 60
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgccgaa
 120

cggttcgggc tcggcggcat cttcttcggt ctaccgacga tggccacgtc caatcccatg
 180
 ttcggctcgag ttcgggaatg gctggacgct gtgccagcca aggacccgtc aagcatttcc
 240
 ctggctcact cgaaagctgg actcaacgag gattaccagc agtcacatgcc gtggaacgcc
 300
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat
 360
 gagtggttct tgggcccga ggcgcgcgac ctggccgacc acgtcgtcgg gaccatcgac
 420
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg
 480
 agcaaggtcg tcattcattga tgaggtccac gccgccgacg tctatatgcg cgaatacctc
 540
 aagtcgtcc tcgaatggct cggcgcctac cgcacgccag tcaccccat gtccgcgacg
 600
 ctgccaccgg cccaacgtca tgaactcgcg ctacggtac
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1				5					10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
			20					25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
	50					55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65				70						75				80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
			85					90						95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100						105					110		
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
		115					120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
	130					135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145				150						155				160	
Ser	Lys	Val	Val	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met	
			165					170					175		
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
		180						185					190		
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
		195					200					205			
Leu	Ala	Leu	Ala	Tyr											
		210													

<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 ncatgggtgtg tgcacgtgtg cnaactgtgta tgcattggtta tgtgcacgtg tgcactgtg
 120
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtggggg gtatgcatgg
 180
 tgtgtgcaca tgagcactgt gtgggtgtgta tgcattggtgn ggtgcacgtg tgcactgtgt
 240
 atgcaatggg gt
 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
 gctagcccgg tcgcgttcgt cgtcgatttg ctggcgccag tcccctcgat cgtcttcggt
 60
 ctgtggggcg gcatcgtctt cggatcgtcg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtggtc ctccggtact
 180
 ggcacggtct accttgccag tctcgtcctg gccatcatga tcctgccaat tatcactgct
 240
 gttagcccgcg acgtcatgcc ccgaacgccc catgatcaag tcgaggccgc gctcgccttc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcacccctc
 420
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
 540
 acctcgctgg gtgccctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc
 600
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg
 660
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg
 720
 gtaaaccggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggccgtccg gcgcggcatc ggatcactat
 840
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccatccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtag
 960
 cgatcgctct gatgaccgcg atcttcctag tcgagtacgc ccgcggaact aagatcgcca
 1020
 aggtcattag cttcgccgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggccctcat gacctcatg gttccgacgg tgctgcgac aaccgaggaa atgtcaagc
 1200
 tt
 1202

<210> 262

<211> 214

<212> PRT

<213> Homo sapiens

<400> 262

Ala	Ser	Pro	Val	Ala	Phe	Val	Val	Asp	Leu	Leu	Ala	Ala	Val	Pro	Ser
1				5				10					15		
Ile	Val	Phe	Gly	Leu	Trp	Gly	Gly	Ile	Val	Phe	Gly	Ser	Ser	Gly	Ile
			20					25					30		
Ile	Asn	Gly	Tyr	Ala	Gly	Ala	Leu	Phe	Lys	Ala	Leu	Gly	Trp	Ile	Pro
			35				40					45			
Ile	Phe	Ser	Glu	Asp	Pro	Ser	Trp	Ser	Ser	Ala	Thr	Gly	Thr	Val	Tyr
	50					55					60				
Leu	Ala	Ser	Leu	Val	Leu	Ala	Ile	Met	Ile	Leu	Pro	Ile	Ile	Thr	Ala
65				70						75				80	
Val	Ser	Arg	Asp	Val	Met	Pro	Arg	Thr	Pro	His	Asp	Gln	Val	Glu	Ala
			85					90					95		
Ala	Leu	Ala	Leu	Gly	Ser	Thr	Arg	Trp	Glu	Val	Ile	Lys	Leu	Ala	Val
			100					105					110		
Phe	Pro	His	Ser	Arg	Ser	Gly	Ile	Ile	Ser	Gly	Ser	Met	Leu	Gly	Leu
		115				120						125			
Gly	Arg	Ala	Leu	Gly	Glu	Thr	Leu	Ala	Val	Thr	Leu	Ile	Leu	Gln	Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

```

```

<210> 263
<211> 424
<212> DNA
<213> Homo sapiens

```

```

<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgccg tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcy aacgtacctc ggaagacggt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggccccagt ccagccggc gatgccgccg tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgc gcagaagcac
420
gann
424

```

```

<210> 264
<211> 99
<212> PRT
<213> Homo sapiens

```

```

<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

```

<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gccttcgact ccctcatcgg caagctcatc atcactgggtg atagccgtga gcaagccctg
 120
 gctcgagctg cccgcgccct cgacgaaatc gtcacgacg gcatgccgac ggtcattccc
 180
 tttcaccagg cggtggttca cgaccgggt ttcactgccg ccgacggctg ctcggcgctc
 240
 tttaccgact ggatcgaaac cgagttcgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgctg tcgaggtcaa cggtaaaccg
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Ala Arg Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natectcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg cggggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttcg aagctcggca ttaccgccag attccgatgc ttgcatcacg tcattggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgccca tcgaggatgc gatgggcatt
 360
 accatcccaa ctcgcgtggc atggatacga accctgctcg ctgagttcag cagaatcacc
 420
 tcacatttca catttttgtc atgggtaggc catcactgtg atgatgccgg c
 471

<210> 268

<211> 157

<212> PRT

<213> Homo sapiens

<400> 268

Xaa	Pro	Gln	Arg	Val	Phe	Ser	Ser	Thr	Arg	Lys	Ile	Met	Phe	Val	Ile
1				5					10					15	
Gly	Ser	Met	Pro	Leu	Thr	His	Pro	Ser	Gln	Ser	Thr	Asp	Gly	Asp	Pro
			20					25					30		
Gly	Lys	Lys	Tyr	Glu	Val	Thr	Trp	Leu	Asp	Leu	Gly	His	Leu	His	Pro
		35					40					45			
Ser	Arg	Pro	Gly	Leu	Val	Thr	Ile	Thr	Thr	Thr	Val	Asp	Asp	Asp	Val
		50				55					60				
Ile	Thr	Ser	Ser	Gln	Val	Asn	Val	Gly	Asn	Leu	His	Arg	Gly	Asp	Glu
65				70					75					80	
Lys	Leu	Phe	Glu	Ala	Arg	Asp	Tyr	Arg	Gln	Ile	Pro	Met	Leu	Ala	Ser
				85				90					95		
Arg	His	Gly	Trp	Thr	Ala	Pro	Phe	Ile	Gly	Glu	Thr	Gly	Ala	Ala	His
			100					105					110		
Ala	Ile	Glu	Asp	Ala	Met	Gly	Ile	Thr	Ile	Pro	Thr	Arg	Val	Ala	Trp
		115					120					125			
Ile	Arg	Thr	Leu	Leu	Ala	Glu	Phe	Ser	Arg	Ile	Thr	Ser	His	Phe	Thr
		130				135					140				
Phe	Leu	Ser	Trp	Val	Gly	His	His	Cys	Asp	Asp	Ala	Gly			
145					150					155					

<210> 269

<211> 387

<212> DNA

<213> Homo sapiens

<400> 269

acgcgtgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
 60
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca
 120
 tttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
 180
 tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa
 300
 ccgggcgttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tgggtcaaat actacgc
 387

<210> 270
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 270
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val
 1 5 10 15
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val
 20 25 30
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys
 35 40 45
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu
 50 55 60
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp
 65 70 75 80
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly
 85 90 95
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu
 100 105 110
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu
 115 120 125
 Arg

<210> 271
 <211> 443
 <212> DNA
 <213> Homo sapiens

<400> 271
 gccggcacca acggaaagtc ctctaccgcg cgcgatggtcg attcgctttt gcgtgccttc
 60
 caccgcccag tgggttttgt aaccagccca cacctgcagc gcgttactga gcgcatcggc
 120
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagttcga ggtcttcgtg
 240
 ggccctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattacccccg
 360
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 272
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 273
 caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctgctcccc cctgctgtcg
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 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc ctagacagc
 180
 tgctgcctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg
 240
 catttcctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcc cctcccttcc agtcacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaattgca
 420
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaagc
 540
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
 660
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
 780
 ccaccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgccttcac gcgt
 864

<210> 274
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
 1 5 10 15
 Lys Leu Leu Glu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
 20 25 30
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
 35 40 45
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
 50 55 60
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
 65 70 75 80
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Gly Phe Gly Phe Ser
 85 90 95
 Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
 100 105 110
 Gln Ser Tyr Phe
 115

<210> 275
 <211> 911
 <212> DNA
 <213> Homo sapiens

<400> 275
 naaatttaaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt
 60
 ttattttcag gaatgaaagg aattaccag ccttctgctt ttataacctac agctgaaagt
 120
 aattcctttc agcctcaggt gaagactttg ccatctccaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa
 240
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattgga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagctcc
 360
 attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
 420

cggcaaagtt cttccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaag actccccaga acgttccagc agtcctggtg ggaatcggtc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctctggggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser
1				5					10					15	
Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala
			20					25					30		
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys
			35				40					45			
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser
	50					55					60				
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile
65					70					75				80	
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro
				85					90					95	
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met
			100					105					110		
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His
			115				120					125			
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg
	130					135					140				
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln
145					150					155				160	
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro
				165					170					175	
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro
			180					185					190		
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser
	195						200					205			
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val
	210					215					220				
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile

<400> 278															
Met	Ser	Glu	Val	Pro	Asp	Glu	Leu	Val	Val	Leu	Arg	Gly	Ala	Ile	Asp
1				5					10					15	
Asn	Met	Asp	Ala	Leu	Ile	His	Leu	Leu	Ala	Glu	Arg		Phe	Arg	Ile
			20				25						30		
Thr	Arg	Glu	Val	Gly	Arg	Leu	Lys	Ala	Glu	Cys	Gly	Leu	Pro	Pro	Ala
		35				40						45			
Asp	Pro	Ala	Arg	Glu	Ala	Glu	Gln	Ile	Ala	Arg	Leu	Arg	Gln	Leu	Ala
	50					55					60				
Val	Glu	Ser	Asn	Leu	Asp	Pro	Glu	Phe	Ala	Gln	Lys	Val	Ile	Thr	Phe
65				70						75				80	
Ile	Val	Ala	Glu	Val	Val	Arg	His	His	Glu	Ala	Ile	Ala	Asp	Asp	Ser

85 90 95
 Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
 100 105 110
 Ser Gly Ser
 115

<210> 279
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 279
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 taccacaatc cttaaaaaga aaagaaagaa aggcataatgg aacccttagt tacctctcat
 120
 ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt
 180
 ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
 240
 ggaagtgtgt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc
 300
 agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
 348

<210> 280
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 280
 Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
 1 5 10 15
 Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
 20 25 30
 Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
 35 40 45
 Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
 50 55 60
 Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
 65 70 75 80
 Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
 85 90 95
 Pro Lys Ile

<210> 281
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 281
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 60

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg
 120
 aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
 180
 acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
 240
 gctgtcaact cagccatggt tccgcttatt aataacgtga caaagaatct tcctaccttg
 300
 caaaaacagg ccaggaatct cgtgtcagtg aacggtagcc tgcagaacct caacggtgat
 360
 tctgtcatta agattcaaca gacc
 384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
1				5				10						15	
Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
		20					25						30		
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
		35					40					45			
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55				60					
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
65					70					75				80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
				85					90					95	
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
			100						105				110		

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

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 120
 ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
 180
 tctgatggcc tatccgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
 240
 tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
 300
 cgcacaaagg aagtcttgca tgaaaaaggg gtcacgttgc cttccacgct gcgcttgatc
 360
 cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
 420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgatttctca gaaatctaca aacgtcagaa ctcgatcttc ggcatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggt gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcggtgcgtt tgtttgcaca accctgggggt tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

1	5	10	15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn			
	20	25	30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu			
	35	40	45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly			
	50	55	60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu			
65	70	75	80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile			
	85	90	95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile			
	100	105	

<210> 287

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 287

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120
gttttgcagg tcacggccag gggctttggg cgcgtgttac agtttgccta cactgccaag
180
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240
cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
300
ggcctgtttg tgtgccggaa ggatgctgcg tgccagcgcc cacacgagga ctgcgagaac
360
tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
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480
gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
540
agctcagaaa aggacgcgtt aacgcagtac cccagatata agaaatacca gcttgcatgt
600
accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
660
gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtgag
720
ccgcccagtg aagagaatga ggaagagagc atcacgctct gctgtcttgg agatgagcct
780
gagccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag ccctgcccct
840
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900
tcctgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
960
acatctcagc agcactttgc caggagtcca gcctgccctt ttgacaaggg gatcactcag
1020

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ggtgacctta aaactgacta cacccttttc acaggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggagggaga gctggaccgg aggagcgtga tcttctctc cagcgcttgc
 1200
 gaccaagtga gcacctcggg gcattcttat tctgggggtga gcagtttgga caaagacctc
 1260
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgag
 1320
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 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
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Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35					40					45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
		50				55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65					70					75				80	
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85						90					95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115				120						125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
		130				135						140			
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145					150					155				160	
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165						170					175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180					185						190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
		195				200						205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210					215						220			
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225					230					235				240	
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245						250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260						265					270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

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      275              280              285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp
 290              295              300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr
 305              310              315              320
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe
      325              330              335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys
      340              345              350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala
      355              360              365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser
 370              375              380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly
 385              390              395              400
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu
      405              410              415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn
      420              425

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<210> 289

<211> 822

<212> DNA

<213> Homo sapiens

<400> 289

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cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcga aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
accctgctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccgt gattttgtgc aggggtgagtt tgatcaggtc
300
aagagccagg tcaaagatga gaaatggtgg cgcgtgcagc ggatcgcgat ggccgcagga
360
gtgctcgtg ccggcgctcg cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgctaccg ctgcgtcgaa gcttgagaag ctgcagcttt ctcaggcgaa gcgggttcga
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccgggggcg
660
tgagaacagt gccgcctagc aaacagcggc cacagcgcaa aacaggtttg gctccgaccc
720
atgggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

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<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgccg acaagactta cgacgggctg cgctgccggg ctgagtgccg ggcccgtcc
 60
 atcaccccc gcacgctcg ccgcggcgtg gagaccagcg agcgcttggg ccggtatcgc
 120
 tgggtcgtcg agcgcacctt cgcttggtc aaccgctttc ggcgctcgc catccgctac
 180
 gagcggcgtg ctgacatcca cgaagccttc gtgacccctg gctgcgccct catctgcctc
 240
 aaccagatca gacggttttg ttaggtgctg taaagggaga atggctgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggtgct catcctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

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Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
          20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
          35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
          50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
          85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

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nncttcacca caccggccat caacgcacct cctcgtgata acttgacott ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcatgttg ctgtcggcca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgcattgc ctacggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcggcca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggtgttg gtgtgcaggc tcgcactatt cattctgcgg cgttgcgcca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccgggtga gtgattctcg tttctcgatg
540
gtggcggaga cgacccatcg cattgggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgcccaga tctcgtgggc gaaggtctca aatgtgccga ctgatcaata cgcacccctg
660
gctagggcgg aaggctcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

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Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

1				5					10					15			
Thr	Ala	Asp	Ala	Ile	Leu	Ala	Ala	Leu	Asp	Leu	Asn	Arg	Phe	Lys	Val		
			20					25					30				
Ala	Lys	Thr	Phe	Asp	Val	Pro	Val	Cys	Val	Ile	Ala	Gly	Ala	Gly	Thr		
		35					40					45					
Gly	Lys	Thr	Arg	Ala	Val	Thr	His	Arg	Ile	Ala	Tyr	Gly	Ala	Ala	Thr		
		50				55					60						
Gly	Lys	Leu	Asp	Pro	Arg	Arg	Thr	Leu	Ala	Val	Thr	Phe	Thr	Thr	Lys		
65					70					75					80		
Ala	Ala	Gly	Thr	Met	Arg	Gly	Arg	Leu	Ala	Asp	Leu	Gly	Val	Val	Gly		
				85					90					95			
Val	Gln	Ala	Arg	Thr	Ile	His	Ser	Ala	Ala	Leu	Arg	Gln	Ile	Lys	Phe		
			100					105					110				
Phe	Trp	Pro	Arg	Ala	Tyr	Asn	Cys	Glu	Leu	Pro	Pro	Val	Ser	Asp	Ser		
		115					120					125					
Arg	Phe	Ser	Met	Val	Ala	Glu	Thr	Thr	His	Arg	Ile	Gly	Leu	Gly	Asn		
		130				135					140						
Asp	Lys	Ala	Leu	Leu	Arg	Asp	Leu	Ser	Ala	Glu	Ile	Ser	Trp	Ala	Lys		
145					150					155					160		
Val	Ser	Asn	Val	Pro	Thr	Asp	Gln	Tyr	Ala	Ser	Leu	Ala	Arg	Ala	Glu		
				165				170						175			
Gly	Arg	Val	Val	Ala	Gly	Val	Ser	Ala	Thr	Asp	Val	Gly	Arg				
			180					185					190				

<210> 295

<211> 417

<212> DNA

<213> Homo sapiens

<400> 295

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ttcatatcag gcagtacccg agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctggtc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttcag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggcg
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcagatcat tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

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<210> 296

<211> 139

<212> PRT

<213> Homo sapiens

<400> 296

Phe	Ile	Ser	Gly	Ser	Thr	Arg	Val	His	Ala	Ile	Asn	Asn	Val	Ser	Val
1				5				10					15		
Ser	Phe	Thr	His	Ser	Gly	Val	His	Leu	Leu	Met	Gly	Glu	Ser	Gly	Ser

```

      20      25      30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35      40      45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50      55      60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
      65      70      75      80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85      90      95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100      105      110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115      120      125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130      135

```

<210> 297

<211> 378

<212> DNA

<213> Homo sapiens

<400> 297

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tacaccatcg gtagcagat tgtcgaagct ctgcagggtgc actcgaagat gtccgacaag
60
gacgcttggg cgcgtgccat cgagctgctc gacttggtgg ggattccgaa tcccagagtg
120
cgtgccaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgtcatcgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggccagat tctcgatttg ctgcgcgtag cccagcgtga aacctatgag
300
ggcgtcggtta tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

<210> 298

<211> 126

<212> PRT

<213> Homo sapiens

<400> 298

```

Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
1      5      10      15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
20      25      30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
35      40      45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
50      55      60
Asn Asp Pro Asp Leu Ile Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
65      70      75      80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Arg Val Ala Gln Arg

```

	85		90		95
Glu Thr His	Ala Gly Val Val Met	Ile Thr His Asp Leu Gly Val Val			
	100	105		110	
Ala Gly Leu Ala Asp Arg Val	Ala Val Met Tyr Ala Gly Arg				
	115	120		125	

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 299
 gtgcacggtt tcgttgcat gcgcaatgac cgggagaact tgcgttttga tccgagactt
 60
 ccagcccaat ggacgtcgat caaacaccac atgctcattg gcgactctca catgctcggt
 120
 ttcctggaac gtgacgcat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
 180
 gtgcgcggtg agctctacca cattgggggt gagccggtga gggtgccgtt gtccgatcag
 240
 gggccggttg gtcctagcct gcgcgttacc catccgatct cgggggttgcg tcgagctgac
 300
 ggttctctta tcactgcaga agtcccggc agcattgctg agacgattgg gtcttctccg
 360
 atctcgac
 368

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 300
 Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
 1 5 10 15
 Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
 20 25 30
 Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
 35 40 45
 Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
 50 55 60
 Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
 65 70 75 80
 Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
 85 90 95
 Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
 100 105 110
 Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
 115 120

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 301
 ggccgggtta ttgccgccc gtttgcggg gaaacccggc agaccttcga gcgcaccggc
 60
 aaccggcgcg actattccgt accgcccgcc gaaccgacct tgctcgacag gcttacggac
 120
 gcgggcccga cggatgatcg aatcggaag attggtgata tctacgcgca caaaggcgtg
 180
 tctcaggtgc gtaaggcaat ggcaatattg gccttggtcg atgaaacact cattgccatg
 240
 gacgacgcgc aggacggcga tctggtcttc accaacttcg tggatttcga catgctctac
 300
 gggcatcgca gggatgtgcc cggctatgcc gccgcgctcg aggctttcga ccggaggctg
 360
 ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc
 420
 tgcgacccga ccctcaaggg aaccgaccac acgcgt
 456

<210> 302
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 302
 Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe
 1 5 10 15
 Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro
 20 25 30
 Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile
 35 40 45
 Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg
 50 55 60
 Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met
 65 70 75 80
 Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe
 85 90 95
 Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala
 100 105 110
 Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg
 115 120 125
 Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr
 130 135 140
 Leu Lys Gly Thr Asp His Thr Arg
 145 150

<210> 303
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 303
 nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcacgtcgc
 60

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc
 180
 atggaccgtc aggggtctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg
 240
 atcgggttaca acgcctggtc gttctacacc cgcagatgc tgttcgtgcc gatcgacgga
 300
 gagatgggtcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg
 360
 cccgccgatc agatcgctcg ttaccgggag agttatgtgc ac
 402

<210> 304
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 304
 Met Tyr Leu Gly Ala Gln Leu Phe Ser Asp Ser Glu Tyr Glu Gln Arg
 1 5 10 15
 Leu Arg Arg Val Arg Glu Leu Met Asp Arg Gln Gly Leu Ser Ala Ile
 20 25 30
 Ile Val Thr Asp Pro Ala Asn Ile Phe Tyr Leu Ile Gly Tyr Asn Ala
 35 40 45
 Trp Ser Phe Tyr Thr Pro Gln Met Leu Phe Val Pro Ile Asp Gly Glu
 50 55 60
 Met Val Leu Tyr Ala Arg Glu Met Asp Arg Met Ala His Ile Xaa Thr
 65 70 75 80
 Thr Ser Leu Pro Ala Asp Gln Ile Val Gly Tyr Pro Glu Ser Tyr Val
 85 90 95
 His

<210> 305
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 305
 nnacgcgtcg gttccgcatc gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgtcgtcct ggcgaatatg ggcgatcagc cggtagcgtt cgggacgctc gctcacctcg
 120
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggccccg
 240
 tcgccatgcy tcggaatcga catgcagcac cctcctgcca ggatcgatgg cgtaatacgt
 300
 gcgacgggtac acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
 360
 acgtcacatc atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 ggtaggaag gctattctct ttggccactc tcctcctaag acctatttgg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatage acctcgca
 180
 ttgatgtct cttcttctca cccactcacc ccacctggg ggttggggca aaaaagtggc
 240
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcaccctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaacca
 360
 gcagaactgg acataatggg aacagggtct gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttggaa
 480
 tggctcagcc tctggacatc accccacca accagagccc tggctcttgc tggatgtcca
 540
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagagggtat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgat ccctgtgcat atggtcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggtcatt gaggtgcaga aatacggtcg cgagccgac
 180
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttgcagga gcagctgcat
 300
 gatgtcctcg ataccttgtc cgagcgagag gccggtgtcg tgtcgatgcg attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcggcaaag tctacggtgt tactcgggag
 420
 cgcacccgcc ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

```

                20                25                30
Pro Thr Pro Glu Glu Leu Ala Asn Glu Leu Asp Met Thr Ala Glu Lys
      35                40                45
Val Ile Glu Val Gln Lys Tyr Gly Arg Glu Pro Ile Ser Leu His Thr
      50                55                60
Pro Leu Gly Glu Asp Gly Asp Ser Glu Phe Gly Asp Leu Ile Glu Asp
      65                70                75                80
Ser Glu Ala Ile Val Pro Ala Asp Ala Val Asn Phe Thr Leu Leu Gln
      85                90                95
Glu Gln Leu His Asp Val Leu Asp Thr Leu Ser Glu Arg Glu Ala Gly
      100                105                110
Val Val Ser Met Arg Phe Gly Leu Thr Asp Gly Gln Pro Lys Thr Leu
      115                120                125
Asp Glu Ile Gly Lys Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln
      130                135                140

```

<210> 311

<211> 358

<212> DNA

<213> Homo sapiens

<400> 311

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acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtgggtggt cattggtcct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

```

<210> 312

<211> 116

<212> PRT

<213> Homo sapiens

<400> 312

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Thr Arg Ile Glu Asn Ile Pro Pro Ile Ile Thr Ala Arg Pro Glu Leu
1      5      10      15
Met Ala His Glu Leu Thr Pro Glu Ser Leu Asp Ala Ser Leu Glu Trp
      20      25      30
Ala Asp Val Val Val Ile Gly Pro Gly Leu Gly Gln Gln Ala Trp Gly
      35      40      45
Lys Lys Ala Leu Gln Lys Val Glu Asn Cys Arg Lys Pro Met Leu Trp
      50      55      60
Asp Ala Asp Ala Leu Asn Leu Leu Ala Ile Asn Pro Asp Lys Arg His
65      70      75      80
Asn Arg Ile Leu Thr Pro His Pro Gly Glu Ala Ala Arg Leu Leu Ser
      85      90      95
Cys Ser Val Ala Glu Ile Glu Asn Asp Arg Leu Leu Xaa Cys Ala Arg

```

100 105 110
 Leu Val Lys Arg
 115
 <210> 313
 <211> 347
 <212> DNA
 <213> Homo sapiens
 <400> 313
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac
 60
 acccctggtg gcgaaccgcg caccatccgc acctcgaacg cgcacatcat tgccgtcacc
 120
 agtggcaaaag gcggcgtggg caagaccttt gtctccgcca acctggccgc cgcgctgacc
 180
 cgcctgggac tgccgctgct ggtactggac gccgacctgg gcctggccaa cttggacgtg
 240
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggcctcgctg
 300
 caagacgcgg tggtcacggc ccccggcggc ttccatgtgc tgctagc
 347

<210> 314
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 314
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
 1 5 10 15
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
 20 25 30
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
 35 40 45
 Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu
 50 55 60
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
 65 70 75 80
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
 85 90 95
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
 100 105 110
 Val Leu Leu
 115

<210> 315
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 315
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggaggggaac catgcttgcc
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggctcgtccc ggggccatcc
 120
 aacaccttgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac
 180
 ctgcttgagg cggtgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcg
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cggtgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaaacttc
 360
 cgccatgggc ccctgcccct gtctgtggca accctgtcga acccgaaggc gctgatcttc
 420
 gccagcgtga tctttcccg caaggcgttc ctcgacttct ggaacaacta cacgatctcg
 480
 ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctgggggccc
 540
 ggta
 544

<210> 316
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 316
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
 1 5 10 15
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
 20 25 30
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
 35 40 45
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
 50 55 60
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
 65 70 75 80
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
 85 90 95
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
 100 105 110
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
 115 120 125
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
 130 135 140
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
 145 150 155

<210> 317
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 317
 nggtcagcct ctcgcccagg caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagagggttt gtccactgag agaagcacat tggaaagggg ggcgtgggccc tgggactgtg
 120
 tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg
 180
 ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg
 240
 tggcatgtgg ggcattgtat catgtggtgt tggcgcagca aactcagctc ttacctggct
 300
 gggggccagcc tctaaaactt ctcacattgg gctcccttct gac
 343

<210> 318

<211> 98

<212> PRT

<213> Homo sapiens

<400> 318

Met	Ser	Thr	Lys	Ala	Arg	Gly	Leu	Ser	Thr	Glu	Arg	Ser	Thr	Leu	Glu
1				5				10						15	
Arg	Gly	Ala	Trp	Ala	Trp	Asp	Cys	Val	Ala	Leu	Tyr	Ala	Arg	Gly	Gly
		20					25					30			
Pro	Lys	Gly	Gly	Gly	Pro	Pro	Thr	Met	His	Xaa	Gly	Trp	Gly	Val	Gly
		35					40					45			
Asn	Met	Pro	Cys	Ile	Leu	Gly	Val	Cys	His	Glu	Trp	His	Thr	Met	Gly
	50					55				60					
Val	Ala	Cys	Gly	Ala	Cys	Met	His	Val	Val	Leu	Ala	Gln	Gln	Thr	Gln
65				70						75				80	
Leu	Leu	Pro	Gly	Trp	Gly	Gln	Pro	Leu	Lys	Leu	Leu	Thr	Leu	Gly	Ser
			85					90						95	

Leu Leu

<210> 319

<211> 429

<212> DNA

<213> Homo sapiens

<400> 319

gaattctcga tgtacccctt cccggcagtc ctattctcga gctgagcggg cacagtggcc
 60
 ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
 120
 agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct
 180
 caactcttcg aacagcatct gctcaaggac ggcgtctctg aaacagtcca tataaaciaa
 240
 gccattcacc gggaatagac ggatggcgtg tcggcgcaga agtgccgggtg ctcgcttata
 300
 cggccccgtc tatggtcaac aatgctagct ggctcggcat gctcgcgcca tcaaaacgca
 360
 catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggactgagt
 420
 atacgtccn
 429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 nggtgcacgac gtgctcgcca agtccctcgg gtcctctaata gcgatcaacg tgggtcacgc
 60
 caccgtcgat gcgttgacgc agctcgagga gcccgaaagag gtcgcccgtc gccgcggcaa
 120
 gtccggttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgagggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc
 240
 accagatca agtctggcat cgctaccaag ccaaatcatc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga cagggtcatc aaggaggacc gcccgaggtt ccgcggcatg
 360
 gtccggaccg ttcgtcacct cgtcaccatg gaagaggtgg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgtc ctggtgcccc caaggccaag acccgcggtg gtcgtggtga
 480
 ggggtccaag ggtaagaccg ctggtcgcgg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

      1             5             10             15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
      20             25             30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
      35             40             45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
      50             55             60

```

<210> 323
 <211> 468
 <212> DNA
 <213> Homo sapiens

```

<400> 323
ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
180
tgcctcagtg aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcctttttg tcagagggaa
300
ctgtatgaag acagcttget ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca tttataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

```

<210> 324
 <211> 156
 <212> PRT
 <213> Homo sapiens

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<400> 324
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
  1             5             10             15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
      20             25             30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
      35             40             45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
      50             55             60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
      65             70             75             80
Pro Leu Gln Glu Leu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
      85             90             95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
      100            105            110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
      115            120            125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

```

130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
 60
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcca gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccaggga tccccactcc cgcagatgac ttgcccgaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcaccactt ggttcactgt gtgcttccgg
 300
 gtccccaggt tttaggtgct tcatgccctg ctgggaacga gacacgtcc tgcctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtgtt ctttctatt ggtctgtcag gtgaaaaact
 60

ccggctgggg gaaaagcgtc cggtggtttg ttggtaaaga gggcgctga tgggctctgg
 120
 ggaatggagg atggcgacc ggctgtgggt ggactgtgga aacggggggg ggcagtgccg
 180
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
 240
 agctcgggat gggctcagag cgaccacga aaataccagg ggccaagtaa aatgaaccca
 300
 ccctttaaca gtgcacaaag cgctggcaca cggtccacgt ctggtgacgc aggctgccc
 360
 aagcgctcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
 420
 cgccctgtc cactctggc cagccggagt tttcaccta cagaccaata ggaaagaaca
 480
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgcc
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40					45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50					55					60				
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65					70					75				80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85						90					95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
			100					105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
 60
 gctcttcagt ctttctgctc cactgagcag tgttttcctg atacccttgg tatcctgcc
 120
 gcagcctcgt tatgactcct aactccattg cctccatgg cccctgggag ctctctctct
 180
 ctttctctcc aggtagtaga gcactgcttc tggcttcttg tgcacagaag gggttccac
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atatcctgcc ccaccttctt
 300
 ctggtagcac acagcaacct tgcatagtat ctggtatcat taccttccca atcaacaggc
 360
 cttgatttct tataggactt tttctctcag atttacattg cttcttt
 407

<210> 330
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1 5 10 15
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
 20 25 30
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
 35 40 45
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
 50 55 60
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
 65 70 75 80
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
 85 90 95
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
 100 105 110
 Arg

<210> 331
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 331
 tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccgg cgccactttc gctgaggcca tggagtcgat cggagccagc
 120
 tacgacggat cggccggggt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg
 180
 ttcgacgcag cggctgaact cttcgtcgaa ttggtgaaca ccacgagcct ggttgaagag
 240
 gacatgccc gtcagatcga cgcggcgcca gcctccctgg ccagaccag ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtggggtc acggtcgtec
 360
 ctgcccacga tcggtaccct ctcgtcgggt gaaaagctca acgccgcagc cgcacgagaa
 420
 ttctgggccc cgcactggac gatctccgat gccgtgctgg tgggtgccgg agagggagtc
 480
 gaggacctcg acttgtcaat attcaaggag tggacgacca gct
 523

<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgaggcga tgacgggtgaa ggtgcccaacc
 60
 gatccccatc accgccccggg agttccattg aagtctgcga aggaccgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccaccac
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccaccac cgggtggcaag
 240
 gaacggggccc gcaactacga tgcggtggcc cagctcgtcg cgcagcgagt cgcgcggtca
 300
 cacggccgga tcaactgcaa acggtgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
      20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
      35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
      50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
      85

```

<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctgggcga gggcgatgcg cctgcgcgca ccttcgtgga cggtagcttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcttggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atgggtccgct ggacatgcgc atggacacca ctccgatgca tggatg
356

```

<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

```

Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
      20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
      35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
      50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
      85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100 105 110
 Thr Thr Pro Met His Gly
 115
 <210> 337
 <211> 447
 <212> DNA
 <213> Homo sapiens
 <400> 337
 cagcctctct ccgaccgcgc cgggtgtgaag cacgggcatg ccggtgtgca agtggcacca
 60
 cagccaaaac agcgagctca cacttcaaac tccttcaaag accccaggcc tctgtaagaa
 120
 ccgctcatct ctgtgccac agctccccg cttccatgtg acccagaaat ggaaccacgc
 180
 agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcagge ttctgtgcaa
 240
 acaggcgcca tcatgtcagc cggtagcagc gagcaacgtg cgtgggtcag ggggtggcca
 300
 cacgtccaac tttataagaa atgacagatt ccctgatggc catagggatc tgcagggcca
 360
 gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg
 420
 tttctgtact gtttttacag ccaattg
 447
 <210> 338
 <211> 111
 <212> PRT
 <213> Homo sapiens
 <400> 338
 Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
 1 5 10 15
 Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
 20 25 30
 Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
 35 40 45
 Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
 50 55 60
 Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
 65 70 75 80
 Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
 85 90 95
 Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Gln Ala
 100 105 110
 <210> 339
 <211> 588
 <212> DNA
 <213> Homo sapiens
 <400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aagggcgta
 60
 gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaacca atggaagaca
 120
 ccgacctgca agcgctgatg gccagactcg aattgctaata tgatcgggtc gagcaactta
 180
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
 240
 tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgcctgaagg
 300
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
 360
 ttcatcatc tgccccagg aagaacgcag cacctgggtga gtgctgcccg ctacctggaa
 420
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcacg ggtgccgacc gcatcgccgt
 480
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
 540
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
 588

<210> 340
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Glu Asp Thr Asp Leu Gln Ala Leu Met Ala Arg Leu Glu Leu Leu
 1 5 10 15
 Ile Asp Arg Val Glu Gln Leu Lys Ser Gln Asn Gly Leu Leu Leu Ala
 20 25 30
 Gln Glu Lys Thr Trp Ala Arg Xaa Arg Ala His Leu Ile Glu Lys Asn
 35 40 45
 Glu Ile Ala Arg Arg Lys Val Glu Ser Met Ile Ser Arg Leu Lys Ala
 50 55 60
 Leu Glu Gln Asp Tyr Glu Leu Ser Asn Ser Val Thr Cys Arg Ser Ser
 65 70 75 80
 Thr Lys Asn Ile Arg Ser Ser Ala Pro Arg Lys Asn Ala Ala Pro Gly
 85 90 95
 Glu Cys Cys Pro Leu Pro Gly Arg Pro Lys Gly Val Lys Ser Ala Ala
 100 105 110
 Ala Ala Lys Ser Ser Val Pro Thr Ala Ser Pro
 115 120

<210> 341
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 341
 ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt
 60
 gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg
 120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctgg ccttcctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgacag atgctgggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
 360
 ctgggggttg acctggcggt tgcgcagcgc tgaggacgcg t
 401

<210> 342

<211> 130

<212> PRT

<213> Homo sapiens

<400> 342

Xaa	Arg	Ala	Ala	Tyr	Leu	Leu	Tyr	Leu	Ala	Tyr	Ala	Thr	Trp	Arg	Asp
1				5					10					15	
Arg	Ser	Ala	Phe	Ala	Met	Asn	Asp	Thr	Pro	Thr	Val	Ala	Thr	Ala	Arg
		20						25				30			
Ser	Leu	Ile	Leu	Arg	Gly	Phe	Leu	Leu	Asn	Ile	Leu	Asn	Pro	Lys	Leu
		35					40					45			
Thr	Ile	Phe	Phe	Leu	Ala	Phe	Leu	Pro	Gln	Phe	Val	Thr	Pro	Gly	Gly
	50					55					60				
Thr	Ala	Pro	Ala	Leu	Gln	Met	Leu	Val	Leu	Ser	Gly	Val	Phe	Met	Ala
65				70					75					80	
Met	Thr	Leu	Ala	Val	Phe	Val	Leu	Tyr	Gly	Leu	Leu	Ala	Asn	Val	Phe
			85					90					95		
Arg	Arg	Ala	Val	Val	Glu	Ser	Pro	Arg	Val	Gln	Asn	Trp	Leu	Arg	Arg
		100					105					110			
Ser	Phe	Ala	Thr	Ala	Phe	Ala	Gly	Leu	Gly	Leu	Asn	Leu	Ala	Phe	Ala
		115					120					125			
Gln	Arg														
130															

<210> 343

<211> 389

<212> DNA

<213> Homo sapiens

<400> 343

gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcacgcac
 60
 ggggtgctcca acttcagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg
 120
 gcggcggttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
 180
 ttcttcacca acgacaaccc cacggtgatc gtcaagctcc aacagctttc cnngggcccc
 240
 aaggcccagg gtgcggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
 300
 atcgtcttct tcgtgctcca gaacttctg gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgtcgt tacatccttg cccctaaagg catgggttgct
60
ggtgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatcc cagttggtac aacagtacac gctgtagaaa tgaaacctgc taaaggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctgctgatgg tgcttacgtt
240
actctacgtt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc
300
ggtgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

                20                25                30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
                35                40                45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
                50                55                60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
65                70                75                80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
                85                90                95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
                100                105                110
Leu Gly Lys Ala Gly Ala Thr Arg
                115                120

```

<210> 347
 <211> 565
 <212> DNA
 <213> Homo sapiens

```

<400> 347
accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgtc gggatcctca cggatgcctt cttggtgcgg
180
atgacctcg tccggccgt gatggccctg ctaggtgaca aggcattgtg gttgcccggg
240
tggctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcggccgtc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggtgaggtc gggaggattg ctgctaccg agcgggcttc cagagtgcgt
540
cgggtgacgt ggttcctcga cgcgt
565

```

<210> 348
 <211> 188
 <212> PRT
 <213> Homo sapiens

```

<400> 348
Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1                5                10                15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
                20                25                30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
                35                40                45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```

```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100             105             110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115             120             125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130             135             140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145             150             155             160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165             170             175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180             185

```

<210> 349
 <211> 339
 <212> DNA
 <213> Homo sapiens

```

<400> 349
ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcggtt cggctaccgc tcatacgttt gcggaacaatt tgccgttcct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

```

<210> 350
 <211> 113
 <212> PRT
 <213> Homo sapiens

```

<400> 350
Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1              5              10              15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20              25              30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35              40              45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50              55              60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65              70              75              80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

85 90 95
 Ala Leu Ala Gly Phe Arg Glu Pro Gln Arg Thr Leu Glu Leu Phe Asp
 100 105 110
 Ala

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgccccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg
 60
 cggcgggacgg agaaaacaac tccaaagtgt gcgaaaggca ccgccccctac tccccggctg
 120
 ccgcgcctc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg
 180
 agccccctg gggaggcggc accagggagc ctgggccccg gggctccgcc gcgaccccat
 240
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccn ntctctctcc tctctcttgg aggcgctctg gcccattcag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 352
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
 1 5 10 15
 Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
 20 25 30
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro
 35 40 45
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
 50 55 60
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
 65 70 75 80
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
 85 90 95
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Trp Arg Arg
 100 105 110
 Ser Gly Pro Ser Arg Pro
 115

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
60
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt
120
gaacccattt cagctgttgt cagcccacac ggctcatgc tgttgctggg gaagcctcaa
180
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggaccc ggccctgcgc
240
ttgcaggcca tcgcggtgt catggcagca gcggtagatt tgggttggcg tatgcgtgac
300
gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac
420
gacacgagcc cttcgagata cgttgctcgc gtcacccatg ccacgcggga cgacgtttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttggga
600
gagttcgccc acgaggcgga ggtggtcgc gtctttggcg gcgacggcac gatcttgca
660
gctgctgaat ggtcattacc tcgccagtt cccatgattg gcgtcaacct tggccatgct
720
ggttttctgg ctgagctgga gcgctccgat atggcggatc tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccga gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccgcg
900
cgcgtgctg acgttctggc gtctgtcgac gagttgccg tgcaacgctg gagttgcgac
960
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcgccccg
1020
gtcatgtggc ccgatctcga cgccatgctc atggtgccgt tgagcgctca cgctctcttt
1080
gtcgcaccgc tggatcatgag ccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
1200
agaatcaccg tcgtccgcca tcccgaccgt ctgcgcattg ctggtctggc cgcgcagccc
1260
ttcacatcgc gtctggtcaa gaagtttgag ctcccggta gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcacgatga gacggtcctc gaacctcat ccgcgctgac ggcagtcacc ggcgagaccg
1440
gcgccggaaa gaccatggtg gtcaccggt
1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

```

Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
          20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
      35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
          85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
      100           105           110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
      115           120           125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
      130           135           140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145           150           155           160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
          165           170           175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
      180           185           190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
      195           200           205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
      210           215           220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225           230           235           240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
          245           250           255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
      260           265           270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
      275           280           285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
      290           295           300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305           310           315

```

<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

```

nggatccac ctccctggaat ggaaaccac ataccagttc tcttctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggcccccatg catccggcgt gaactccatc
120

```

ctgcccagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
 240
 gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
 300
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
 360
 agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttcctgtggg
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagtga aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356
 <211> 186
 <212> PRT
 <213> Homo sapiens

<400> 356
 Xaa Ile Pro Pro Pro Gly Met Glu Thr His Ile Pro Val Leu Phe Leu
 1 5 10 15
 Asp Leu Asn Ala Asp Asp Leu Ser Ala Asn Glu Gln Leu Val Gly Pro
 20 25 30
 His Ala Ser Gly Val Asn Ser Ile Leu Pro Lys Glu His Gly Ser Gln
 35 40 45
 Phe Phe Tyr Leu Pro Ile Ile Lys His Ser Asp Asp Glu Val Ser Ala
 50 55 60
 Thr Ala Ser Trp Asp Ser Ser Val His Asp Ser Val His Leu Asn Gly
 65 70 75 80
 Val Thr Pro Gln Asn Glu Arg Ile Tyr Leu Ile Val Lys Thr Thr Val
 85 90 95
 Gln Leu Ser His Pro Ala Ala Met Glu Leu Val Leu Arg Lys Arg Ile
 100 105 110
 Ala Ala Asn Ile Tyr Asn Lys Gln Ser Phe Thr Gln Ser Leu Lys Arg
 115 120 125
 Arg Ile Ser Leu Lys Asn Ile Phe Tyr Ser Cys Gly Val Thr Tyr Glu
 130 135 140
 Ile Val Ser Asn Ile Pro Lys Ala Thr Glu Glu Ile Glu Asp Arg Glu
 145 150 155 160
 Thr Leu Ala Leu Leu Ala Ala Arg Ser Glu Asn Glu Gly Thr Ser Asp
 165 170 175
 Gly Lys Thr Tyr Ile Glu Lys Tyr Thr Arg
 180 185

<210> 357
 <211> 323
 <212> DNA
 <213> Homo sapiens

<400> 357

acgcgtgcgt gtgttggtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
 60
 gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
 120
 cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
 180
 cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggcttga cagagtggat
 240
 ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
 300
 gtcacatgg gtcagcgagg atn
 323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5					10					15	
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35					40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50					55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70				75					80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
				85					90					95	
His	Thr	Thr	His	Ala	Arg										
															100

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgcgc ggtgatggcc gaccttcgcg aatcgggcgc aatcgagcag
 60
 gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg
 120
 gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
 180
 aagctgaagt tcttcggcga gtacaccggt ttcgacaacc tggcccacaa ctcggttggg
 240
 tcgttcgaat aacggatgat tccgg
 265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1             5             10             15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
      20             25             30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
      35             40             45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
      50             55             60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65             70             75             80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

```

gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catcccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtgggtc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtggttg ggctttcaga agcctttgtt tccgtgggtt atgaatatga atcctgcccc
300
gatctaatacc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaaagggg atggnagagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1             5             10             15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
      20             25             30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
      35             40             45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
      50             55             60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

```

<210> 363
<211> 502
<212> DNA
<213> Homo sapiens

```

```

<400> 363
ggtagcaaaa aagtttgcca cagtattcac actccagggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaag
120
cggtgatgcc tgaccggtgc tcaggggagc ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggc ctcagctggg tttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttcccccta
300
gggggctctg ggcgccatgg ctttctgat ctgaccagc actctgggccc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

```

<210> 364
<211> 136
<212> PRT
<213> Homo sapiens

```

```

<400> 364
Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```

				85						90					95				
Ala	Phe	Met	Lys	Val	Leu	Asn	Ser	Leu	Gln	Lys	Lys	Gln	Met	Asn	Thr				
			100						105				110						
Ser	Leu	Cys	Glu	Arg	Ile	Trp	Lys	Val	Tyr	Gly	Asp	Leu	Glu	Cys	Glu				
		115					120					125							
Tyr	Cys	Gly	Lys	Leu	Phe	Trp	Tyr												
		130					135												

<210> 365

<211> 333

<212> DNA

<213> Homo sapiens

<400> 365

atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
60
ccactgatcg ttgggattct atttgggggt gagaccctct ctggagtcct tgctgggtgcc
120
cttgctctctg gtgttcagat tgccatttct gcatccaaca ctgggtggtgc ctgggacaac
180
gccaagaagt acattgaggc tggagtttca gagcatgcca ggacccttgg cccaaaaggt
240
tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
300
tctggccctt ccctcaacat cctcatcaag ctt
333

<210> 366

<211> 111

<212> PRT

<213> Homo sapiens

<400> 366

Ile	Ser	Thr	Asp	Ala	Ser	Ile	Lys	Glu	Met	Ile	Pro	Pro	Gly	Ala	Leu				
1				5				10					15						
Val	Met	Leu	Thr	Pro	Leu	Ile	Val	Gly	Ile	Leu	Phe	Gly	Val	Glu	Thr				
		20					25					30							
Leu	Ser	Gly	Val	Leu	Ala	Gly	Ala	Leu	Val	Ser	Gly	Val	Gln	Ile	Ala				
		35				40					45								
Ile	Ser	Ala	Ser	Asn	Thr	Gly	Gly	Ala	Trp	Asp	Asn	Ala	Lys	Lys	Tyr				
	50				55			60											
Ile	Glu	Ala	Gly	Val	Ser	Glu	His	Ala	Arg	Thr	Leu	Gly	Pro	Lys	Gly				
65				70				75				80							
Ser	Asp	Pro	His	Lys	Ala	Ala	Val	Ile	Gly	Asp	Thr	Ile	Gly	Asp	Pro				
			85				90				95								
Leu	Lys	Asp	Thr	Ser	Gly	Pro	Ser	Leu	Asn	Ile	Leu	Ile	Lys	Leu					
		100					105						110						

<210> 367

<211> 381

<212> DNA

<213> Homo sapiens

<400> 367

gcgttcgctcg cactaccgg cgggcgcgga acccttgacg agctactcga agcatggaca
60
tggcagcagc tcggtgtaca cagcaaacc gtngccttg tacgactcga cnncttctgg
120
gcaccgctga ccgcgtact caaccacatg accatcgaaa gtttcattcg ccctgaggac
180
cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
240
accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
300
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
360
cngttcaggt ggcccgaat g
381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1				5					10					15	
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
			20					25					30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
		35					40					45			
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50					55				60					
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70					75				80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
				85											

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatat cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa
60
acttgcgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
120
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
180
acattctacg agcagcaagc gaccagtttc cttcgccagc tgaacgacct cccacccgaa
240
gagcttcccc acgtcatcga ggacttcttc cgctgtcca ctgatgtcct tctttaccat
300
ttccagcaag ctt
313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacgggtc acgtcatcct ggcgattcca cagggtggtga cgtcatggat cggcctcatc
 60
 tgcacgcgcca ttggcacggg ctttatcaag ccgaacctct ccacgggtggt aggaggtctt
 120
 tacgatgacg gtgacccccg ccgcgatcag gggttctctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
 240
 gtaggtttca ttgccgctgc tatcggtatg gctctgggtc tgatgcctt cttccacggt
 300
 cgttccaaac tgcgtgagct cgccttcgac atcccgaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgctccgcgg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100             105             110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115             120             125

```

<210> 373
 <211> 475
 <212> DNA
 <213> Homo sapiens

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<400> 373
acatgttggg aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggc ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttcctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
180
ttggctgggc actgcctctc agaaagaagt cccagggtccc tgtcagcccc agagcgccctg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggaccacctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaagggtcca atccactcag ttcttaaagt aaaaacagtt
420
gcccatgagt ccccccaaa gacgtccgca catatgccaa acattcggtg tgcac
475

```

<210> 374
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 374
Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1      5      10      15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20      25      30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35      40      45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50      55      60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65      70      75      80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85      90      95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100     105

```

<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcggt ttttcacccat ggccgaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct ccttcatagc ggcatgtggg gcgaagctgg gctgcccgc ggcactatg
 240
 ggacggcgcc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 cgcgtagccag gtatgtcaac tgatctgtcg gatatttccg aggttgagta ccgtcaactg
 60
 aggctggaac gagggtgct gtgttcggtg tggactcagg gaactgccgc agacgccgag
 120
 aacgctatgg cggagctgaa agcccttget gaaacggcgg gatctcaggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttggttcggg caaggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cgggtgaactt
 300
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggtcg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttatc tgtaaataat aaattcatta tttctagttg gttagggtact
 60
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
 120
 gttagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctgtt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcattaaa
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tgggtgtaaa ggctatgttg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatggctcaa gatgttccaa caatcggt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100          105          110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115          120          125
Ala Gln Asp Val Pro Thr Ile Val
      130          135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

```

naccggtcat aggcggggccc agtgggaagac cacgccaaca cagttggttg agatccgcgt
60
tgaggggcaag gtcctgcgcg tcccgcgaaa tctggtcaag gcctaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
acaaaaacgc gtcgatcccc taggggtgtc gtcgatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcggttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgacactac gtcggcggtgg ccttaagcaa tggctcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggtcg gtggacgacg caaactcgtc
480
atccccccacc accttgctta cgggtccgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctggtct tcgtctgcga ccttgtaaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
 50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

```

nggagcaaca cctgggcctt gggaatgaag ttaggaggtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctcccccggt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

```

<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```

50	55	60
Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser		
65	70	75
Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile		80
85	90	

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

<400> 385
 gccggcgcca cgaaatgcaa aatgcgccct tcaccggacg ccaggttgat cgagccgcca
 60
 gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca
 120
 caaaaacgca tcatgaggca gacgccaggg aagtacaga agccgcagca ggcgcgcggc
 180
 gattggaaat atcggtgagg ctaatgggtca ccagcgcttg caggttgat tccgtggcca
 240
 attcgcggaa cgacagcacc gccagttcca gtcgccgcg cagcaccagg cgacgcaagc
 300
 tgcggcgcaa ctccgggtgc accaacaaca ccgcactgtt ca
 342

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 386
 Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
 1 5 10 15
 Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
 20 25 30
 Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
 35 40 45
 Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
 50 55 60
 Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
 65 70 75 80
 Ser Thr Ala Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
 85 90 95
 Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
 100 105

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 387
 acgcgtgacg cgccggcatc ggaagcgttg actgcagaga agaccgcgca cgtggctgtg
 60

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgcgtgat ctgcccattg cgcggcagca agcgctcgat
 180
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgccca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg catcccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 388
 Met Arg Leu Val Arg Asp Gln Val Leu Ala Ala Cys Lys Gln Arg Pro
 1 5 10 15
 His Gly Ala Pro Gly Ile Trp Asp Ala Leu Ala His Asp His Leu Ala
 20 25 30
 His Ala Ala Ala Ala Ala Gly Thr Arg His Met Leu Ala Ala Leu Arg
 35 40 45
 Ala Ala Arg Asn Glu Gln His Arg Ala Leu Ala Ala Ala His Gly Arg
 50 55 60
 Asp His Ala His Cys Gln Ala Pro Leu Ala Trp His Ala Gln Ala Lys
 65 70 75 80
 Arg Arg Arg Val His Ala Pro Cys Gln Thr Cys Gln His Val Pro Gln
 85 90 95
 Pro Arg Ala Arg Ser Ser Leu Gln Ser Thr Leu Pro Met Pro Ala Arg
 100 105 110
 His Ala

<210> 389
 <211> 382
 <212> DNA
 <213> Homo sapiens

<400> 389
 ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg
 60
 ggcttcccac gtgtcccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag
 120
 gtattgcgtt tggagacgct tggggtaaat tacggccagg tgcgcgccgt cgatgccctg
 180
 acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtgggagat ccaaggggca acaaagtcct caggaggagg actggtcaac
 300
 cacgaggggt cttgggctga cccccgaaa gccgacgccg cgaccgctcg acgaatgggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgcctat cacgggtgaca ctctcgggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcacgcctntg ttcagcgact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcttgacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggcgg
360
actggcacaac ttttcgcatg cgagtgggcc gatatcggtc ctgacatcat ggtgggtggg
420
aaatccatga ctggcgata cctgacccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1 5 10 15
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
 20 25 30
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
 35 40 45
 Asp Val Val Gln Arg Gly Arg
 50 55

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact
 60
 gagcgggacc ggtaccgggc ttcccgatt cgcacgggtgt gcatcccggc ttctatcgac
 120
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
 180
 gaggcgatgg acaagattaa ggagtcgggt atcgcggtcca gacgctgctt cgtcgtcgag
 240
 acgatgggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgtgag
 300
 cggatctata ccaacgagga cggtatctcc ctggacgata tagccaacga cgtccattgg
 360
 ttgcgggagt c
 371

<210> 394

<211> 123

<212> PRT

<213> Homo sapiens

<400> 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1 5 10 15
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
 20 25 30
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
 35 40 45
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
 50 55 60
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
 65 70 75 80
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
 85 90 95
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
 100 105 110
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
 115 120

<210> 395
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 395
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
 60
 gcgacagggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc
 120
 tctcatttct gttttctact ttacgattta tggtatctca tactcccat gttgcctgtt
 180
 ctccagtttt ttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag
 240
 ggcagaattg tgtccaacag ctcttaaagt cagcgcagaa actgtgatgt taaaaacatc
 300
 ttgttatccg gccccaaaac atgttgcctc tggtaactct tactggtttg t
 351

<210> 396
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
 1 5 10 15
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
 20 25 30
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
 35 40 45
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
 50 55 60
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
 65 70 75 80
 His Val Val Leu Gly Asn Ser Tyr Trp Phe
 85 90

<210> 397
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 397
 gccgtcatta aagagatcac ccctctctc caacctggtg atgtcctcgt cgacgggtggt
 60
 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
 120
 tatgttggtg ctggcatctc cgggtggggga gtcggggccc tgagggtccc atcaattatg
 180
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc
 240
 cacgtcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acatttcgtc
 300

aagatggtcc ataatggcat cgagtaggcc gatatgcagt tcattggcga ggcgcccttc
 360
 ctttttgcgn tgcccgccgg tttagcaaat gctgaggccg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaag
 480
 gat
 483

<210> 398
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 398
 Ala Val Ile Lys Glu Ile Thr Pro Leu Leu Gln Pro Gly Asp Val Leu
 1 5 10 15
 Val Asp Gly Gly Asn Ala Tyr Phe Gly Asp Thr Arg Arg Arg Glu Glu
 20 25 30
 Glu Ile Arg Pro Thr Gly Ile His Tyr Val Gly Thr Gly Ile Ser Gly
 35 40 45
 Gly Gly Val Gly Ala Leu Arg Val Pro Ser Ile Met Pro Gly Gly Val
 50 55 60
 Lys Glu Ser Tyr Glu Ile Ile Gly Pro Val Leu Glu Lys Ile Ser Ala
 65 70 75 80
 His Val Asp Gly Glu Pro Cys Cys Ala Trp Met Gly Thr Asp Gly Ala
 85 90 95
 Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met
 100 105 110
 Gln Phe Ile Gly Glu Ala Pro Phe Leu Phe Ala Xaa Pro Ala Gly Leu
 115 120 125
 Thr Asn Ala Glu Ala Ala Asp Ala Phe Glu Ser Trp Asn His Gly Asp
 130 135 140
 Leu Asn Ser Tyr Leu Val Glu Ile Thr Ser Arg Val Leu Arg Ala Lys
 145 150 155 160
 Asp

<210> 399
 <211> 314
 <212> DNA
 <213> Homo sapiens

<400> 399
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 gggtcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt
 120
 cattcactca ttgtgccatc cactcatgta cccatccact cattcgccca tttatccatc
 180
 cactcaacca tccactcatc caccatcca nctcatcatc cgtccagtca cccatctatc
 240
 caccatgta tccatccact catccaccca tccactcatc tgtccatcca cttatccacc
 300

catctactca ccca
314

<210> 400
<211> 104
<212> PRT
<213> Homo sapiens

<400> 400
Xaa Gly Met Lys Thr Thr Gln Pro Phe Leu Ser Ser Asn Leu Leu Gln
1 5 10 15
Ala Ser Val His Gly Ser Ser Thr His Pro Leu Ile His Pro Ser Ile
20 25 30
His Pro Leu Ile His Pro Ser Ser His Ser Leu Ile Cys Pro Ser Thr
35 40 45
His Val Pro Ile His Ser Phe Ala His Leu Ser Ile His Ser Thr Ile
50 55 60
His Ser Ser Thr His Pro Xaa His His Pro Ser Ser His Pro Ser Ile
65 70 75 80
His Pro Cys Ile His Pro Leu Ile His Pro Ser Thr His Leu Ser Ile
85 90 95
His Leu Ser Thr His Leu Leu Thr
100

<210> 401
<211> 2165
<212> DNA
<213> Homo sapiens

<400> 401
gagaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta
60
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtg
120
caaaatgaaa gatctattga agtttacta tacattgcat tgattgaacc ttggagagtt
180
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt
240
gaaatgcctg cctctttttt gccagattg tttcctgacc atccgaactc agatggggtc
300
ctctaagttc ttctggata ttcacaaatc ccttcacaag gccacgtgc gaagtgaatg
360
atctggaggt gcctgggcat ctgtgttgga agggagtcaa gactcaccag ccagtcagtt
420
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctcccctctg ggcccctaca
480
gctgggactg atcatagcct cagattagaa gaaatactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct
660
tgaggattta tagcagctaa agggtaaag ctgttatgca aaagggtccc atatgaactt
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatga
780
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggcccgagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttgtggc cttttgatcc gccccggaa tgcccaccgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagagaca
1080
ctgcccgggc ctttttccct gcaatcaciaa ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgccgc cccaatgttc tacgggctca ttttccggtg caggattggg tggaccatgc
1200
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1260
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttggggg
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gccctgtggt ggaatgagcc agggccagga ccttgccggt aggtttgtgc gggttcttgg
1440
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1500
cttgacaggtg caggggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag
1560
gaaaagaact gttttccgat tccctgtaca tgtccctgga agggatattg gatgtctgtt
1620
cattatgaag atggtgctcg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc ccttttctct aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggtgat
1800
gcttgagaaa gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggtg tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atggtgggtc tgggacaaac
1980
tggaacacaa gtcaccccta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggtg gctgctggag aggctggccc cactcacttg ggacaaaagc ttttcttgg
2100
ccagtgggga catcatgcct gggttgcccc tagagtagag caggggcgtg taattaagtc
2160
catgg
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

```

Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1           5           10           15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
          20           25           30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
          35           40           45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
          50           55           60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65           70           75           80
Pro Asn Pro Pro Gly Cys Ala
                      85

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<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

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cccatgggtg tgtcccagga cggcgatcatg aagcgatcagg taaatgacaa ggaaacgggtc
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gcgcaattgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgatccag
120
ccttcgccca cgatgcacga caacctcgatg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggatgtctt ggtggacgtc ggcacgaagc ccggccacct cgccctatac
300
catctatggc aggcattcta tcaccgacct accttggggc gtgcttgagg cgaaattcat
360
gctatgatc
369

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<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

```

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1           5           10           15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
          20           25           30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
          35           40           45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
          50           55           60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65           70           75           80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

85 90 95
 Leu Ala Leu Tyr His Leu Trp Gln Ala Phe Tyr His Arg Pro Thr Leu
 100 105 110
 Gly Gly Ala Cys Gly Glu Ile His Ala Met Ile
 115 120

<210> 405
 <211> 840
 <212> DNA
 <213> Homo sapiens

<400> 405
 gaattcccg gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgcttc
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 gactcgccct ggaccacgag ggccctgtcg gagacagtgg tggaggagag cgacccaag
 120
 ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
 180
 gtggaggcca ccgtgcccat gctgcagcgg accaagtcac ggatcgagca gggatcgtg
 240
 gaccgctcag agacgggctg gctggacaag aaggaggggg agcaagccaa ggcgtgttt
 300
 gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
 360
 atgcggcaga ccatcatcaa ggtgatcaag ttcacccca tcactctgta caccgtctac
 420
 tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
 480
 taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
 540
 tacatcagcc tagtcatctt ctacggcctc atctgcatgt atacactgtg gtggatgcta
 600
 cggcgctccc tcaagaagta ctcgtttgag tcgatccgtg aggagagcag ctacagcgac
 660
 atccccgacg tcaagaacga cttgccttc atgctgcacc tcattgacca atacgacccg
 720
 ctctactcca agcgcttcgc cgtcttcctg tcggaggtga gtgagaacaa gctgcccag
 780
 ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
 840

<210> 406
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 406
 Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
 1 5 10 15
 Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
 20 25 30
 Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
 35 40 45
 Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

```

      50      55      60
Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu
65      70      75      80
Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg
      85      90

```

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

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<400> 407
gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgcccc
60
aggtcttact ttgctctgcc tggcttcagg gtgtagggga tggagagctg gacttccagc
120
ctgtctcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
180
caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgccaagg
240
agatgctcgc tcggagtggg tgctctgggt ctgggattcc aaaccaagct gccttctctg
300
atgtggcctt agtgcctctg gcggatgtac cttggctctg cctggaccct ctctctcttc
360
caggcctctg tcccaccagg atgatgccta tccagagctc attgtcctct cccacttctt
420
ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtggt
480
gcactgagga ccacagcagc cctcgcatc ccacgggcaa aggggtatgt gtagg
535

```

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

```

<400> 408
Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
1      5      10      15
Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
      20      25      30
Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
      35      40      45
Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
      50      55      60
Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
65      70      75      80
Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
      85      90      95
Val

```

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

nggtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg
 60
 ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct
 120
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
 180
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact
 240
 gcagccttcc aagaagtgca acaattgttc ggctttataa ctacgattat tagtgccatt
 300
 gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcggtg
 360
 acggagcgta cgcgt
 375

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1			5						10					15	
Phe	Gly	Ile	Gly	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn
			20					25					30		
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
		35					40				45				
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
	50					55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr
65				70					75					80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
		100						105					110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
	115						120					125			

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

ccacatactt caccctcctc accccctcca cctactccac cacctggcag tcgccatcga
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 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
 120
 gcacgcggtc ggggccccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc
 180

tggctcgagg gcacgtcgta ctggtgcgag acgcggaagc acttgtggcc gatgtaggcg
 240
 cgatcggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgtactc
 300
 ccggtccacc acgatcatgg gctgggactc gtgttccagg tggggggcca gggcttgggc.
 360
 ctgcggtgag cgcggtggggg ggatggggca tagcgtcggt gaggaggtg
 409

<210> 412
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 413
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggg agggactcca
 60
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccgg ccacacatcca gctggacccc ctgtcatata gcagccaaca
 180
 acacccatgt ttgtagctcc cccccaaag acccagcggc ttcttcaactc agaggcctac
 240
 ctgaaatata ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
 300
 ctggcagctc ggagacgcga cgctcatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414
 <211> 119
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1             5             10             15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
          20             25             30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
          35             40             45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
 50             55             60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65             70             75             80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
          85             90             95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Arg Asp Val His Leu Ser Lys
          100             105             110
Glu Gln Glu Ser Arg Leu Pro
          115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

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tctagagcca acttggttat cgtaatgaat agagagacta catctatatc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccatttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1             5             10             15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
          20             25             30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
          35             40             45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
 50             55             60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

```
<210> 417
<211> 483
<212> DNA
<213> Homo sapiens
```

```
<210> 418
<211> 161
<212> PRT
<213> Homo sapiens
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639

	130		135		140	
Gly	Pro	Arg	Ala	Leu	Asn	Ala
145				150		
Arg					155	160
						Pro
						Asp
						Ala
						Val
						Ile
						Gly
						Asn
						Ala
						Leu
						Arg
						Pro

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
 atttcacccc aggaaaacca gtaaggacca atgattaagc ccaagggttg gtaccgagtt
 60
 cggatccata agtaccggcc gcccgagggtg ctggaatttg ggctcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg gggtaggggtg ggctgagctc
 180
 aagcccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
 240
 gaacttctag taagcgcccc ccgctgcaag cgaaagcact cccttgccaa gaaacagatc
 300
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga aggggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 tttcagtggtg gcagtgcacg cagattcttc attggtgtta gtgtatttcc atacgggtatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
 660
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

50		55		60											
Thr	Leu	Ser	His	Thr	Asn	Val	Leu	Ser	Pro	Glu	Asn	Val	Lys	Asp	Phe
65					70					75					80
His	Gln	Pro	Leu	Pro	Asp	Ser	Pro	Asn	Leu	Glu	Asn	Val	Met	Ser	Thr
			85						90					95	
Leu	Gln	Ile	Met	Tyr	Thr	Leu	Phe	Val	Gln						
			100					105							

<210> 421
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 421
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 60
 aacccaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
 120
 tttgcctggg gccctctcta cctcctctgc tttctggaga acccttgac tcctcccaag
 180
 ccttcaagtt ggaaagtga cagtcagcat atgtctctag ctgagccctt actgcgtgga
 240
 ttcataaga ttggttcact gtcagccctt gaccagaacg tgtgttttag gaaagcagga
 300
 accaagtctt accaatgtct gtagtcccag cctccaccct ggcatacagt aggtgctcat
 360
 tgaatgtggg agggaaagag gagacacatg gaaggaatg tcattc
 406

<210> 422
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 422
Met Met Glu Pro Thr His Pro Ser Ser Val His Leu Leu Gln Leu Leu
1 5 10 15
His Asn Pro Thr Gln Val Asn Leu Val Ser Leu Asn Thr Pro Cys Ala
20 25 30
Leu Met Leu Pro Trp Phe Ala Trp Gly Pro Leu Tyr Leu Leu Cys Phe
35 40 45
Leu Glu Asn Pro Cys Thr Pro Pro Lys Pro Ser Ser Trp Lys Val Asn
50 55 60
Ser Gln His Met Ser Leu Ala Gln Pro Leu Leu Arg Gly Phe Met Lys
65 70 75 80
Ile Gly Ser Leu Ser Ala Pro Asp Gln Asn Val Cys Phe Arg Lys Ala
85 90 95
Gly Thr Lys Ser Tyr Gln Cys Leu
100

<210> 423
 <211> 628
 <212> DNA
 <213> Homo sapiens

<400> 423

ngccacccta cgctcgcct gcaatggcaa cttcagatcc cgggtggcac cgtagtctta
 60
 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa
 120
 ggagatgggg atttgctgac gcagacccaa gcccacacgc cgactccagc acccgcttgg
 180
 ccggcgcccc cagccacacc gcgcttcttg gccctcgcaa atggctccct gttggtgcc
 240
 ctctgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc
 300
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aaccgacgg acaggccccg acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtcttgcc ttccaaaccc gagggcaaaa tcaaaggcca aggcctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
 540
 gaggccgaag accagatcct cgcggaccgc gcggaggagc agcgctgtgg caacggggag
 600
 ccctctcggg acgtttctaa ccacgcgt
 628

<210> 424

<211> 209

<212> PRT

<213> Homo sapiens

<400> 424

Xaa His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro Gly Gly
 1 5 10 15
 Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp Gly Val
 20 25 30
 Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu Thr Gln
 35 40 45
 Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala Pro Pro
 50 55 60
 Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu Val Pro
 65 70 75 80
 Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala His Asn
 85 90 95
 Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala Ala Thr
 100 105 110
 Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp Gly Gln
 115 120 125
 Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly Asn Ser
 130 135 140
 Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly Leu Ala
 145 150 155 160
 Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu Asp Thr
 165 170 175
 Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro Ala Glu

	180		185		190
Glu Gln Arg Cys Gly Asn Gly Asp Pro Ser Arg Tyr Val Ser Asn His					
	195		200		205
Ala					

<210> 425

<211> 471

<212> DNA

<213> Homo sapiens

<400> 425

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ccggccgctcg aagactttga ggacgatgta gctcgcagcg cagcggttacg agccctggag
60
tacgtggatt tgaccccgagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
120
ggatcgtgca cgaatggccg tgaggactta cggtggctg ctgaggttcc caaaggacga
180
catatcgtag cgggcacccg gatgctcgtc gccctggat ctgctcgtgt ccgtctgcag
240
gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac
300
tctgcaaca atggcttggt actggctcag gttgacccg aggtcgtcga agagttgtgg
360
gactttgccg agcagcatcc tgggtgagcag ctcaccgtct ccctcgagaa tcggacgatc
420
aaccttcggt gtcgcacgac ctaccggttc catattgatg acgtcacggt t
471

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<210> 426

<211> 157

<212> PRT

<213> Homo sapiens

<400> 426

Pro	Ala	Val	Glu	Asp	Phe	Glu	Asp	Asp	Val	Ala	Arg	Ser	Ala	Ala	Leu
1			5						10					15	
Arg	Ala	Leu	Glu	Tyr	Val	Asp	Leu	Thr	Pro	Gly	Thr	Xaa	Val	Arg	Val
		20						25					30		
Ile	Ala	Ile	Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Gly	Arg	Glu
		35					40					45			
Asp	Leu	Arg	Leu	Ala	Ala	Glu	Val	Pro	Lys	Gly	Arg	His	Ile	Ala	Ala
	50					55					60				
Gly	Thr	Arg	Met	Leu	Val	Ala	Pro	Gly	Ser	Ala	Arg	Val	Arg	Leu	Gln
	65				70				75					80	
Ala	Met	Glu	Glu	Gly	Leu	Asp	Glu	Ile	Gly	Ser	Arg	Phe	Ala	Asp	Ile
				85					90					95	
Phe	Arg	Asn	Asn	Ser	Ala	Asn	Asn	Gly	Leu	Leu	Leu	Ala	Gln	Val	Asp
		100						105					110		
Pro	Glu	Val	Val	Glu	Glu	Leu	Trp	Asp	Phe	Ala	Glu	Gln	His	Pro	Gly
		115					120					125			
Glu	Gln	Leu	Thr	Val	Ser	Leu	Glu	Asn	Arg	Thr	Ile	Asn	Leu	Pro	Gly
	130						135					140			
Arg	Thr	Thr	Tyr	Pro	Phe	His	Ile	Asp	Asp	Val	Thr	Arg			

145

150

155

<210> 427

<211> 546

<212> DNA

<213> Homo sapiens

<400> 427

ctagcggtag tagaaggat gcagtttgat cgcggtact tgtctccgta tttcatcaac
60
aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa
120
atttctaata tccgtgactt gctaccaatt ttggaagggtg ttgctaaagc atcgcgccca
180
ttgttgatca ttgcggaaga cgttgaaggc gaagcgttgg caaccttgggt tgttaacact
240
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
300
gcaatgcttc aagacattgc tgtgctaacy ggttcaactg ttatttcaga agaaattggc
360
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcggt tacattgaca
420
aaagaaagta caacgattgt tgatggtgcy ggtgttgcag ctaatattac tggctcgtgtt
480
gagcaaattc gtgcagaaat tgctaactct tcttctgggt acgataaaga gaaattgcaa
540
gaacgc
546

<210> 428

<211> 182

<212> PRT

<213> Homo sapiens

<400> 428

Leu	Ala	Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro
1			5						10					15	
Tyr	Phe	Ile	Asn	Asn	Gln	Glu	Thr	Met	Asn	Ala	Glu	Leu	Glu	Asn	Pro
			20					25					30		
Phe	Ile	Leu	Leu	Val	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Asp	Leu	Leu
		35				40					45				
Pro	Ile	Leu	Glu	Gly	Val	Ala	Lys	Ala	Ser	Arg	Pro	Leu	Leu	Ile	Ile
	50					55					60				
Ala	Glu	Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr
65				70						75				80	
Met	Arg	Gly	Ile	Val	Lys	Val	Ala	Ala	Lys	Ala	Pro	Gly	Phe	Gly	
			85					90					95		
Asp	Arg	Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Val	Leu	Thr	Gly	Ser
			100					105					110		
Thr	Val	Ile	Ser	Glu	Glu	Ile	Gly	Ile	Lys	Leu	Glu	Glu	Ala	Thr	Ile
		115					120					125			
Glu	Gln	Leu	Gly	Thr	Ala	Lys	Arg	Val	Thr	Leu	Thr	Lys	Glu	Ser	Thr
	130					135					140				
Thr	Ile	Val	Asp	Gly	Ala	Gly	Val	Ala	Ala	Asn	Ile	Thr	Gly	Arg	Val

145 150 155 160
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
 165 170 175
 Glu Lys Leu Gln Glu Arg
 180

<210> 429

<211> 425

<212> DNA

<213> Homo sapiens

<400> 429

gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc
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 ccgttgccagc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca
 120
 ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcaggggtt
 180
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc
 240
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
 300
 tgcattgaca ctttcagcac ctccctgggc tgagatgaac aggagtgcag aggtcgggtc
 360
 cagttcagag cctgaagtcc agactctgcc atatcttcct cactacattc caggagtggg
 420
 tcctg
 425

<210> 430

<211> 130

<212> PRT

<213> Homo sapiens

<400> 430

Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
 1 5 10 15
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
 20 25 30
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
 35 40 45
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
 50 55 60
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
 65 70 75 80
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
 85 90 95
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
 100 105 110
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
 115 120 125
 Asp Pro
 130

<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 ctagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcattccacac gggcgagaag
 120
 cctnaccgt gcccgactg cgagcggcgc ttctctcct cctctcgctt ggtcagtcac
 180
 cggcgtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtgagta tctttggtac
 60
 ctcatggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg
 120
 accgaccgag gcgcgtggga cagctttgtg tgctgctacc tcgagcggca ccaaagggat
 180
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcgagt cctcgcacag ctgtacatgg ccgcacatca gcccggcaag
 420
 gctctgacat actacatgcg cctgcgtgat ccattgcgtgt ttgatctcat tcgcgagtac
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccca
 600
 tcgattccca tccagcgcgc catggcgcag ctgca
 635

<210> 434
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 434
 Xaa Pro Ala Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu
 1 5 10 15
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala
 20 25 30
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr
 35 40 45
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro
 50 55 60
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu
 65 70 75 80
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr
 85 90 95
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala
 100 105 110
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu
 115 120 125
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr
 130 135 140
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr
 145 150 155 160
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu
 165 170 175
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met
 180 185 190
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met
 195 200 205
 Ala Gln Leu
 210

<210> 435
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 435
 nncgtacgtt cgcgtatttt ccgcgcccgc gaagctatcg ataataaagt tcaaccgctg
 60
 atccagcgtt agcaatggcg ggcacaggaa gggctacttag gcatgcagaa agaaaagctt
 120
 tccgctctga tggatgggtga atcggttcgac agcgagctgt tgagttctct gtcgcaagat
 180
 cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 cccgcccggc tggcgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgtccc tgggcgagcc agattacgca aatcggtatg
 420
 gcggcctgcg tgtcgtggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg
 480
 ccatcgaacg cgt
 493

<210> 436
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 436
 Met Gln Lys Glu Lys Leu Ser Ala Leu Met Asp Gly Glu Ser Phe Asp
 1 5 10 15
 Ser Glu Leu Leu Ser Ser Leu Ser Gln Asp Arg Thr Leu Gln Gln Ser
 20 25 30
 Trp Gln Gly Tyr His Leu Ile Arg Asp Thr Leu Arg Gly Asp Val Gly
 35 40 45
 Gln Val Met His Leu Asp Ile Ala Asp Arg Val Ala Ala Ala Leu Glu
 50 55 60
 Lys Glu Pro Ala Arg Leu Val Pro Ser Ala Val Gln Glu Ser Gln Pro
 65 70 75 80
 Gln Pro His Thr Trp Gln Lys Met Pro Phe Trp Asp Lys Val Arg Pro
 85 90 95
 Trp Ala Ser Gln Ile Thr Gln Ile Gly Met Ala Ala Cys Val Ser Leu
 100 105 110
 Ala Val Ile Val Gly Val Gln Gln Tyr Asn Gln Pro Ser Ala Pro Ser
 115 120 125
 Asn Ala
 130

<210> 437
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 437
 ntggtaaccg gtgtccctga tatggaccct gctgtgttag agcgtaaatt atttatttta
 60
 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac
 120
 attaatacat tctcatataa aacaatcggt tataaagggtc agttaaccac tgaacaagtg
 180
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcattagc gcttgttcac
 240
 tcacgtttct caacaaatac atttcctcgt tggcgttttag cacaaccatt ccgttacatc
 300
 gtcataatg gcgaaatcaa tacgggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt ttctactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag
 60
 cttcccaggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggctctgag tgactgcatg
 180
 ctcagcgagg aaggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcgggggc ctggc
 395

<210> 440

<211> 128
 <212> PRT
 <213> Homo sapiens

<400> 440
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1 5 10 15
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
 20 25 30
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
 35 40 45
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
 50 55 60
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
 65 70 75 80
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
 85 90 95
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
 100 105 110
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
 115 120 125

<210> 441
 <211> 364
 <212> DNA
 <213> Homo sapiens

<400> 441
 gccagtgact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagcccg
 60
 ggcgggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
 120
 gacgggttga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
 180
 ggcggtccga aaggcttga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
 240
 gacaagccgg cgtacggcgg aatccacgaa atggtcgagg ccagagcggc cgggatgggc
 300
 caattgggca tgtccaacga gcctcgcac catattccct acatctacaa ctatgccggc
 360
 gcgc
 364

<210> 442
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 442
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1 5 10 15
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
 20 25 30
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
      50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100              105              110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115              120

```

<210> 443
 <211> 430
 <212> DNA
 <213> Homo sapiens

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<400> 443
accggttacg gctcagtga acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatggtgc tggcaatccc ctctcgccaag atcctctcga cgaccctgtc catcggatcg
120
ggcgggtccgg cggcgctcttc cggccctggc atgggtcatcg gcggagccac tggcgcgga
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag tttcgtcatt
240
gtcggcatga tcgcctgctt cgggtgcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccgaaa cctgtcgctg ctgcgtcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgcctggag
420
ggcgacgcgt
430

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<210> 444
 <211> 143
 <212> PRT
 <213> Homo sapiens

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<400> 444
Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1              5              10              15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
      20              25              30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
      35              40              45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
      50              55              60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65              70              75              80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
      85              90              95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

```

          100          105          110
Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr
          115          120          125
Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala
          130          135          140

```

<210> 445
 <211> 360
 <212> DNA
 <213> Homo sapiens

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<400> 445
ccatggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
60
tcttgcttta ttgctcacc tgtccagggt tcctctgtt tgtgaggag ctgctgccac
120
cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtggagg acttttcctt
180
agttttcttt gctcttctgc tctgagtcca gccctggctg gacctttgat cccttctctc
240
tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
300
caagtgggaa caagccatga aggagctgca ccccgaaaag tctgagggtg ggacacgcgt
360

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<210> 446
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 446
Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
 1          5          10          15
Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
          20          25          30
Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
          35          40          45
Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
          50          55          60
Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
65          70          75          80
Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
          85          90          95
Gly Leu Pro Arg Gly
          100

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<210> 447
 <211> 487
 <212> DNA
 <213> Homo sapiens

```

<400> 447
acgcgtgaag ggggaaattg ctcggtgccac ctgaggatta atcattaccc tggaaccctt
60

```

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
 120
 gagtgaggct gaggtcatgg agaagggaat ggggggcccc catggccagc tggacctgat
 180
 cactgcctcc ccaactcagcc acagccctca gggccctgtg ccagtccaga agccattca
 240
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttcccc gtgccccaac
 300
 catagcgttt tccccaaac accctcagga aggagggacc actacctgtg cagggggggg
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc ccattgcct
 420
 ttctctccta cttccacctg gccagcttcc ctcagtcccc ctctgcctc agtgccctt
 480
 cacgcgt
 487

<210> 448

<211> 117

<212> PRT

<213> Homo sapiens

<400> 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1				5					10					15	
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
		20						25					30		
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
		35					40					45			
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
	50					55					60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65					70					75				80	
Ala	Ser	Tyr	Gly	Glu	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser
			85						90				95		
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100					105					110		
Cys	Pro	Phe	Thr	Arg											
			115												

<210> 449

<211> 353

<212> DNA

<213> Homo sapiens

<400> 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
 60
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
 120
 gggaggctgg ccaggaaggt gacctcctg gagacagcca ccgagaaagt cgaggccctg
 180
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
 300
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
 353

<210> 450
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 450
 Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His Arg Asp Leu
 1 5 10 15
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
 20 25 30
 Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr
 35 40 45
 Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
 50 55 60
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
 65 70 75 80
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
 85 90 95
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
 100 105 110
 Arg Arg Arg Gln Arg
 115

<210> 451
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 451
 gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa
 60
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cggttaatggt
 120
 gcagaagttt taatgttggg agaaatgctg actttaccac agaattttgg gaatatattt
 180
 ttgggagaga ccttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
 240
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaactct ttcagcctcc
 300
 aatgctgcag tggctgaact taaaccggat tgttgatttg atgatgtcat acatcatgaa
 360
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
 420
 gaaaaaatgt atttcagaaa attt
 444

<210> 452
 <211> 148
 <212> PRT

<213> Homo sapiens

<400> 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

```

gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gccccagatg acctgggggt
120
tgaaaggcac tcccgctggg tgcttcctgg gagcaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttcctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

```

                20                25                30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
                35                40                45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
                50                55                60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
65                70                75                80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
                85                90                95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
                100                105

```

<210> 455

<211> 602

<212> DNA

<213> Homo sapiens

<400> 455

```

cctaggcaaa gcatgccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccaccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcaggtg gggaagcaga gatctgcgtc tcttgagct
420
ggagctggtg ggtggggctc cttcctggtg ctgcgaggc tcattgggga ggtggcagcg
480
acccctcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

```

<210> 456

<211> 100

<212> PRT

<213> Homo sapiens

<400> 456

```

Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
1                5                10                15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
                20                25                30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
                35                40                45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr

```

50 55 60
 Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
 65 70 75 80
 Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
 85 90 95
 Leu Ala Thr Tyr
 100

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 457
 acgcgtcatg tggatattcc tgggagggtc ccaggaacgt ttctggacgg gcccccgacc
 60
 agagggtcagg gaacttttct tattattctg cacgtgcccc gggatagtca aaccaggctct
 120
 tcccccttctg ctggccgcaa cacgccagcc gccgccacga ccgcacgctg aattcatgac
 180
 ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
 240
 tcgttttctg tccactggcc agcgccacta tgatcagggtg gggatatccgc ccggcgggcg
 300
 gagcaccggg acgccggggc gccg
 324

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 458
 Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
 1 5 10 15
 Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
 20 25 30
 Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
 35 40 45
 Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
 50 55 60
 Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
 65 70 75 80
 Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
 85 90 95
 Gly Gly Ser Thr Gly Thr Pro Gly Arg
 100 105

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgagg cagagagtgc
60
gggtgtcgaa caggaactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
120
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccgggtggtt
180
tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
240
agaggcctca cccgacagct gggcatcgga tttacgaagc ccacgacgaa tcttcctcgc
300
ctcctcaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttoga tcaacacact
360
aggatcgttg gggccacca catacaccga gcggcaatcg agcggatacg acctc
415

<210> 460
<211> 105
<212> PRT
<213> Homo sapiens

<400> 460
Met Pro Met Ile Gly Phe Glu Glu Ala Arg Lys Ile Arg Arg Gly Leu
1 5 10 15
Arg Lys Ser Asp Ala Gln Leu Ser Gly Glu Ala Ser Pro Phe Lys His
20 25 30
Val Gln Ile Pro Arg Glu Gly Arg Ala Gln Ser Ser Ala Gly Ser Ile
35 40 45
Asn His Arg Asn Arg Ala Ala Arg Asp Gln Glu Arg Glu Arg Lys Arg
50 55 60
Leu Glu Ala Gln Arg Gln Asp Pro Ser Arg Pro Val Val Glu Thr Ile
65 70 75 80
Thr Glu Val Ser Cys Ser Thr Pro Ala Leu Ser Ala Ala Pro Pro Arg
85 90 95
Arg Lys Ser Met Glu Ala Asp Ala Glu
100 105

<210> 461
<211> 357
<212> DNA
<213> Homo sapiens

<400> 461
acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt gggtcacaac
60
cgggtcacat gcatgatgac aaaaactggc agaataagat tgatgtcatc ccgtctacca
120
gtccttagaa ccagctcaga ggtcccggt gtcggtaccg tcgagactca gtacacaact
180
gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact
240
gtcgtctacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt
300
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtgggtgcga tgcgaggaat gcgatcgat cctgggtgcgt
 120
 accggagagt ccatctgagc ccttcttgtg gcggtgatgc cgggatatcc gtagaattag
 180
 cggctcggacg agccatccgg gtgatcgcgg cagcgggtgag ttgtcgagga aagtccgggc
 240
 tccatagagc aggggtggtgg gtaacgcca cccggggtga cccgcgggaa agtgccacag
 300
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gcccaccgcg
 360
 tcatcggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
 420
 ggtcgcggac gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1             5             10             15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20             25             30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35             40             45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50             55             60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65             70             75             80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85             90             95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100            105            110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115            120            125

```

<210> 465
 <211> 438
 <212> DNA
 <213> Homo sapiens

```

<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tggtaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggtat cattacgggt aatgatgaat atggcatgta ccttgtttgg tatgacacct
240
gaaaccgccc ttgcaggggt aacaattcat gcggcaaaag cgttggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattgggt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466
 <211> 143
 <212> PRT
 <213> Homo sapiens

```

<400> 466
Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
1             5             10             15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20             25             30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35             40             45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50             55             60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

```

65          70          75          80
Glu Thr Ala Leu Ala Gly Val Thr Ile His Ala Ala Lys Ala Leu Gly
          85          90          95
Ile Ser Asp Ser His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe
          100          105          110
Val Cys Trp Asp Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly
          115          120          125
Glu Gln Leu Val Lys Gln Arg Ile Gln His Gly Val Ser His Glu
          130          135          140

```

<210> 467
 <211> 460
 <212> DNA
 <213> Homo sapiens

```

<400> 467
ntttccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcggttaagc
60
tgcattccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcgagcgtt
120
ctcgcagtga agatggcggt ggaggaatgg atgccctggc tagaagaggc ggaatatctg
180
ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
240
tccaggcaag caagaagggc ccagctgttt acctggttcc acttttccct ctectaccgg
300
ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggccca
360
ttctccagg cttgcctgtc acccgggtc ccgtcaaacc ctggccttcg tgcgacaaca
420
ctcttggtgc cttctatggt tctgtatggt gccgcaattg
460

```

<210> 468
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 468
Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
1          5          10          15
Pro Trp Leu Glu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
          20          25          30
Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
          35          40          45
Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
          50          55          60
Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
65          70          75          80
Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
          85          90          95
Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
          100          105          110
Leu Tyr Val Ala Ala Ile

```

115

<210> 469
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 469
 cttgtgcaca cgttatTTTT ccaatacaaa tagtttaaaa agtaaaactcc aaatacctat
 60
 aagccccctc aaagcacctt ccaaatatga accttggttaa tgcccaaggt ccagaggggt
 120
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcggggtccc catgctgact
 180
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
 240
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
 300
 ccctgagttc ctggctagct gtggttaacc acaaaaaatg cggggggtga tgattttcga
 360
 agtccatcgg caaagaaaga c
 381

<210> 470
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
 1 5 10 15
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
 20 25 30
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
 35 40 45
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
 50 55 60
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
 65 70 75 80
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
 85 90 95
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
 100 105 110

<210> 471
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 471
 accggtgact acctgcagca ctggattgac atgggttaaaa agggcggcga ccgcatgccca
 60
 gaggtcttcc tgggttaactg gttccgccgc ggcgacgatg gccgcttcct gtggccgngg
 120

cttggcgaaa acttcccggc cctanagtgg atcatcgacc gcattgaagg caacgtagag
 180
 gccgaggaca cgggtggcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
 240
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgcgttg acccgaagga atgggaaggg
 300
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg
 360
 tggaaccagt tccgcgcc
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5				10						15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
		20						25					30		
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
		35					40					45			
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
	50					55				60					
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65				70					75					80	
Asp	Phe	Asp	Val	Asp	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Lys
			85					90					95		
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
		100					105						110		
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
		115					120					125			

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaaggg acccatccca tgccacctgt cctagaaaat gtttcccctt
 60
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
 120
 aggcaccaag taaaagaagg gggaagctgc caaaaccccc cctgcaaaa ctctcccacc
 180
 ctgcttccat ttccctctcc agggaacagg tgtacctccc ctctccctg tctctctcag
 240
 atgccccagg ggctctctac ttcatctctg ccgacctgc caggagtggc ctgaggggta
 300
 gaggctccta gttggagaat ttgcttgagc gaaggtgaa
 339

<210> 474

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
 20 25 30
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
 35 40 45
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
 50 55 60
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65 70 75 80
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
 85 90 95
 Glu

<210> 475
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 475
 agcgcgtgaag ggtccctccc aaactctgag cctccttcca agccttgctg ggagctcccc
 60
 agcgcctgcc ggagaggcct ctcctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtcccacagc cataatcccc
 180
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa
 240
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
 300
 ctttgatgga tcttgtaga agtgggttgt tcattctggg gtttt
 345

<210> 476
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1 5 10 15
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
 20 25 30
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
 35 40 45
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
 50 55 60
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

```

<400> 478
Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
 1           5           10           15
Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
      20           25           30
Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
      35           40           45
Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
      50           55           60
Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
65           70           75           80
Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
      85           90           95
Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
      100           105           110
Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
      115           120           125
Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
      130           135           140

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<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
 cgcggtggcca ttggccgggc gctggtgcgg caccgcgac tggtgattgc cgatgagccg
 60
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
 120
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac
 180
 gcccaaccggg tggcggtgat gagcgagggc aggggtggtg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgagca cccctacacc cgcaagctgc tggccgccgc cagccccctg
 300
 gagaaaacttg aaaacggtgg ctaccgcac cgccagggcc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
 aagcttctga ctgtggcatt ctccctgctt aatatgtcct caatatcccc tacttactgg
 60
 gcaaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc
 120
 cctgccctgc cggcttgccg tggcttctct agtgtagga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgcccctgct cccagcaggg cccacaan
 240
 cccagtcacag gacctggctc acgctgggtg gcgcatgccc aggaatgggg ctctggatct
 300
 gcctcttctc ctgcaggacc aggaaccgc tgccctgtcc ctgcccagg aaaccctcag
 360
 taaatcccca gtcatttgag tttccctca ggcagagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgct t
 441

<210> 482
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 482
 Lys Leu Leu Thr Val Ala Phe Ser Leu Leu Asn Met Ser Ser Ile Ser
 1 5 10 15
 Pro Thr Tyr Trp Ala Lys Ser Cys Leu Cys Phe Gly Thr Ser Ser Lys
 20 25 30
 Thr Thr Pro Leu Asp Gly Ala Phe Pro Ala Leu Pro Ala Cys Ala Gly
 35 40 45
 Phe Leu Ser Val Arg Ile Thr Ile Thr Leu His His Glu Ser Arg Arg
 50 55 60
 Pro Ser Pro Cys Asp Cys Cys Pro Cys Ser Gln Gln Gly Pro Gln Xaa
 65 70 75 80
 Pro Ser Pro Gly Pro Gly Ser Arg Trp Val Ala Asp Ala Gln Glu Trp
 85 90 95
 Gly Ser Gly Ser Ala Ser Ser Pro Ala Gly Pro Gly Asn Arg Cys Pro
 100 105 110
 Val Pro Ala Pro Gly Asn Pro Gln
 115 120

<210> 483
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 483
 acgcgttcat tcctgatgg ccacgcacga gctaacggag ggatggggcg aaggggaaggc
 60
 caagggttgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttta aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccaggctccg
 180
 agcgtctgcc cagcccagca tcctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgctgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctggggcc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484
 Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1 5 10 15
 Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
 20 25 30
 Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
 35 40 45
 Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
 50 55 60
 Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
 65 70 75 80
 His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
 85 90 95

<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485
 acgcgtgctc gcgcggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
 60
 gcccgattcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
 120
 cgggggatac caaaggaatc ttgtcgaggg cttcgcgggc ctcgacgtgg atcacctgta
 180
 cccgacggac gtggggaagc cgtcccgcaa gctcacggga ctccgcgaca tcgatgtgcg
 240
 atacgatttg caccgtcgtc ggctgcgtgc gcgacacatg ctccgcgacg gcctcagcgg
 300
 tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
 360
 cattcccatt cctcggg
 377

<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486
 Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1 5 10 15
 Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
 20 25 30
 Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
 35 40 45
 Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
 50 55 60
 Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

669

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgtactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
 60
 aaccagcacg gttgctacaa agtgcgcttt ccattttacc gcgatcaaaa gcccagcact
 120
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac
 180
 tttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggctgcgt accaaactcg gaaaccccg gcatggctcg tgagcgtaac
 300
 gccacccaga gcggcttctc caccggcggg gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct ggggtgcgct ggcggaaca gcgtcttcac actgggcaat
 420
 ggcaaagtcg ccggcgcgca actgcgccac aacgccccac atgcaattga catcgtcttc
 480
 gctcaaacac gaagtgcccg gcgtgtactc attgtcgatg ggcaccgggg acccgggcggc
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly
1			5					10						15	
Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe
		20					25						30		
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg
		35					40					45			
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu
		50				55					60				
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg
65				70						75				80	
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val
			85					90						95	
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His
			100					105					110		
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly
		115					120				125				
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala
		130				135					140				
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe
145				150						155				160	
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg
				165					170					175	
Gly	Pro	Gly	Gly												

180

<210> 491
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 491
 nacgcgtcga ggcgacggc ggcgccgtca tggcgactgt tctcgagggc acatgggaac
 60
 gcatcggtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tgggcggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggaggggtca atcgaattgg
 240
 tcgacgtgtc ggtcgggtgac gaagagcgca ggtcgcacgt caccatgaag ggagcatgcc
 300
 gaggttgccc ggcagccatc agaccctaca tcagcgcttg gaacatcaac tgagtctgag
 360
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaagccac tcgtagacgc attcctcctc ggcatccaat
 480
 tcctcccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
 540
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgcg catcacaggg
 600
 ttcattggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcg
 660
 tcttcccagc gcgccgcgac atcctcggcg tcatggtcga catggaattg cgcgtcagct
 720
 ggtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
 780
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
 825

<210> 492
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 492
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493
 <211> 863

<212> DNA

<213> Homo sapiens

<400> 493

nacgcgttcc aacctcgtca aaacggctat cgcaggaaat gacccaact ggggtcgcac
 60
 cctcgcggcg atcgatgtg ttcctgagaa tatagctccc ttcgatcccg accaggtgga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc
 420
 gtgaaatatg gcggcaacgc gatggttgat cccggtctgc agcaggcctt cgccgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacggtgg tggccctcag
 540
 atcaatgcca tgcttgctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
 600
 acatctccgg aggtcatgga ggttgccgg atggtgctcg tcgggcagggt gggccgtcag
 660
 ctcggttaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
 720
 ggcctttttt cggcccgaa gtcgcggtta attgttgatg gcgagcaaat agacatgggt
 780
 ttagtgggag acatcggtga cgtcaacatc gatctcgta tctctatgct tgatcgcggt
 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala
 1 5 10 15
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg
 20 25 30
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val
 35 40 45
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala
 50 55 60
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile
 65 70 75 80
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly
 85 90 95
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu

```

      100      105      110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala
      115      120      125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala
      130      135      140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu
      145      150      155      160
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu
      165      170      175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro
      180      185

```

<210> 495
 <211> 514
 <212> DNA
 <213> Homo sapiens

```

<400> 495
gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tccccgggcc ttgatgacc ttgagccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcggtt ttgcgcggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggtaactg ctgtgggacc ttgg
514

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<210> 496
 <211> 171
 <212> PRT
 <213> Homo sapiens

```

<400> 496
Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr
1      5      10      15
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser
      20      25      30
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro
      35      40      45
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly
      50      55      60
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
      65      70      75      80
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu

```

```

      85              90              95
Met Ile Tyr Arg Ile Ala His Asn Phe Gly Gly Thr Ser Val Phe Ala
      100              105              110
Gly Val Gly Glu Arg Thr Arg Glu Gly Asn Asp Leu Ile Asn Glu Met
      115              120              125
Asp Glu Ala Gly Val Leu Lys Asp Thr Ala Leu Val Phe Gly Gln Met
      130              135              140
Asp Glu Pro Pro Gly Thr Arg Tyr Glu Leu Ser Arg Trp Gln Pro Cys
145              150              155              160
Gly Pro Cys Leu Val Asn Cys Cys Gly Thr Leu
      165              170

```

<210> 497

<211> 662

<212> DNA

<213> Homo sapiens

<400> 497

```

acgcgtcctg ggatctcaac cccagcagtc tggcttgttt ctcattccca caatttcctg
60
ggttcacca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgtcagc acaggcctgg gacctcccc ggcaggcacc tgtggggggg gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg ccgagaggcg
420
tgtctgtgaa gacaggtacc aggatggcag gaccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcttc ctacttctgc ttagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

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<210> 498

<211> 191

<212> PRT

<213> Homo sapiens

<400> 498

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Met Asn Glu Glu Lys Thr Gln Pro His Lys Arg Asp Thr Arg Trp Arg
  1              5              10              15
Gly Glu Thr Gln Gln Ser Ser Phe Leu Ser Val Asp Ser Glu Gln Arg
      20              25              30
Arg Gly Ala Pro Ser Phe Val Phe Ser Ser Ser Gly Glu Arg Met Asp

```

```

      35          40          45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
 50          55          60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
65          70          75          80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85          90          95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100          105          110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115          120          125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130          135          140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
145          150          155          160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165          170          175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180          185          190

```

<210> 499

<211> 444

<212> DNA

<213> Homo sapiens

<400> 499

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acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
60
ctgccttctg cctgaccctc tggcttctca agcagtctat acgtgagaag ccctttcttc
120
aagtgaaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
180
tcctcaactg gggggttgga ggagggttact tcacttctca aaacctcaat ttccttatct
240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaatgc ctggcacagt
300
agggcagtta ccgtcatgga gaacagaaaag gccccgagct atcctggatg tggtgagaat
360
gggtcctgga tctgcctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
420
aagggcctct gaaaacacag ggtg
444

```

<210> 500

<211> 105

<212> PRT

<213> Homo sapiens

<400> 500

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Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
 1          5          10          15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20          25          30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

      35              40              45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
   50              55              60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
   65              70              75              80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
              85              90              95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100              105

```

<210> 501
 <211> 800
 <212> DNA
 <213> Homo sapiens

```

<400> 501
agatctgata cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
ggtactcctt attcaatgag aggcctgagg tgagaccgcg catgcggcgc gtggatcgca
120
tggtgttagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gaccttgtag tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccggcca aagctgagga gtttgtgggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcaccca aaattgcaag acctttcata
360
gagggcctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtagt cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agcttttagct
780
atcttgcttc agaaactgaa
800

```

<210> 502
 <211> 103
 <212> PRT
 <213> Homo sapiens

```

<400> 502
Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
  1              5              10              15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
      65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503
 <211> 538
 <212> DNA
 <213> Homo sapiens

```

<400> 503
nnacgcgttg tcgtctctcc gatcattgat tttgttgat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataaggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttcagct attggaaggg gaaggtcccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctgggccct tcacgcgt
538

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<210> 504
 <211> 179
 <212> PRT
 <213> Homo sapiens

```

<400> 504
Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
1      5      10      15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
      50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
      65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

```

      85              90              95
Lys Asn Ala Pro Leu Leu Leu Pro Asp Val Ile Lys Val Ser Thr Arg
      100              105              110
Ser Ser Glu His Phe Phe Ser Val Phe Leu Asn Ile Asn Glu Thr Phe
      115              120              125
Lys Leu Met Glu Gln Leu Ala Asn Ile Ala Met Arg Gln Leu Leu Asp
      130              135              140
Asn Glu Gly Phe Glu Gln Asp Arg Ser Leu Pro Lys Leu Lys Arg Lys
      145              150              155              160
Ser Pro Lys Lys Val Ser Ala Leu Lys Arg Asp Leu Asp Ala Trp Ala
      165              170              175
Leu His Ala

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<210> 505
 <211> 381
 <212> DNA
 <213> Homo sapiens

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<400> 505
gtgcacgaca ccgaacggta cgaacgtatc tcccaggcac gtcgcgagga acagcaggcc
60
atgctcggct acgacngctc aagaacctgt cgcattgacct tgctcaccgg gcagctggac
120
gacccctcca cgactccttg cggacgctgc gacgtctgtg ctggcccgtg gtactcagtc
180
gaggtcgtac agtcagccgc tgtgagagcc gtccaatccc tcaaccgggt gggagttccg
240
gtggaaccac gcgccgcctg gcccgagggt atggacgccc tccaggttgc gctcaagggt
300
cgcattcagtg ccgaggagat cgctgcagag ggccgcgtca tcgccagact ctccgatctg
360
ggttggggag gggcgctgcg c
381

```

<210> 506
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 506
Val His Asp Thr Glu Arg Tyr Glu Arg Ile Ser Gln Ala Arg Arg Glu
1      5      10      15
Glu Gln Gln Ala Met Leu Gly Tyr Asp Xaa Ser Arg Thr Cys Arg Met
20     25     30
Thr Leu Leu Thr Gly Gln Leu Asp Asp Pro Ser Thr Thr Pro Cys Gly
35     40     45
Arg Cys Asp Val Cys Ala Gly Pro Trp Tyr Ser Val Glu Val Asp Gln
50     55     60
Ser Ala Ala Val Arg Ala Val Gln Ser Leu Asn Arg Val Gly Val Pro
65     70     75     80
Val Glu Pro Arg Ala Ala Trp Pro Ala Gly Met Asp Ala Leu Gln Val
85     90     95
Ala Leu Lys Gly Arg Ile Ser Ala Glu Glu Ile Ala Ala Glu Gly Arg

```

	100		105		110									
Val	Ile	Ala	Arg	Leu	Ser	Asp	Leu	Gly	Trp	Gly	Gly	Ala	Leu	Arg
	115			120								125		

<210> 507
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 507
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 60
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa
 120
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
 180
 tcctcctccc aaggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgtc
 240
 gccaccgcca tcccagcgat ctgctgcctc ggcgctgccc tgctcatgct gggctaccg
 300
 ctcaccgcg acaaggtggt cgccaacgcc gacgagttgg ctgctcgcca cgcagtacag
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgtca tgcggatcac
 420
 cgaccacttg acaacctcgc cggttatcca attgaaaatt gacaagcgat ggggtgcctc
 480
 cgtcacattt gtgacgcgt
 499

<210> 508
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 508
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1 5 10 15
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
 20 25 30
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
 35 40 45
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
 50 55 60
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
 65 70 75 80
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
 85 90 95
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
 100 105 110
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
 115 120 125

<210> 509
 <211> 360

<212> DNA

<213> Homo sapiens

<400> 509

ttggccatgg atttggtcgc caagttcagt cccaaagatg tcacgctcta tctaattggac
 60
 ttctgggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt
 120
 ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
 180
 cgtaagaagc tcttggtccga ctacggtgtt ggtacactag agctctaccg tcaggctagc
 240
 ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag
 300
 gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc
 360

<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

Leu	Ala	Met	Asp	Leu	Ala	Arg	Lys	Phe	Ser	Pro	Lys	Asp	Val	Thr	Leu
1				5					10				15		
Tyr	Leu	Met	Asp	Phe	Gly	Thr	Asn	Gly	Val	Ala	Pro	Leu	Gly	Gln	Leu
			20					25				30			
Pro	Gln	Val	Ala	Asp	Thr	Leu	Leu	Leu	Asp	His	Thr	Glu	Lys	Ile	Ala
			35				40					45			
Lys	Phe	Val	Arg	Ile	Met	Glu	Arg	Glu	Leu	Asn	Arg	Arg	Lys	Lys	Leu
			50			55					60				
Leu	Ser	Asp	Tyr	Gly	Val	Gly	Thr	Leu	Glu	Leu	Tyr	Arg	Gln	Ala	Ser
65					70					75				80	
Gly	Gln	Gln	Glu	Pro	Ala	Ile	Val	Ile	Leu	Leu	Asp	Ser	Tyr	Glu	Ser
				85					90					95	
Met	Lys	Glu	Glu	Ala	Tyr	Glu	Ala	Glu	Leu	Phe	Thr	Leu	Leu	Val	Arg
				100				105						110	
Ile	Ser	Arg	Glu	Gly	Leu	Ser	Ile								
			115				120								

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

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 actgcgttcg gcatgccgg catcgccag atcgggcgca agatgcagga cgatctcgac
 120
 gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc
 180
 ggggcctcct atggcggcta tgccgcgatg tggggcgca tccgcaatcc cgaacgctat
 240

cgctgcgcgg cgagcctggc gggggttgcc gattaaggcc atgctcaaataa acccggcg
 300
 ctatctcgac aaggaggcgg gcaagcgctg gccgccccgn tcaaccggcg aaccggaatt
 360
 c
 361

<210> 512
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 512
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser
 1 5 10 15
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
 65 70 75 80
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
 nnatgcagac tagaagatgg catgacgggt ttggctggcg gtttcgggct atgcggcatt
 60
 ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca
 120
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatggtgt cttcttatgt ggggtgaaaat gcactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
 300
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa
 360
 gacacgcgt
 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

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1           5           10           15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
20           25           30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
35           40           45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
50           55           60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
65           70           75           80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
85           90           95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
100          105          110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
115          120

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<210> 515
 <211> 387
 <212> DNA
 <213> Homo sapiens

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<400> 515
gcggtgggacg agaagggcgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttctctt cggacgacgg gcagatcctg
180
cgggcgttcc agaagggcgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
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360
gccgacctga ccggtgcgcc gttgtac
387

```

<210> 516
 <211> 129
 <212> PRT
 <213> Homo sapiens

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<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
1           5           10           15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
20           25           30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
35           40           45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
50           55           60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
65           70           75           80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

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683

<212> DNA

<213> Homo sapiens

<400> 519

gcgcgccagg gggaagggag agaaaacaca gaaaaatgag ggggaaatac cagatactga
 60
 agaattttaa ttattataaa ggaacctttt ctgcaactct gaaaaatggt agaatatcca
 120
 aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaate
 180
 gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgcca aacctggaat
 240
 tcatgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc
 300
 cagaacttaa g
 311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1				5				10						15	
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20				25					30			
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
		35				40				45					
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50				55				60						
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65				70				75					80		
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

<400> 521

nnngatgcc a cgcggtcta cggaatctcc accggcttcg gcgcgcttgc ccgcgccac
 60
 attccagaag agatgcgcgc gcagctgcag ctgtccctgg tgcgctccca cgcggccggc
 120
 accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc
 180
 ctgtgtaccg gccgtaccgg cgtgcgcccc gtggtggtag aaacttatgc caaggcgtc
 240
 aacgcggca tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg
 300
 gccccgctgg ctactgcgc cctagcgctg ttgggtgagg gtgaggtacg cn
 352

<210> 522
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 522
 Xaa Asp Ala Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly Ala Leu
 1 5 10 15
 Ala Arg Arg His Ile Pro Glu Glu Met Arg Ala Gln Leu Gln Leu Ser
 20 25 30
 Leu Val Arg Ser His Ala Ala Gly Thr Gly Pro Glu Val Glu Glu
 35 40 45
 Val Ile Arg Ala Leu Met Leu Leu Arg Leu Ser Thr Leu Cys Thr Gly
 50 55 60
 Arg Thr Gly Val Arg Pro Val Val Val Glu Thr Tyr Ala Lys Ala Leu
 65 70 75 80
 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
 85 90 95
 Ser Gly Asp Leu Ala Pro Leu Ala His Cys Ala Leu Ala Leu Leu Gly
 100 105 110
 Glu Gly Glu Val Arg
 115

<210> 523
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 523
 agcgcttcca cagtcgcgca aactcctctt ggtctagccg cccattcact ttcagttcca
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 tcagagccac caagctgcgg caccatctaa ggagaacatg tcccctggag gtcctgttag
 120
 aagctcctgg ttgagaaggc cctgaagctg ggtggcatca atgtccagcc tctgctgagc
 180
 atatctgttg aaaatgcttt gttgggagcc atgttctgaa gggcttcctt tcattctgag
 240
 gttgaaatgg ctgctcaggt gcctgtcact gtctggcatt ttcaggaaga ttcggagcaa
 300
 gaactccgct gattttctcc gtgtctgtgc aaccacaaca tagttcccag ggctcagatg
 360
 gtaagtcatg gtgaagtgc ggcggaattt attatttgag ctttggacag tgtttctgaa
 420
 cgaggaaaaa aacacgggtg gaaatttctc ccggaaccgc tgtgagccag ccagaatcac
 480
 ttggaaatcg agtggaaatt ttgcatcttc tgctttcaaa tttgatggtg tgacagcaac
 540
 tgtgacgcac acgacaacat tggcgccttc cattggctct tgcacagaga agttgaattg
 600
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 660
 tgggaccatc cttcgtggag tgtgtttcca tgg
 693

<210> 524
 <211> 193
 <212> PRT
 <213> Homo sapiens

<400> 524
 Met Ile Leu Gly Asn Thr Pro Gly Gly Pro Gly Asn Asp Ala Gln Phe
 1 5 10 15
 Asn Phe Ser Val Gln Glu Pro Met Glu Gly Thr Asn Val Val Val Cys
 20 25 30
 Val Thr Val Ala Val Thr Pro Ser Asn Leu Lys Ala Glu Asp Ala Lys
 35 40 45
 Phe Pro Leu Asp Phe Gln Val Ile Leu Ala Gly Ser Gln Arg Phe Arg
 50 55 60
 Glu Lys Phe Pro Pro Val Phe Phe Ser Ser Phe Arg Asn Thr Val Gln
 65 70 75 80
 Ser Ser Asn Asn Lys Phe Arg Arg Asn Phe Thr Met Thr Tyr His Leu
 85 90 95
 Ser Pro Gly Asn Tyr Val Val Val Ala Gln Thr Arg Arg Lys Ser Ala
 100 105 110
 Glu Phe Leu Leu Arg Ile Phe Leu Lys Met Pro Asp Ser Asp Arg His
 115 120 125
 Leu Ser Ser His Phe Asn Leu Arg Met Lys Gly Ser Pro Ser Glu His
 130 135 140
 Gly Ser Gln Gln Ser Ile Phe Asn Arg Tyr Ala Gln Gln Arg Leu Asp
 145 150 155 160
 Ile Asp Ala Thr Gln Leu Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr
 165 170 175
 Gly Pro Pro Gly Asp Met Phe Ser Leu Asp Gly Ala Ala Ala Trp Trp
 180 185 190
 Leu

<210> 525
 <211> 1101
 <212> DNA
 <213> Homo sapiens

<400> 525
 nggcaagttg caaagagagc ctcagaggtc cgaagagcgc tgcgctccta ctcgcgttcg
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 120
 gtcctaccga gaccgatccg cagcgtttgg cccggtcgcg cctattgcat cgggagcccc
 180
 cgagcaccgg cgaaggactg gcgggtgggg tagggagggtg gcggcggcgg catggcgagg
 240
 ttcccgaagg ccgacctggc cgctgcagga gttatgttac ttgcccactt cttcacggac
 300
 cagttttcagt tcgccgatgg gaaacccgga gaccaaatec ttgattggca gtatggagtt
 360
 actcaggcct tcctcacac agaggaggag gtggaagttg attcacacgc gtacagccac
 420

aggtggaaaa gaaacttgga ctttctcaag gcggtagaca cgaaccgagc aagcgtcggc
 480
 caagactctc ttgagcccag aagcttcaca gacctgctgc tggatgatgg gcaggacaat
 540
 aacactcaga tcgaggagga tacagaccac aattactata tatctcgaat atatggtcca
 600
 tctgattctg ccagccggga tttatgggtg aacatagacc aaatggaaaa agataaagtg
 660
 aagattcatg gaattattgtc caatactcat cggcaagctg caagagtga tctgtccttc
 720
 gattttccat tttatggcca cttcctacgt gaaatcactg tggcaaccgg gggtttcata
 780
 tacactggag aagtcgtaca tcgaatgcta acagccacac agtacatagc acctttaatg
 840
 gcaaatttcg atcccagtg atccagaaat tcaactgtca gatattttga taatggcaca
 900
 gcacttggtg tccagtggga ccatgtacat ctccaggata attataacct gggaagcttc
 960
 acattccagg caaccctgct catggatgga cgaatcatct ttggatacaa agaaattcct
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 gtcttggtca cacagataag ttcaaccaat catccagtga aagtcggact gtccgatgca
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<210> 526

<211> 290

<212> PRT

<213> Homo sapiens

<400> 526

Met	Ala	Arg	Phe	Pro	Lys	Ala	Asp	Leu	Ala	Ala	Gly	Val	Met	Leu
1				5				10					15	
Leu	Cys	His	Phe	Thr	Asp	Gln	Phe	Gln	Phe	Ala	Asp	Gly	Lys	Pro
			20			25						30		
Gly	Asp	Gln	Ile	Leu	Asp	Trp	Gln	Tyr	Gly	Val	Thr	Gln	Ala	Phe
	35					40					45			
His	Thr	Glu	Glu	Glu	Val	Glu	Val	Asp	Ser	His	Ala	Tyr	Ser	His
	50					55					60			
Trp	Lys	Arg	Asn	Leu	Asp	Phe	Leu	Lys	Ala	Val	Asp	Thr	Asn	Arg
65				70					75				80	
Ser	Val	Gly	Gln	Asp	Ser	Leu	Glu	Pro	Arg	Ser	Phe	Thr	Asp	Leu
			85					90					95	
Leu	Asp	Asp	Gly	Gln	Asp	Asn	Asn	Thr	Gln	Ile	Glu	Glu	Asp	Thr
			100					105					110	
His	Asn	Tyr	Tyr	Ile	Ser	Arg	Ile	Tyr	Gly	Pro	Ser	Asp	Ser	Ala
		115				120						125		
Arg	Asp	Leu	Trp	Val	Asn	Ile	Asp	Gln	Met	Glu	Lys	Asp	Lys	Val
	130					135					140			
Ile	His	Gly	Ile	Leu	Ser	Asn	Thr	His	Arg	Gln	Ala	Ala	Arg	Val
145				150					155				160	
Leu	Ser	Phe	Asp	Phe	Pro	Phe	Tyr	Gly	His	Phe	Leu	Arg	Glu	Ile
			165					170					175	
Val	Ala	Thr	Gly	Gly	Phe	Ile	Tyr	Thr	Gly	Glu	Val	Val	His	Arg

	180		185		190
Leu Thr Ala Thr Gln Tyr Ile	Ala Pro Leu Met Ala Asn Phe Asp Pro				
195	200		205		
Ser Val Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala					
210	215		220		
Leu Val Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu					
225	230		235		240
Gly Ser Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile					
	245		250		255
Phe Gly Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr					
	260		265		270
Asn His Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His					
	275		280		285
Arg Ile					
290					

<210> 527

<211> 5343

<212> DNA

<213> Homo sapiens

<400> 527

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120
gcctcccag agctagacat ccctctccct gaggacagtg agacggctta cgactgggag
180
tacgtgggt tcaccccttg cacagcaaca tgcttgggag gccatcaaga agccatagca
240
gtgtgcttac atatccagac ccagcagaca gtcaatgaca gcttgtgtga tatgggtccac
300
cgctctccag ccatgagcca ggctgtaac acagagccct gtccccccag gtggcatgtg
360
ggctcttggg ggccctgctc agctacctgt ggagttggaa ttcagaccg agatgtgtac
420
tgctgcacc caggggagac ccctgcccct cctgaggagt gccgagatga aaagcccat
480
gctttacaag catgcaatca gtttgactgc cctcctggct ggcacattga agaatggcag
540
cagtgttcca ggacttgtgg cgggggaact cagaacagaa gagtcacctg tcggcagctg
600
ctaacggatg gcagcttttt gaatctctca gatgaattgt gccaaaggacc caaggcatcg
660
tctcacaagt cctgtgccag gacagactgt cctccacatt tagctgtggg agactggtcg
720
aagtgttctg tcagttgtgg tgttggaaac cagagaagaa agcaggtgtg tcaaaggctg
780
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Asp Leu Gln Leu Gly Ile Pro Pro Ser Phe Met Arg Phe Gln Pro Arg
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Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
 370          375          380
Tyr Ser Ala Val Asp Gly Gln Pro Pro Arg Arg Gly Met Asp Ser Ala
 385          390          395          400
Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

```

405 410 415
 Asn Ala Asn Ala Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile
 420 425 430
 Gln Tyr Gly Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile
 435 440 445
 Leu Asp Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr
 450 455 460
 Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
 465 470 475 480
 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg
 485 490 495
 Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys
 500 505 510
 Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu
 515 520 525
 Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe
 530 535 540
 Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile
 545 550 555 560
 Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser
 565 570 575
 Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile
 580 585 590
 Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe
 595 600 605
 Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu
 610 615 620
 Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe
 625 630 635 640
 Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe
 645 650 655
 Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys
 660 665 670
 Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp
 675 680 685
 Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val
 690 695 700
 Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
 705 710 715 720
 Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg
 725 730 735
 Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
 740 745 750
 Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
 755 760 765
 Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
 770 775 780
 Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn Asn Gly Ser Val Arg
 785 790 795 800
 Thr Ala

<210> 531

<211> 321

<212> DNA

<213> Homo sapiens

<400> 531

ngatgatgaa tccccccgca gcctcgtcaa tatggggggc ttcctacccc agcaaaaggc
 60
 acggcaatac gtctcgaaca aaggctctttt gtttcgaaat aacaaggggt tagagctaag
 120
 aggaagaagc gtgaaacgct gtaggaccag cgtttcgaac gcccccgagg tgaaccctcg
 180
 ggggcgtctg aatcaggcca gttgggcctg ggacgacagc ggttgacgag gcagcaatgg
 240
 cgcgtgcgga tcagccttga tcgattcacg ccaggcgccg agccactcgg cgtggccttc
 300
 gttccacacc tgctggtgca g
 321

<210> 532

<211> 96

<212> PRT

<213> Homo sapiens

<400> 532

Met	Gly	Gly	Phe	Leu	Pro	Gln	Gln	Lys	Ala	Arg	Gln	Tyr	Val	Ser	Asn
1				5					10					15	
Lys	Gly	Leu	Leu	Phe	Arg	Asn	Asn	Lys	Gly	Leu	Glu	Leu	Arg	Gly	Arg
			20					25					30		
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
		35				40					45				
Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
	50				55					60					
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
65				70						75				80	
Gln	Ala	Pro	Ser	His	Ser	Ala	Trp	Pro	Ser	Phe	His	Thr	Cys	Trp	Cys
			85					90						95	

<210> 533

<211> 335

<212> DNA

<213> Homo sapiens

<400> 533

nagttttccgg tgaacccgct cgcaatgcct cgtgacatcg acttcagcga agccaacagg
 60
 agcatcatcg acaacatggc aactgcctca atcccgtttt tccgaaccca caaaaactgg
 120
 gagacgtggt cgagtcaggt ccggcatttc attagccttt tacacccaaa agtcaccctc
 180
 accaacattg acaacgtcct caacaaagat cacctgcgtt ggctacactt tcttttggag
 240
 ggtcgccctgg agccaaacgt gcgcctgatt gtccagggct actgttcgcc tggcaagctg
 300
 taccgcaagc ttgaggagct atatgcccct tctgc
 335

<210> 534
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 534
 Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp
 1 5 10 15
 Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp
 20 25 30
 Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro
 35 40 45
 Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu
 50 55 60
 Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg
 65 70 75 80
 Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu
 85 90 95
 Glu Glu Leu Tyr Ala Pro Ser
 100

<210> 535
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 535
 acgcgtctct acagccggac taagcacagg ctcagccccg gtcgccatgc gccaggctc
 60
 gggtatcagc cgaggaatcc acggcgaaat gaccagtagc ggccctaata caactatgct
 120
 gccgagcagc agacgtcgag gtcgggtcat gaggatgccg acggccaccg cgaccgggta
 180
 taccacaat gcaggaacaa ggctgatagc tagggctgac cacagagcca ggccgcctgc
 240
 cgaggaaaacg cccccacct ggtgactgcc agtatcagca ccgcgcagct caacgacgtc
 300
 aacagtctcg ggattgacca accgccacgt atgcagggcc atgtggggga gaatcacccc
 360
 caacgccaat gctgtcaccc agcctcgggc taggcgccgc gc
 402

<210> 536
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 536
 Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val
 1 5 10 15
 Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val
 20 25 30
 Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

```

      35              40              45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
      50              55              60
Met Thr Arg Pro Arg Arg Leu Leu Gly Ser Ile Val Val Leu Gly
65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
      85              90              95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
      100              105              110
Thr Arg

```

<210> 537
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<400> 537
gtgcacatcg gcggcaccga cttcgacaaa caactctcgc tggctggcat gatgccgctg
60
ttcggctacg gcagccgcat gaagagcggc gcctacatgc ccaccagcca ccacatgaac
120
ctggcgacct ggacacccat caactcgggtg tactcgcaaa aatcccagct ggccctgggc
180
agcatgcgct acgacatcga agacaccggc ggcacgcacc gcctgttcaa gctgatcgaa
240
cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcacccat
300
caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
360
cgggcgctgt tcgaatcgtc catcgacaac ctgctcgaac gcgt
404

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<210> 538
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 538
Met Met Pro Leu Phe Gly Tyr Gly Ser Arg Met Lys Ser Gly Ala Tyr
1              5              10              15
Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
      20              25              30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
      35              40              45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
      50              55              60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65              70              75              80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
      85              90              95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
      100              105              110
Asp Asn Leu Leu Glu Arg

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115

<210> 539
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 539
 nnacgcgtga aaaagaagaa aatgaaggaa agcgaggctg acagcgaggt gaagcatcaa
 60
 ccaatttttca taaaagaaag attgaagctt tttgaaatac tgaagaaaga ccatcagctc
 120
 ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct
 180
 gatgggcaaa cagtgcagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
 240
 attagtcagg aactggctga aagcacggta atagccaaag tcaatgggtga actgtgggac
 300
 ctggaccgcc cattggaagg ggactcttct ctagagctgc ttacatttga taatgaggaa
 360
 gctcaagctg tgagtatttt aaaaccagac agccaaactt tgggtagtta tgttgtaaac
 420
 tacattatat aagaggccac atattgaatt cacgaatgtt gagttttttg ggggtttcta
 480
 agatttaaaa tttgattatt gatgtttaat aaatatttgc ctcatgaatg ttaa
 534

<210> 540
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 540
 Xaa Arg Val Lys Lys Lys Lys Met Lys Glu Ser Glu Ala Asp Ser Glu
 1 5 10 15
 Val Lys His Gln Pro Ile Phe Ile Lys Glu Arg Leu Lys Leu Phe Glu
 20 25 30
 Ile Leu Lys Lys Asp His Gln Leu Leu Leu Ala Ile Tyr Gly Lys Lys
 35 40 45
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
 50 55 60
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
 65 70 75 80
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
 85 90 95
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
 100 105 110
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
 115 120 125
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
 130 135 140

<210> 541
 <211> 551

<212> DNA

<213> Homo sapiens

<400> 541

ggtaccgagc tgcgcgtgtg gtatgcggcc ttctatgcc aagaatgga caagcccatg
 60
 ctgaagcagg ccggtctctg cgtccacgct gcaggcacc cagaaaacag cgcctccgtg
 120
 gagtcggagc ccagccagtg ggcgtgtaaa gtgtgttctg ccaccttctt ggagctgcag
 180
 ctctcaatg gtaaggagga cgtgtgggga gcccagttg taaaactctt gtgtcgattt
 240
 ctctctgact tacgtgtca cctgtctgcg gctgtcgggg gtgtcccaga ctttgtcttg
 300
 tctgccccat tgccccacaa tgtagtcgcc agaaccaagg ctttctcagg gtttaaagct
 360
 tctgggcagt cccgcttccc acccccgacc cctgcaggcc tcaactctca ctctctctgg
 420
 ttgggaagtt gcatttcagc tgggcgcctt gactctggag cactggcagg ggccaggggc
 480
 caggagccag ccgtggcatg tggtgtgcac tcttgccctt gttgtctcta cttgacagcc
 540
 ccctcacgcg t
 551

<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

Met	Asp	Lys	Pro	Met	Leu	Lys	Gln	Ala	Gly	Ser	Gly	Val	His	Ala	Ala
1				5					10					15	
Gly	Thr	Pro	Glu	Asn	Ser	Ala	Pro	Val	Glu	Ser	Glu	Pro	Ser	Gln	Trp
			20					25					30		
Ala	Cys	Lys	Val	Cys	Ser	Ala	Thr	Phe	Leu	Glu	Leu	Gln	Leu	Leu	Asn
		35					40					45			
Gly	Lys	Glu	Asp	Val	Trp	Gly	Ala	Pro	Val	Val	Lys	Leu	Leu	Cys	Arg
	50					55					60				
Phe	Leu	Ser	Asp	Leu	Arg	Cys	His	Leu	Ser	Ala	Ala	Val	Gly	Gly	Val
65					70					75				80	
Pro	Asp	Phe	Val	Leu	Ser	Ala	Pro	Leu	Pro	His	Asn	Val	Val	Ala	Arg
			85						90					95	
Thr	Lys	Ala	Phe	Ser	Gly	Phe	Lys	Ala	Ser	Gly	Gln	Ser	Arg	Phe	Pro
			100					105					110		
Pro	Pro	Thr	Pro	Ala	Gly	Leu	Thr	Pro	His	Ser	Ser	Trp	Leu	Gly	Ser
		115					120					125			
Cys	Ile	Ser	Ala	Gly	Arg	Leu	Asp	Ser	Gly	Ala	Leu	Ala	Gly	Ala	Arg
	130					135					140				
Gly	Gln	Glu	Pro	Ala	Val	Ala	Cys	Val	Val	His	Ser	Cys	Leu	Cys	Cys
145					150					155				160	
Leu	Tyr	Leu	Thr	Ala	Pro	Ser	Arg								
					165										

<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
 nnaaagccgg acatgaatac ccgcattgct ggcaaaactg tcctgaccat cattctggcc
 60
 gggggcaaaag gcagccgcct ggccccgatg accgatcagg tggccaaacc agccgtgccg
 120
 tttatgggga cgtaccgcct gattgacttt tcgctgtcca acattgtcca cagcggcttg
 180
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
 240
 gggcgctcct gggatctgga ccgcaccgcg ggtggcctga aggtcatgcc gcccttttcc
 300
 ggccctgccg atgaggacgg tggcttttcc gaaggcaacg cacacgcgt
 349

<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
 Xaa Lys Pro Asp Met Asn Thr Arg Ile Ala Gly Lys Thr Val Leu Thr
 1 5 10 15
 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
 100 105 110
 Asn Ala His Ala
 115

<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
 catgatgcaa aaacagacat gcttatttca aaatataaaa gtgaaaaaga tcgttttagca
 60
 caagaaattg ttggtgtcat cacaggttct gcaatgccgg gtggttcagc aaaccgtatc
 120
 ccaataaaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
 240
 gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcggaat
 300
 acgttatata cctataaaat ggaaagttca ttagtgaaac aagtgttga agatgcaatg
 360
 ctatttgctt tgggtccccc ccccccccc
 390

<210> 546
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 546
 His Asp Ala Lys Thr Asp Met Leu Ile Ser Lys Tyr Lys Ser Glu Lys
 1 5 10 15
 Asp Arg Leu Ala Gln Glu Ile Val Gly Val Ile Thr Gly Ser Ala Met
 20 25 30
 Pro Gly Gly Ser Ala Asn Arg Ile Pro Asn Lys Ala Gly Ser Asn Pro
 35 40 45
 Glu Gly Ser Ile Ala Thr Arg Phe Ile Ala Glu Thr Met Tyr Asn Glu
 50 55 60
 Leu Lys Thr Val Asp Leu Thr Ile Gln Asn Ala Gly Gly Val Arg Ala
 65 70 75 80
 Asp Ile Leu Pro Gly Asn Val Thr Phe Asn Asp Ala Tyr Thr Phe Leu
 85 90 95
 Pro Phe Gly Asn Thr Leu Tyr Thr Tyr Lys Met Glu Ser Ser Leu Val
 100 105 110
 Lys Gln Val Leu Glu Asp Ala Met Leu Phe Ala Leu Gly Pro Pro Pro
 115 120 125
 Pro Pro
 130

<210> 547
 <211> 306
 <212> DNA
 <213> Homo sapiens

<400> 547
 aagcttggtt ttctgatttt tattcaaact tctatcatgg atgaagcatg cagtttcaga
 60
 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcat
 120
 gaagcctcca acatattttg tgggatacca tctttgtcag gcattgtgct aggcaactgtc
 180
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
 240
 tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcactaaact cnnnnncnn
 300
 nncnn
 306

<210> 548

<211> 90
 <212> PRT
 <213> Homo sapiens

<400> 548
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
 1 5 10 15
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
 20 25 30
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
 35 40 45
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
 50 55 60
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
 65 70 75 80
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa
 85 90

<210> 549
 <211> 780
 <212> DNA
 <213> Homo sapiens

<400> 549
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat
 60
 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcataatca gaaatatttc
 120
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttgttc tttttcacca
 180
 tgttattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
 240
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgc
 300
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
 360
 aagatttcta aggatgcagg gatgcccatc cagggccagc catgcttctg caaatatgca
 420
 cagggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta
 480
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta
 540
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca
 600
 tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaaactcg aggatcaat
 660
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
 720
 gccgatgtca ctcatccacc tgctggtgat ggaaagaagc cttctattgc tgctgttgta
 780

<210> 550
 <211> 192
 <212> PRT

<213> Homo sapiens

<400> 550

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Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
           20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
           35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
 50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
 65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
           85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
           100          105          110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
           115          120          125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
           130          135          140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
 145          150          155          160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
           165          170          175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
           180          185          190

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<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
 60
gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttccgag
 120
gaaccgtcct cgtcgtcaat cgcaccgggtc ccgccggccc cgacgactgc agtaccacg
 180
actagtctgt cgtcggggccg ctgaccgatg cgcccatcgg cggggtcatc tggctggcgc
 240
tagcggggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
 291

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<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

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Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

```

```

                20                25                30
Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ser Ile Ala
      35                40                45
Pro Val Pro Pro Ala Pro Thr Ala Val Pro Thr Thr Ser Ser Ser
      50                55                60
Ser Gly Arg
65

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<210> 553
 <211> 471
 <212> DNA
 <213> Homo sapiens

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<400> 553
ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
60
gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
120
gggtgtgttt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
180
gaagggtgat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
240
aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
300
tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
360
atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgtttaaa
420
gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
471

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<210> 554
 <211> 157
 <212> PRT
 <213> Homo sapiens

```

<400> 554
Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
 1                5                10                15
Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
      20                25                30
Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
      35                40                45
Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
      50                55                60
Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
      65                70                75                80
Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
      85                90                95
Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
      100                105                110
Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
      115                120                125
Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

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130 135 140
 Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg
 145 150 155

<210> 555
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 555
 tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag
 60
 attcgggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg
 120
 tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
 180
 ttaataaagt acctagaatt gtctgcctgc ttctccggct tagtggtgtc gtcgctgcgg
 240
 caataggtgc cgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt
 300

<210> 556
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 556
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
 1 5 10 15
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
 20 25 30
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
 35 40 45
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
 50 55 60
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
 65 70 75 80
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
 85 90

<210> 557
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 557
 atcttcccg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
 60
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac
 120
 gtgttcccg ctaccacta tgctgcggc ccggaacgta tggagcgggc catagcgtcc
 180
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggctcggtgcc
 300
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccgg ctcagccccg
 360
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atccccacgtg
 420
 accgtcccgc agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta
 480
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
 540
 acccagcggg tccggccagac tgtctacctg tccgccacgc cccgttcgta cgagaccgaa
 600
 cgagctcacg gcgtcgtcga acaaatcatt cgtccgacag gtctggtgga tccggagatt
 660
 atcgtcaagc ctacgcgt
 678

<210> 558
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 558
 Ile Phe Pro Val Tyr Glu Glu Asn Ala Leu Arg Val Glu Phe Phe Gly
 1 5 10 15
 Asp Glu Ile Glu Ala Leu Thr Thr Met His Pro Leu Thr Gly Glu Val
 20 25 30
 Ile Ser Glu Asp Glu Gln Val Tyr Val Phe Pro Ala Thr His Tyr Val
 35 40 45
 Ala Gly Pro Glu Arg Met Glu Arg Ala Ile Ala Ser Ile Gln Gln Glu
 50 55 60
 Leu Glu Glu Arg Leu Ala Val Leu Glu Arg Asp Gly Lys Leu Leu Glu
 65 70 75 80
 Ala Gln Arg Leu Arg Met Arg Thr Thr Tyr Asp Ile Glu Met Met Gln
 85 90 95
 Gln Val Gly Ala Cys Ala Gly Ile Glu Asn Tyr Ser Arg His Ile Asp
 100 105 110
 Gly Arg Ala Pro Gly Ser Ala Pro Asn Cys Leu Leu Asp Tyr Phe Pro
 115 120 125
 Glu Asp Phe Val Leu Val Ile Asp Glu Ser His Val Thr Val Pro Gln
 130 135 140
 Ile Gly Gly Met Tyr Glu Gly Asp Met Ser Arg Lys Arg Thr Leu Val
 145 150 155 160
 Glu His Gly Phe Arg Leu Pro Ser Ala Met Asp Asn Arg Pro Leu Lys
 165 170 175
 Phe Asp Glu Phe Thr Gln Arg Ile Gly Gln Thr Val Tyr Leu Ser Ala
 180 185 190
 Thr Pro Gly Ser Tyr Glu Thr Glu Arg Ala His Gly Val Val Glu Gln
 195 200 205
 Ile Ile Arg Pro Thr Gly Leu Val Asp Pro Glu Ile Ile Val Lys Pro
 210 215 220
 Thr Arg
 225

<210> 559
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 559
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa
 60
 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag
 120
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
 180
 tatgggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
 240
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta
 300
 gggtcacaaa cattcagtct gggaccatat ctaga
 335

<210> 560
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 560
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1 5 10 15
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
 20 25 30
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
 35 40 45
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
 50 55 60
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
 65 70 75 80
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
 85 90

<210> 561
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 561
 ngcgcgcccc ctccctccgat ggcggcgagg atccagccca agcctctgac ccgcaagccg
 60
 atcctgctgc agcggatgga ggggtcccag gaggtggtga atatggccgt gatcgtgccc
 120
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga
 180
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga
 240
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgacgat
 300

gacacctgtt gtcctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
 360
 ctggcactgc tctgagagtg ggagcgcct gggagggttat cggaccagtg ctgtggcctc
 420
 aggcctgcaa tttgatgttg aaaccggca tgtgtttatc ggtgaccact caggcca
 477

<210> 562
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 562
 Xaa Ala Pro Pro Pro Met Ala Ala Glu Ile Gln Pro Lys Pro Leu
 1 5 10 15
 Thr Arg Lys Pro Ile Leu Leu Gln Arg Met Glu Gly Ser Gln Glu Val
 20 25 30
 Val Asn Met Ala Val Ile Val Pro Lys Glu Glu Gly Val Ile Ser Val
 35 40 45
 Ser Glu Asp Arg Thr Val Arg Val Trp Leu Lys Arg Asp Ser Gly Gln
 50 55 60
 Tyr Trp Pro Ser Val Tyr His Ala Met Pro
 65 70

<210> 563
 <211> 403
 <212> DNA
 <213> Homo sapiens

<400> 563
 ccattggcaga cagggagctg agcggcctgc ggaccaggt gcaccagagc atggtgcccc
 60
 tgctcctaca cctgaaggac caatgcccac ctgtcgccac gggcaatgcc caccacaaga
 120
 aaagggaaggg aaaaggcctc aaccttgccc agggctggaa cccacaggag gccagggtac
 180
 ggggcagacg gatggcagca gcactgcctg agagtgggg gagctccac ggggcagcaa
 240
 gtggcgggca gaggtcttg ccattctgac tggtttctgt gaccacagtt ggctgccccg
 300
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
 360
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
 403

<210> 564
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 564
 Met Ala Asp Arg Glu Leu Ser Gly Leu Arg Thr Gln Val His Gln Ser
 1 5 10 15
 Met Val Pro Leu Leu Leu His Leu Lys Asp Gln Cys Pro Thr Val Ala

```

                20                25                30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
      35                40                45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
      50                55                60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
      65                70                75                80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
      85                90                95
Gly Leu Pro Ala Pro Pro Leu His His
      100                105

```

<210> 565

<211> 311

<212> DNA

<213> Homo sapiens

<400> 565

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ncctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
60
ccaccaccca gcgaccacag agaggctgcg cggaggacac aggagagagg gagcccacgg
120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctctctctc
180
tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttggggccg cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

```

<210> 566

<211> 101

<212> PRT

<213> Homo sapiens

<400> 566

```

Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
  1                5                10                15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
      20                25                30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
      35                40                45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
      50                55                60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
      65                70                75                80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
      85                90                95
Ala Gln Glu Ala Pro
      100

```

<210> 567

<211> 929

<212> DNA

<213> Homo sapiens

<400> 567

atcacatcgg tcgctgaacc ccgacgagcc tcaccttgtc gaaatattca tccttgagat
 60
 cagcccacgt gccgtcgacc tctacctcgg tgagggtcgc gggcgggtac caacagccga
 120
 cctcgtcctc ggctccactc atggcggcaa gttccgctgc cagtccgggg atcgtcgggg
 180
 catgggcat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgccgacgca
 240
 cggatatcagt gccgcagtaa tagagggtc gcatgaattc gaccggacaa tccagttgga
 300
 ggcatccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
 360
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacgtcg gtgagcggac
 420
 gctcccgatc ccgcccga gcatgggatg cgggctgtgc atgtctcatg aggaacagag
 480
 tgtgcatgga tccatcggtg cacttcgagg tcgccgagg tctacgatgt tggcatgccg
 540
 ttgacggatt tgggcattga tgaggcggc acctaccgcc cgaacgtccc tgaacccgat
 600
 gggttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg
 660
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg
 720
 gggatcaca actctcgggt gagcgggtga ttacatgccc cagccgctgt gaacggccca
 780
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
 840
 gtcttcgctg ctgctggcta tgcacatc gtcgtcgatc cacgtgggtca ggggtggggc
 900
 caccacacct tgacggaaaa ctgtccgga
 929

<210> 568

<211> 71

<212> PRT

<213> Homo sapiens

<400> 568

Met Pro Leu Thr Asp Leu Gly Ile Asp Glu Ala Arg Thr Tyr Arg Pro
 1 5 10 15
 Asn Val Pro Glu Pro Asp Gly Phe Asp Ser Phe Trp Ala Glu Thr Leu
 20 25 30
 Asp Glu Tyr Ser Gly Val Pro Gln Asp Leu Thr Ala Val Pro Phe Asp
 35 40 45
 Asn Arg Gln Ala Leu Ile Asp Thr Trp Asp Leu Ser Trp Val Gly Tyr
 50 55 60
 His Asn Ser Arg Val Ser Gly
 65 70

<210> 569
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 569
 ncgcaaactt caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
 60
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac
 120
 ctgctgatta cttaatgggc gaaggaacgg aacttggtga ttcaaactg gaagaactac
 180
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac
 240
 tcaaggaaca accaacagcc gttgctctct tctcggatgt tgataaacgg ccagagatta
 300
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt
 360
 cccatgtcta n
 371

<210> 570
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 570
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1 5 10 15
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
 20 25 30
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
 35 40 45
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
 50 55 60
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
 65 70 75 80
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
 85 90 95
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
 100 105 110

<210> 571
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 571
 nacgcgtatc ttcgctgggc cacaccagac gtggcattaa acgacgtcac aagaacgaca
 60
 ccgggccttg acggggccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc
 120
 gttccacact ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tcccgattgc cgtcgagggc
 240
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgcctt cggcatcacc
 300
 atcttgacgc gcatcacctt gcccggtgac gaaggttggg aagaactcac caccaaaggc
 360
 aagcccccaa gcactcgtga tgtgccccta cccgggagct aggtcgg
 407

<210> 572

<211> 100

<212> PRT

<213> Homo sapiens

<400> 572

Leu	Thr	Glu	Thr	Thr	Val	Ser	Val	Pro	Thr	Ser	Phe	Ala	Asp	Leu	Gly
1				5					10					15	
Val	Arg	Glu	Asp	Ile	Cys	Gln	Ala	Leu	Glu	Gly	Val	Gly	Ile	Val	Ser
			20					25					30		
Pro	Phe	Pro	Ile	Gln	Ala	Met	Ser	Ile	Pro	Ile	Ala	Val	Glu	Gly	Thr
		35				40					45				
Asp	Leu	Ile	Gly	Gln	Ala	Arg	Thr	Gly	Thr	Gly	Lys	Thr	Leu	Ala	Phe
	50					55					60				
Gly	Ile	Thr	Ile	Leu	Gln	Arg	Ile	Thr	Leu	Pro	Gly	Asp	Glu	Gly	Trp
65				70					75					80	
Glu	Glu	Leu	Thr	Thr	Lys	Gly	Lys	Pro	Pro	Ser	Thr	Arg	Asp	Val	Pro
				85				90						95	
Leu	Pro	Gly	Ser												
			100												

<210> 573

<211> 393

<212> DNA

<213> Homo sapiens

<400> 573

acgcgtctac cgtaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
 60
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
 120
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
 180
 ccacccgcga ggcagccgag gactttggcc gccgactggc tcacaccac gcagccgggg
 240
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg
 300
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagtgttac gctcagtgc
 360
 gcatcgaacc atatatggac agtctcgacg ctg
 393

<210> 574

<211> 124

<212> PRT

<213> Homo sapiens

<400> 574

```

Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
          20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
          35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
          50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
          65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
          85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
          100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
          115          120

```

<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

```

nntatccatg cagacatggg accaggggtct ctgagggcag gaagcaaagt gggtgagggg
60
gatgggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctgggag ccagtgggct
180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttccagg gcctcagggg
240
actgggggtca gaacagccta tggagaaagg tcaagggggc ttgggcctag gagtacaggg
300
ccaggggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
360
gatggggccg gt
372

```

<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

```

Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
          20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
          35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

```

<210> 577
 <211> 432
 <212> DNA
 <213> Homo sapiens

```

<400> 577
nagcgc aatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagc gcc gggcgcg gat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgcctct tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccgt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgaccgc
300
ccaaagcaag gcccgaaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacggttt tcggatcatc tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 578
Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1              5              10              15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20              25              30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35              40              45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50              55              60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65              70              75              80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85              90              95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100              105              110
Ala Thr Gly Ser Tyr Ala

```

115

<210> 579
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 579
 ggccccaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc
 60
 ctgctcccag ggatcaccac cttaccacagc gggccacctg ctccccggtt ccccgcggcg
 120
 cccggcccct ggctgcgcag acccctcttc agcctgaagc tgtccgacac agaggacgtc
 180
 ttctctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgcgtggt cgtgcaggcg
 240
 gccttgcccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg
 300
 tcttcacgcc cggccccggg
 320

<210> 580
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
 1 5 10 15
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro
 20 25 30
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
 35 40 45
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
 50 55 60
 Val Phe Val Gln Ala Ala Ala Arg Pro Ser Pro Arg Trp Gly Leu
 65 70 75 80
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Ser Arg Pro Ala Pro
 85 90 95

<210> 581
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 581
 nacgacggca accattcgct gtggaaggag ctgaacggcc agctcgacgt gcagtttttc
 60
 cacgtcggca tgggttcaa gacgccagta cgcattcaca gcgtcgaccc caagaccgcg
 120
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggag
 180
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgcgggaa
 240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca
 300
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
 360
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
 419

<210> 582
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 582
 Xaa Asp Gly Asn His Ser Leu Trp Lys Glu Leu Asn Gly Gln Leu Asp
 1 5 10 15
 Val Gln Phe Phe His Val Gly Met Gly Phe Lys Thr Pro Val Arg Met
 20 25 30
 His Ser Val Asp Pro Lys Thr Arg Glu Ala Arg Glu Val His Phe Arg
 35 40 45
 Pro Ser Leu Phe Asn Tyr Ala Lys Thr Thr Val Asp Thr Lys Gln Leu
 50 55 60
 Thr Gly Asp Leu Gly Phe Ser Gly Phe Lys Leu Phe Lys Ala Pro Glu
 65 70 75 80
 Leu Asp Arg His Asp Val Leu Ser Phe Leu Gly Ala Ser Tyr Phe Arg
 85 90 95
 Ala Val Asp Ala Thr Arg Gln Tyr Gly Leu Ser Ala Arg Gly Leu Ala
 100 105 110
 Ile Asp Thr Tyr Ala Lys Lys Arg Glu Glu Phe Pro Asp Phe Thr Gln
 115 120 125
 Phe Trp Phe Glu Thr Pro Ser Lys Asp Pro Arg
 130 135

<210> 583
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 583
 cttttgatca atgctgatgg cacgaagcta tcgaaaaggt cgggtgatgt ccgcgtagct
 60
 gattatatgg agcagggatg ggagccggag acgctggtga acctagttgc cctcacgggc
 120
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc
 180
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt
 240
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag
 300
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
 360
 tcagatgatt atatcctgcy cgtcgtaaca ctgggacccc aacgcgt
 407

<210> 584

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 584
 Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
 1 5 10 15
 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
 20 25 30
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
 35 40 45
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
 50 55 60
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
 65 70 75 80
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
 85 90 95
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
 100 105 110
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
 115 120 125
 Val Thr Leu Gly Pro Gln Arg
 130 135

<210> 585
 <211> 502
 <212> DNA
 <213> Homo sapiens

<400> 585
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 240
 caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgccgat
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 catectggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt
 360
 cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc
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 480
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 502

<210> 586
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 586

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 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
 20 25 30
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
 35 40 45
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
 50 55 60
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
 65 70 75 80
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
 85 90 95
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
 100 105 110
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
 115 120 125
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
 130 135 140
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
 145 150 155 160
 Gly Asp Asp Ala Ser Glu Ala
 165

<210> 587

<211> 746

<212> DNA

<213> Homo sapiens

<400> 587

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 tgcctgcagc gctctgaccc ggccctctac ggggggtgtcc aggcgcctt ccctggcgcc
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 420
 actgtggcag gctatatctg caggtgccca gagacctggg gtgggcgcga ctgttctgtg
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 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc
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 720

actcgcaatg acaccaagga aagctt
746

<210> 588
<211> 248
<212> PRT
<213> Homo sapiens

<400> 588
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Gly Tyr Ser Gly Glu Leu Cys Glu Val Asp Glu Asp Glu Cys Ala Ser
20 25 30
Ser Pro Cys Gln His Gly Gly Arg Cys Leu Gln Arg Ser Asp Pro Ala
35 40 45
Leu Tyr Gly Gly Val Gln Ala Ala Phe Pro Gly Ala Phe Ser Phe Arg
50 55 60
His Ala Ala Gly Phe Leu Cys His Cys Pro Pro Gly Phe Glu Gly Ala
65 70 75 80
Asp Cys Gly Val Glu Val Asp Glu Cys Ala Ser Arg Pro Cys Leu Asn
85 90 95
Gly Gly His Cys Gln Asp Leu Pro Asn Gly Phe Gln Cys His Cys Pro
100 105 110
Asp Gly Tyr Ala Gly Pro Thr Cys Glu Glu Asp Val Asp Glu Cys Leu
115 120 125
Ser Asp Pro Cys Leu His Gly Gly Thr Cys Ser Asp Thr Val Ala Gly
130 135 140
Tyr Ile Cys Arg Cys Pro Glu Thr Trp Gly Gly Arg Asp Cys Ser Val
145 150 155 160
Gln Leu Thr Gly Cys Gln Gly His Thr Cys Pro Leu Ala Ala Thr Cys
165 170 175
Ile Pro Ile Phe Glu Ser Gly Val His Ser Tyr Val Cys His Cys Pro
180 185 190
Pro Gly Thr His Gly Pro Phe Cys Gly Gln Asn Thr Thr Phe Ser Val
195 200 205
Met Ala Gly Ser Pro Ile Gln Ala Ser Val Pro Ala Gly Gly Pro Leu
210 215 220
Gly Leu Ala Leu Arg Phe Arg Thr Thr Leu Pro Ala Gly Thr Leu Ala
225 230 235 240
Thr Arg Asn Asp Thr Lys Glu Ser
245

<210> 589
<211> 381
<212> DNA
<213> Homo sapiens

<400> 589
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120
gtgggttggtg taacttcagc tttagggtcag cagccttcca tttccagttt ggctcaaccc
180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttcagg ggcaccacca
 240
 ccccaacagt tacagtatgg acaacagcaa ccaatgggtt ctacacagat ggccccaggc
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 360
 caaacagcaa tgtcctccgg a
 381

<210> 590
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 590
 Ile Ser Gln Val Gln Leu Gln Ser Gln Glu Leu Ser Tyr Gln Gln Lys
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 Gln Gly Leu Gln Pro Val Pro Leu Gln Ala Thr Met Ser Ala Ala Thr
 20 25 30
 Gly Ile Gln Pro Ser Pro Val Asn Val Val Gly Val Thr Ser Ala Leu
 35 40 45
 Gly Gln Gln Pro Ser Ile Ser Ser Leu Ala Gln Pro Gln Leu Pro Tyr
 50 55 60
 Ser Gln Ala Ala Pro Pro Val Gln Thr Pro Leu Pro Gly Ala Pro Pro
 65 70 75 80
 Pro Gln Gln Leu Gln Tyr Gly Gln Gln Gln Pro Met Val Ser Thr Gln
 85 90 95
 Met Ala Pro Gly His Val Lys Ser Val Thr Gln Asn Pro Ala Ser Glu
 100 105 110
 Tyr Val Gln Gln Gln Pro Ile Leu Gln Thr Ala Met Ser Ser Gly
 115 120 125

<210> 591
 <211> 684
 <212> DNA
 <213> Homo sapiens

<400> 591
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 180
 naaaaagcgc gcctgcgtca ggaagccgaa gccctggccc agcgcgatgca gttcgagcac
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 gccaccgcgc cggtagcga cagacagaag ctggggccgta acgaactgtg ctactgcggt
 360
 tcgggcaaga agtacaagca ctgccacggt cagatcagct aaggtcttta ccggatactg
 420
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<211> 133
<212> PRT
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<210> 593
<211> 615
<212> DNA
<213> Homo sapiens
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725

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<210> 594
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 594
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 Gly Ser Gln Thr Cys Glu Thr Val Thr Val Glu Arg Arg Gly Gly Leu
 20 25 30
 Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly
 35 40 45
 Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr
 50 55 60
 Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp
 65 70 75 80
 Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu
 85 90 95
 Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu
 100 105 110
 Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg
 115 120 125
 Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser
 130 135 140
 Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met
 145 150 155 160
 Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu
 165 170 175
 Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe
 180 185 190
 Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg
 195 200 205

<210> 595
 <211> 303
 <212> DNA
 <213> Homo sapiens

<400> 595
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 120
 gcctgtgccc gcaaccgccc cgaaattctc tcctggcac cgtgtccgct ttacggagcc
 180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgctg tcacaggca
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 300
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 303

<210> 596
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 596
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 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val
 35 40 45
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln
 50 55 60
 Lys His Gly Thr Cys Leu Ser Ser Gly Lys Ser Ser Lys Ser Gly Trp
 65 70 75 80
 Asp Gln Gly Pro Arg Asp Leu Val
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<210> 597
 <211> 2709
 <212> DNA
 <213> Homo sapiens

<400> 597
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 aagaaccaca tggaggagaa gacctacgaa tgtaaagaat gcgggaaatc ctttggcgat
 120
 ctctgtgtccc ggaggaaaca catgaggatt cacatcgtca agaaacccgt ggaatgtcgg
 180
 cagtgcggga agaccttccg aaaccagtcc atccttaaga ctcacatgaa ctctcacact
 240
 ggagagaaac catacgggtg cgatctctgc gggaaagctt tcagcgcgag ttcaaacctc
 300
 accgcacaca ggaagataca cacgcaagag agacgctacg aatgcgccgc ctgcgggaaa
 360
 gtcttcggtg actatttatc ccggcggagg cacatgagcg ttcaccttgt aaagaaacga
 420
 gttgagtgtg ggcattgtgg caaggccttc aggaaccagt caacgctgaa gacgcacatg
 480
 cgaagccaca cgggggagaa accgtacgaa tgcgatcact gtgggaaggc cttcagcata
 540
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 660

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1320
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1380
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1740
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1860
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1980
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2040
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2160
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2220
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2280

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 2340
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 2520
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 2580
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 2709

<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

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			20				25						30		
Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met
		35					40					45			
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys
		50				55					60				
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr
65					70					75				80	
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala
				85				90						95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg
			100					105					110		
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg
		115					120					125			
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg
		130				135					140				
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met
145					150					155				160	
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys
			165					170					175		
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr
			180				185						190		
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp
		195					200					205			
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu
		210				215					220				
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu
225						230					235				240

<210> 599
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 599
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 120
 caggcatgtt tgccggggccg catcccttgc acttgcagtc cgtggcctat cggccgaggg
 180
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta
 240
 tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgtattc
 300
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<210> 600
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 600
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 1 5 10 15
 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Ser Asp Glu Pro His
 20 25 30
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
 35 40 45
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
 50 55 60
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
 65 70 75 80
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
 85 90 95
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
 100 105 110

<210> 601
 <211> 421
 <212> DNA
 <213> Homo sapiens

<400> 601
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 ccgcgctcca ccattttgat ggacggcgtc ccgctggcgg tcgcgcctta cggccagccc
 120
 cagctgtcga tggccccgct gtctatcggg aatctgcaat cggtaggagc ggtgcgcggc
 180
 ggcggcgcgg tgcgctacgg gccgcagaac gtccggcgcg tgatcaactt cgttaccgca
 240

gacattccca aaacgtttgg cgggtgccgc agcgtacaaa ccagggtgc cagccacggc
 300
 ggcctgaaga ccctgaccag cgcctccgtg ggcggcaccg cagacaacgg cctcggcgcc
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 421

<210> 602
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 602
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 Ser Arg Leu Ser Pro Arg Ser Thr Ile Leu Met Asp Gly Val Pro Leu
 20 25 30
 Ala Val Ala Pro Tyr Gly Gln Pro Gln Leu Ser Met Ala Pro Leu Ser
 35 40 45
 Ile Gly Asn Leu Gln Ser Val Asp Val Val Arg Gly Gly Gly Ala Val
 50 55 60
 Arg Tyr Gly Pro Gln Asn Val Gly Gly Val Ile Asn Phe Val Thr Arg
 65 70 75 80
 Asp Ile Pro Lys Thr Phe Gly Gly Ala Ala Ser Val Gln Thr Gln Gly
 85 90 95
 Ala Ser His Gly Gly Leu Lys Thr Leu Thr Ser Ala Ser Val Gly Gly
 100 105 110
 Thr Ala Asp Asn Gly Leu Gly Ala Glu Leu Leu Tyr Ser Gly Leu His
 115 120 125
 Gly Gln Gly Tyr Arg Asp Asn Asn Asp Asn Thr Asp
 130 135 140

<210> 603
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 603
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 gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcgtt
 180
 ggcaaaccgg aagacctcgt agagggtgtg cgccgcggtg tggacatgtt cgattgcgtg
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 300
 cgtaacgcg
 309

<210> 604

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 604
 Xaa Gly Gly Met His Glu Ser Leu Arg Lys Arg Ser Leu Glu Gly Leu
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 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
 20 25 30
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
 35 40 45
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
 50 55 60
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
 65 70 75 80
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
 85 90 95
 Val Leu Lys Ile Arg Asn Ala
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<210> 605
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 605
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 actggcccaa ggctgggcta tagtcagggtg catagtactt ggtgaagtag cgtacgtccg
 120
 caccacatc acatttcagt accttggcta tcttcaatcg gaaaaaaga ttggagtaaa
 180
 tggttagttt tggtaatggc aacgccgttt gactggaaga gttttggaag gtaatgaccg
 240
 attcccagtg caaagggtccc catgctacat cctgcgacaa tgaggccgtt agcacgttta
 300
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 428

<210> 606
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 606
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 20 25 30
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
  50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
  65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100              105              110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115              120              125
Asn Tyr Pro Ile Val Asn Ala
      130              135

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<210> 607
 <211> 366
 <212> DNA
 <213> Homo sapiens

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<400> 607
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gacattgtgt gtaaaggatt ctttagaaaa ttggaaaacg tagtgaccgg agtcaatttg
  120
gtttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
  180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
  240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
  300
ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccag
  360
gacgcg
  366

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<210> 608
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<400> 608
Asp His Asp Glu Leu Trp Ala Tyr Thr Tyr Glu Asn Val Met Ala Leu
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Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
  65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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100 105 110
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala
 115 120
 <210> 609
 <211> 291
 <212> DNA
 <213> Homo sapiens
 <400> 609
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 tgggtcgggtt ggaacgagtc cgtcatgagc ccggtcgcca tggacgactc cagcagtcgg
 120
 taccagcctt ggaagcagga ccccccacgcg acggaatcgc cggtttccaa gtcgtcgccc
 180
 ccgaagcctc aaacttcccc cgccccgtac gccggggccgg ctccgaagac accggccaca
 240
 cctggaccat ctggggcggg ggcgcgcgcg tggtgggtggc gggtaggagcc g
 291

<210> 610
 <211> 69
 <212> PRT
 <213> Homo sapiens
 <400> 610
 Met Ser Pro Val Ala Met Asp Asp Ser Ser Ser Pro Tyr Pro Ala Trp
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 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro
 20 25 30
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
 35 40 45
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
 50 55 60
 Trp Arg Val Glu Pro
 65

<210> 611
 <211> 393
 <212> DNA
 <213> Homo sapiens
 <400> 611
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 tgtacccaag tagagaggtg ttcatgcca cacagtccgg aagaaaagaa gcaagcactg
 120
 acgcgcacaa ggcgcacaa aggtcaggta gcgactcttg agcaagcgct tgatgcaggt
 180
 gcgaaatgtc ctgcaattct tcagcagctt gcggccgttc gtggcgagct caacggattg
 240
 atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc
 300

gattcgcaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag
 360
 aggcaccagg gtgtcctcgg tgagggcaaa ttt
 393

<210> 612
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 612
 Xaa Ile Leu Cys Arg Phe Ser Val Ala Tyr Thr Met Gly Glu Tyr Cys
 1 5 10 15
 Ile Met Arg Arg Cys Thr Gln Val Glu Arg Cys Ser Met Pro His Ser
 20 25 30
 Pro Glu Glu Lys Lys Gln Ala Leu Thr Arg Ile Arg Arg Ile Lys Gly
 35 40 45
 Gln Val Ala Thr Leu Glu Gln Ala Leu Asp Ala Gly Ala Lys Cys Pro
 50 55 60
 Ala Ile Leu Gln Gln Leu Ala Ala Val Arg Gly Ala Val Asn Gly Leu
 65 70 75 80
 Met Ala Thr Val Leu Glu Ser Tyr Leu Arg Glu Glu Phe Pro Ser Ser
 85 90 95
 Glu Ile Arg Ser Asp Ser Gln Asn Lys Ser Ile Asp Glu Thr Ile Ser
 100 105 110
 Ile Val Arg Ser Tyr Leu Arg
 115

<210> 613
 <211> 567
 <212> DNA
 <213> Homo sapiens

<400> 613
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 120
 acactggata aagagagtgg agaaagcctc agagtgttga gtgtcaaag cattttttac
 180
 tagaaattca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga
 240
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctgggtca atgactgggt
 300
 agacacccaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt
 360
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga
 420
 tttatgtggc tatttgagg aagaagagga aagtaccacc gttcaaaaat ttatagacca
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 tctgctccat aaaaatgtgg tagattctgc aatgatggaa gatcttgga ggaaggaaaa
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 567

<210> 614
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 614
 Met Leu Leu Ala Pro Gln Gly Arg Ser Phe Ser Lys Lys Arg Met Gly
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 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr
 20 25 30
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala
 35 40 45
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
 50 55 60
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
 65 70 75 80
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
 85 90 95
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
 100 105 110
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
 115 120 125
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
 130 135 140
 Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu
 145 150 155 160
 Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg
 165 170 175
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp
 180 185

<210> 615
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 615
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 ggccatgaac gggccctagc gagggccgga ctgcggccccg tggccggatg cgacgaggcg
 120
 gggcggggcg cgtgtgcagg gccattggta gccgcagctg tcattcttga tgatcgaga
 180
 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc
 240
 ctgtttaacg tcatcatgga taaagctttg gcagtgtcgt gggtagctgt agaagccgac
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 gaatgcgatc ggttggggat gcaggaggca gatatcagcg gcttgaggcg tgccgtggtg
 360
 aggctgggag ttgaaccggg ctacgtgctg tcggacggtt tcccggtcga cggactgacg
 420
 gttcccgatc tgggaatgtg gaagggcgat tcagtgtgtg cgtgtgtggc agctgcctcc
 480

atcgtggcca aagtggccag ggatcgcatc atgatcgcta tggacgccga gattcctggg
 540
 tacgattttg cgggtgcacaa ggggtacgcg acagccttac accagcgctcg tctgaaggag
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 660
 cattcatcat gagtgccgaa gatct
 685

<210> 616
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 616
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 Ala Arg Ala Gly Leu Gly Pro Val Ala Gly Cys Asp Glu Ala Gly Arg
 20 25 30
 Gly Ala Cys Ala Gly Pro Leu Val Ala Ala Ala Val Ile Leu Asp Asp
 35 40 45
 Arg Arg Ser Gly Arg Ile Ala Gly Leu Ala Asp Ser Lys Thr Leu Ser
 50 55 60
 Ala Ala Lys Arg Glu Ala Leu Phe Asn Val Ile Met Asp Lys Ala Leu
 65 70 75 80
 Ala Val Ser Trp Val Arg Val Glu Ala Asp Glu Cys Asp Arg Leu Gly
 85 90 95
 Met Gln Glu Ala Asp Ile Ser Gly Leu Arg Arg Ala Val Val Arg Leu
 100 105 110
 Gly Val Glu Pro Gly Tyr Val Leu Ser Asp Gly Phe Pro Val Asp Gly
 115 120 125
 Leu Thr Val Pro Asp Leu Gly Met Trp Lys Gly Asp Ser Val Cys Ala
 130 135 140
 Cys Val Ala Ala Ala Ser Ile Val Ala Lys Val Ala Arg Asp Arg Ile
 145 150 155 160
 Met Ile Ala Met Asp Ala Glu Ile Pro Gly Tyr Asp Phe Ala Val His
 165 170 175
 Lys Gly Tyr Ala Thr Ala Leu His Gln Arg Arg Leu Lys Glu Leu Gly
 180 185 190
 Pro Ser Arg Gln His Arg Met Ser Tyr Ala Asn Val Arg Arg Ala Ala
 195 200 205
 Arg Leu His Ser Ser
 210

<210> 617
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 617
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 gctcgtttcc cggcttcaac cccatcgctc agctgtcgct gtcgttccac aacctcgctc
 120

tcggcgccaa cggccagcgc caggccatgt tcctcgaaaa cgtttccggc cttcccggag
 180
 cgaatectcc gaaacttcga cctgtcccaa caagactctg cactcgtgat ttcataaagc
 240
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 337

<210> 618

<211> 112

<212> PRT

<213> Homo sapiens

<400> 618

Xaa	Thr	Cys	Leu	Ala	Arg	Gly	Thr	Arg	Gly	Ser	Trp	Ser	Arg	Lys	Cys
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Gly	Arg	Ala	Thr	Ala	Arg	Phe	Pro	Ala	Ser	Thr	Pro	Ser	Ser	Ser	Cys
			20					25				30			
Arg	Cys	Arg	Ser	Thr	Thr	Ser	Ser	Ser	Ala	Pro	Thr	Ala	Ser	Ala	Arg
		35				40					45				
Pro	Cys	Ser	Ser	Lys	Thr	Phe	Pro	Ala	Phe	Pro	Glu	Arg	Ile	Leu	Arg
	50				55					60					
Asn	Phe	Asp	Leu	Ser	Gln	Gln	Asp	Ser	Ala	Leu	Val	Ile	Ser	Ser	Ser
65					70					75				80	
Ala	Ala	Thr	Ser	Cys	Gln	Ser	Arg	Trp	Pro	Arg	Ser	Ser	Ser	Val	Ala
			85					90						95	
Ala	Ser	Ala	Ser	Ser	Arg	Ser	Ser	Arg	Trp	Arg	Thr	Arg	Arg	Arg	Arg
			100					105						110	

<210> 619

<211> 425

<212> DNA

<213> Homo sapiens

<400> 619

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 120
 gttttatagc atctttgtca gaaggcaaac ctgccaaacc agatgaatcg atgccactct
 180
 caaacttgct caaatgttca attaaatcat ccaagttgtg gccatgctta ccgcttccag
 240
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 300
 caatagaagc ccgctcattt ttaaagctca gtatgtcact aatgcctttt tcgaagtggc
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 420
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 425

<210> 620

<211> 137
 <212> PRT
 <213> Homo sapiens

<400> 620

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Met Ala Ser His Ser Asn Gln Ser Ala Ser Asn Met Ala Gln Gly Ile
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Trp Ser His Phe Glu Lys Gly Ile Ser Asp Ile Leu Ser Phe Lys Asn
      20           25           30
Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys
      35           40           45
Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly
      50           55           60
His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly
      65           70           75           80
Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile
      85           90           95
Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu
      100          105          110
Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu
      115          120          125
Glu His Lys Ile Gly Ile Lys Asn Ala
      130          135

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<210> 621
 <211> 453
 <212> DNA
 <213> Homo sapiens

<400> 621

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atcgctcgata accatctcgt gagecgtggat gtccccgccg aggtcgcagg gcgcgccatg
120
gtcgttgagg aactcgacat gttccccgtc gaatgcgtcg tgcgggggcta cctcaccggt
180
tcagggtggg ccgaatatca gcgcaaccag gccgtgtgcg gaatccgcct tcccagaggg
240
ctgcagaatg ggtccccggt cgaagagccc attttcaccc cggcaattaa ggccccgcag
300
ggagaacatg acgagaacat cgactatcta cgcttgtag aactcgtcgg tccngatgn
360
tcagcgcagc tgcattgacct ttcgctgcgg gtctaccagc gtgcagagga gatcgtcgg
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453

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<210> 622
 <211> 151
 <212> PRT
 <213> Homo sapiens

<400> 622

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Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

```

```

      1           5           10           15
Gln Leu Ala Asp Ile Val Asp Asn His Leu Val Ser Val Asp Val Pro
      20           25           30
Ala Glu Val Ala Gly Arg Ala Met Val Val Glu Glu Leu Asp Met Phe
      35           40           45
Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
      50           55           60
Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
      65           70           75           80
Leu Gln Asn Gly Ser Arg Leu Glu Glu Pro Ile Phe Thr Pro Ala Ile
      85           90           95
Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
      100          105          110
Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
      115          120          125
Leu Arg Val Tyr Gln Arg Ala Glu Glu Ile Ala Arg Lys Arg Gly Ile
      130          135          140
Leu Leu Ala Asp Thr Lys Leu
      145          150

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<210> 623

<211> 345

<212> DNA

<213> Homo sapiens

<400> 623

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acgcgtccag tatgtccacg gaggacatgc ttgacctcga ctggaacgtc tctactacg
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cgaggaacta tcaggccgcg caatcagttg tggcgaaatt cgacgcgggc accattgccc
120
aagccgaaga cctgccacct gacgacaccc acacggggggc ggaactggta aagagcgtgg
180
tcaacagcat cacctgtgtg tcaccctgtg acatcgaaga tttcaccacc atagagatcc
240
aggggctggg actgcactgt gtcaggctct gggcgcttgg gctgctcgcc ctgtcactgc
300
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345

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<210> 624

<211> 111

<212> PRT

<213> Homo sapiens

<400> 624

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Met Ser Thr Glu Asp Met Leu Asp Leu Asp Ser Asn Val Ser Tyr Tyr
      1           5           10           15
Ala Arg Asn Tyr Gln Ala Ala Gln Ser Val Val Ala Lys Phe Asp Ala
      20           25           30
Gly Thr Ile Ala Gln Ala Glu Asp Leu Pro Pro Asp Asp Thr His Thr
      35           40           45
Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
      50           55           60
Pro Leu Tyr Ile Glu Asp Phe Thr Thr Ile Glu Ile Gln Gly Leu Gly

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cgcgagact gaggtcctga caagegataa catttctgat aaagaccga tcttactgca
120
atctctagcg tcctcttttt tggtgctgct ggtttctcca gacctcgct cctctcgatt
180
gctctctcgc cttcctatct cttttttttt tttttaaaca aaaaacaaca cccctcccc
240
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420
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660
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Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile
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Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
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Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
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Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
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Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
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<210> 636

<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

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Tyr	Leu	Leu	Asp	Val	Val	Asp	Ser	Glu	Glu	Gln	Asp	Met	Ala	Leu	Asn
		35				40					45				
Ile	His	Ala	Phe	Ser	Ala	Gly	Leu	Gly	Gly	Ala	Ile	Gly	Tyr	Val	Leu
	50					55				60					
Gly	Gly	Leu	Asp	Trp	Thr	Gln	Thr	Phe	Leu	Gly	Ser	Trp	Phe	Arg	Thr
65				70				75						80	
Gln	Asn	Gln	Val	Leu	Phe	Phe	Phe	Ala	Ala	Ile	Ile	Phe	Thr	Val	Ser
			85					90						95	
Val	Ala	Leu	His	Leu	Phe	Ser	Ile	Asp	Glu	Glu	Gln	Tyr	Ser	Pro	Gln
			100					105					110		
Gln	Glu	Arg	Ser	Ala	Glu	Glu	Pro	Gly	Ala	Leu	Asp	Gly	Gly	Glu	Pro
		115					120					125			
His	Gly	Val	Pro	Ala	Phe	Pro	Asp	Glu	Val	Gln	Ser	Glu	His	Glu	Leu
	130					135				140					
Ala	Leu	Asp	Tyr	Pro	Asp	Val	Asp	Ile	Met	Arg	Ser	Lys	Ser	Asp	Ser
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Ala	Leu	His	Val	Pro	Asp	Thr	Ala	Leu	Asp	Leu	Glu	Pro	Glu	Leu	Leu
			165					170						175	
Phe	Leu	His	Asp	Ile	Glu	Pro	Ser	Ile	Phe	His	Asp	Ala	Ser	Tyr	Pro
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Ala	Thr	Pro	Arg	Ser	Thr	Ser	Gln	Glu	Leu	Ala	Lys	Thr	Lys	Leu	Pro
		195					200					205			
Arg	Leu	Ala	Thr	Phe	Leu	Lys	Glu	Ala	Ala	Lys	Glu	Asp	Glu	Thr	Leu
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Leu	Asp	Asn	His	Leu	Asn	Glu	Ala	Lys	Val	Pro	Asn	Gly	Ser	Gly	Ser
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Pro	Thr	Lys	Asp	Ala	Leu	Gly	Gly	Tyr	Thr	Arg	Val	Asp	Thr	Lys	Pro
			245					250						255	
Ser	Ala	Thr	Ser	Ser	Ser	Met	Arg	Arg	Arg	Arg	His	Ala	Phe	Arg	Arg
			260					265					270		
Gln	Ala	Ser	Ser	Thr	Phe	Ser	Tyr	Tyr	Gly	Lys	Leu	Gly	Ser	His	Cys
		275					280					285			
Tyr	Arg	Tyr	Arg	Arg	Ala	Asn	Ala	Val	Val	Leu	Ile	Lys	Pro	Ser	Arg

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Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg				
305		310		315
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser				320
	325		330	335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met				
	340		345	350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu				
	355		360	365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met				
	370		375	380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr				
385		390		395
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu				400
	405		410	415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys				
	420		425	430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly				
	435		440	445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn				
	450		455	460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met				
465		470		475
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile				480
	485		490	495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly				
	500		505	510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu				
	515		520	525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg				
	530		535	540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr				
545		550		555
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu				560
	565		570	575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly				
	580		585	590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly				
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Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val				
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<210> 637

<211> 370

<212> DNA

<213> Homo sapiens

<400> 637

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<210> 638
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 638
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 35 40 45
 Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly
 50 55 60
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 Ile Val Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu
 85 90 95
 Ser Ala Met

<210> 639
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 639
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<210> 640
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 640

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Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu
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Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly
      20           25           30
Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
      35           40           45
Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
      50           55           60
Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
      65           70           75           80
Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn Pro Asp Trp
      85           90           95
Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe
      100           105           110

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<210> 641

<211> 491

<212> DNA

<213> Homo sapiens

<400> 641

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<210> 642

<211> 163

<212> PRT

<213> Homo sapiens

<400> 642

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Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His
 1           5           10           15
His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly
      20           25           30
Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
      35           40           45
Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```

```

      50              55              60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65              70              75              80
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      85              90              95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100             105             110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115             120             125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130             135             140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145             150             155             160
Leu Gln Cys

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<210> 643

<211> 628

<212> DNA

<213> Homo sapiens

<400> 643

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tggtttgtcc gcaccaagcc caccaagtcc agcccctcac ggcagggctg ggtgtcacca
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<210> 644

<211> 209

<212> PRT

<213> Homo sapiens

<400> 644

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Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1           5           10           15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

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```

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Leu Asp Ala Ala His Pro Leu Arg Trp Leu Val Arg Thr Lys Pro Thr
      35      40      45
Lys Ser Ser Pro Ser Arg Gln Gly Trp Val Ser Pro Ala Tyr Leu Asp
      50      55      60
Arg Arg Leu Lys Leu Ser Pro Glu Trp Gly Ala Ala Glu Ala Pro Glu
65      70      75      80
Phe Pro Gly Glu Ala Val Ser Glu Asp Glu Tyr Lys Ala Arg Leu Ser
      85      90      95
Ser Val Ile Gln Glu Leu Leu Ser Ser Glu Gln Ala Phe Val Glu Glu
      100      105      110
Leu Gln Phe Leu Gln Ser His His Leu Gln His Leu Glu Arg Cys Pro
      115      120      125
His Val Pro Ile Ala Val Ala Gly Gln Lys Ala Val Ile Phe Arg Asn
      130      135      140
Val Arg Asp Ile Gly Arg Phe His Ser Ser Phe Leu Gln Glu Leu Gln
145      150      155      160
Gln Cys Asp Thr Asp Asp Val Ala Met Cys Phe Ile Lys Asn Gln
      165      170      175
Ala Ala Phe Glu Gln Tyr Leu Glu Phe Leu Val Gly Arg Val Gln Ala
      180      185      190
Glu Ser Val Val Val Ser Thr Ala Ile Gln Glu Phe Tyr Lys Lys Tyr
      195      200      205
Ala

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<210> 645

<211> 417

<212> DNA

<213> Homo sapiens

<400> 645

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120
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417

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<210> 646

<211> 95

<212> PRT

<213> Homo sapiens

<400> 646

Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

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Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
      20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
      35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
      50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
      85           90           95

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<210> 647

<211> 421

<212> DNA

<213> Homo sapiens

<400> 647

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120
cggtagccat gcgtggcgaa ctcccttggc atgggaaaat cgggtgaggc caacgggcac
180
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240
ggatttccgt tgaatgaagg caagaagtcg ggcacgcac cacctgctac cgctcgggtg
300
tacgatagcc gcggcgccac caggttggtt acattccaaa cgcaacgcag gaaccgcgcat
360
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420
c
421

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<210> 648

<211> 90

<212> PRT

<213> Homo sapiens

<400> 648

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Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
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Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
      20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
      35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
      50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
      85           90

```

<210> 649
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 649
 cgcaacatgc ataaacacat gtgctcctcc gagactcagc tacttccttt gccctctctg
 60
 gacctcagtg tccaggcttg tgcatttagg ggctcagggt tgggctctgt gcctatgagc
 120
 cagtctatgt gtgcactgtc tgtctgtctg tccgtctgcc agcaaccttc aaggccccag
 180
 gaggggaagg caccaatgga aggtgggggc agggaaggag gtagcgttga caagttccaa
 240
 tgtctggctt tccctcctgg aaaccccgag ctggggctgg ccccccttc ccttcctgtc
 300
 tctctcgctc aagcacgtcc cttctaagag cccctctctg cagacgcccc cagtggaacc
 360
 aagcctagat tcgctgccaa gaaggccgac attttttaga cttgccacgt taaaggggcc
 420
 tgacaggca cgactcaaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa
 480
 cccgaaacac acaaagacac ggttggacac agcgccacc tgtgcacaca ggaggtagca
 540
 catggagcgc atctgacccc ggg
 563

<210> 650
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 650
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
 1 5 10 15
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu
 20 25 30
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
 35 40 45
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
 50 55 60
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
 65 70 75 80
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
 85 90 95
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
 100 105

<210> 651
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac
 60
 cataatggag tccatggggg caaagttatc tcctggagct cagcagttga tggatatggg
 120
 taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttgggcaa
 180
 ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia
 240
 gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
 300
 cttacaagcg tacattgata aaagtaaca actgcctggg ggagagaatt c
 351

<210> 652

<211> 95

<212> PRT

<213> Homo sapiens

<400> 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1				5				10						15	
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
			20					25					30		
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
		35				40					45				
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
	50				55					60					
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65				70				75						80	
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
			85					90					95		

<210> 653

<211> 399

<212> DNA

<213> Homo sapiens

<400> 653

nncccggtg gggctggggg ggggccagca tcagaggagg acatgaccaa gctgtgcaac
 60
 caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgtctca
 120
 cactcttctc ctggagaggg agcgagcccc caaatgttcc aactgtgtc cccagggcc
 180
 ccctctgccc gccctccctg tcgagtctct cctacaactc cacttaatgg gggctctggc
 240
 tcccttcccc cagaaccacc ctgagtttcc caggccttcc ccactctagc aggccttggg
 300
 gggcttttcc cccaaggct tgctgaccca gtcccttctg ggggcagtag cagccccgt
 360
 ttccctccaa ggggcaatgc cccctctcca gccccacct
 399

<210> 654

<211> 133
 <212> PRT
 <213> Homo sapiens

<400> 654

```

Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
 1           5           10           15
Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
          20           25           30
Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
          35           40           45
Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
          50           55           60
Pro Pro Cys Arg Val Pro Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
65           70           75           80
Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
          85           90           95
Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
          100          105          110
Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
          115          120          125
Ser Pro Ala Pro Pro
          130

```

<210> 655
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 655

```

tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
60
gatgagggtgg gaagtgcact gggatctggg ggaagaagcc cgggggttcaa gactcagcta
120
ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
180
gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
240
cttgacaaat gcaagggtgcc atacaaacag gaactgcaca atctcaccgc cgggcctact
300
cagcattgtt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
360
ttgttttc
368

```

<210> 656
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 656

```

Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
 1           5           10           15
Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

```

```

      20      25      30
Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
      35      40      45
Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
      50      55      60
Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
65      70      75      80
Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
      85      90      95
His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
      100      105

```

<210> 657
 <211> 330
 <212> DNA
 <213> Homo sapiens

```

<400> 657
gtcgaccacg gcatgaaaaa gccgggggatg atcctcatca acaaccctg gggcgagtec
60
aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cgggtgctgag
120
cgtattcagg acagcgacct ggacgtggtg ccgcaattga cccgcctga aaaacgccgg
180
tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtcctt
240
ggaccgcatg ggttgggacg tgctgtggt gtctcactgg gggccggccg gnggtcgctt
300
tggcgagctg gcggggccta acgcttctcg
330

```

<210> 658
 <211> 102
 <212> PRT
 <213> Homo sapiens

```

<400> 658
Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
 1      5      10      15
Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
      20      25      30
Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
      35      40      45
Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
      50      55      60
Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
65      70      75      80
Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
      85      90      95
Trp Arg Ala Gly Gly Ala
      100

```

<210> 659
 <211> 1505

<212> DNA

<213> Homo sapiens

<400> 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tcctcctgtc catcctgggg
60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac
120
aaccctgtca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccage catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcatc gtcctgggtg ccattggcct cctggtatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgcca agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct
420
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tgggtgcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cactactaatt gggggtgtga tgatgtgcat cgctgcggg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt
660
gttgccctaca agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgcccgacac gaggacgagg tacaatctta tccttccaag
780
cacgactatg tgtaatgctc taagacctct cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga
900
agttagaaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg
960
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
atcttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat tttgatgatt tagacagact cccctctctc ctcttagtca
1140
ataaacccat tgatgatcta tttccagct tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctggt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccagatct cggttttctt aactgtgat cttaaaagt accaaaccaa agtcattttc
1380
agtttagggc aaccaaacct ttctactgct gttgacatct tcttattaca gcaacacat
1440
tctaggagtt tcctgagctc tccactggag tcctcccctt ctgtcgtctt ctgcagcgg
1500

tacc

1505

<210> 660

<211> 261

<212> PRT

<213> Homo sapiens

<400> 660

```

Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
 1           5           10           15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
          20           25           30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
          35           40           45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
          50           55           60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
          65           70           75           80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
          85           90           95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
          100          105          110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
          115          120          125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
          130          135          140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
          145          150          155          160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
          165          170          175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
          180          185          190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
          195          200          205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
          210          215          220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
          225          230          235          240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
          245          250          255
Lys His Asp Tyr Val
          260

```

<210> 661

<211> 451

<212> DNA

<213> Homo sapiens

<400> 661

```

nnacgcgtgt agtttgtgta tcggcgcgga actcgccgcg tctgatctcg aggagcttcc
60
cccatggacg agattttaac cttgcttgcc ggaggcggtg acgacgagcc agagtggcat
120

```

gacaaggcat tatgtgcca gactgatccg gaggcattct tccctgaaa ggggtggatcc
 180
 acccgtgagg ccaagegcat ctgtgagtc tgtgaggtcc gccaggagt cttggagtac
 240
 gcccttgca atgacgagag gttcggaaac tggggcggat tgtccgagat ggagaggcgt
 300
 cggctgcgca agcgggcggt acctgacgtc ggagcgcggt tattgacacg gcccggtaaa
 360
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcgatg atgcgagacg
 420
 tgggtgtgcat cccgtgctcc atgacgtcga c
 451

<210> 662

<211> 85

<212> PRT

<213> Homo sapiens

<400> 662

Met	Asp	Glu	Ile	Leu	Thr	Leu	Leu	Ala	Gly	Gly	Gly	Asp	Asp	Glu	Pro
1				5					10					15	
Glu	Trp	His	Asp	Lys	Ala	Leu	Cys	Ala	Gln	Thr	Asp	Pro	Glu	Ala	Phe
			20					25					30		
Phe	Pro	Glu	Lys	Gly	Gly	Ser	Thr	Arg	Glu	Ala	Lys	Arg	Ile	Cys	Glu
			35				40					45			
Ser	Cys	Glu	Val	Arg	Gln	Glu	Cys	Leu	Glu	Tyr	Ala	Leu	Ala	Asn	Asp
	50				55					60					
Glu	Arg	Phe	Gly	Ile	Trp	Gly	Gly	Leu	Ser	Glu	Met	Glu	Arg	Arg	Arg
65				70					75					80	
Leu	Arg	Lys	Arg	Ala											
				85											

<210> 663

<211> 552

<212> DNA

<213> Homo sapiens

<400> 663

ctcgagcgtc tcgacgccga cgccgcccag ggagccaagg aagacctctc gcagcgcgac
 60
 ccctacgacg tgctcgtcgt agggggcgggt cccgcgggtg ccgcggccgc cgtgtacgag
 120
 gctcgtaagg gcattcgcac cgccatggtc ggggtctcgga tcggcggcca ggtactcgat
 180
 accgaggcca tcgacaacct catctcgggt cgcacacca ccggtccgag tctggccgac
 240
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgagcgtca gaccgccagc
 300
 gccatagaga ccaccggcgg tatgaccacc gtgcattctga ccgacggcga cctgcggggc
 360
 cgctcagtca tcgtggccac cgggtccccg tggcgcaacc ttggcgtacc tggcgaggag
 420
 gaataccgca ccaagggtgt gacctactgc ccgcaactgc atggcccgtt attcacaggc
 480

aaaaaggtgg ccgctcgtcg aggtggaaac tccggtattg aggccgctat cgacctcgcc
 540
 ggcgtcgtcg ac
 552

<210> 664
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 664
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
 1 5 10 15
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
 20 25 30
 Gly Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
 35 40 45
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
 50 55 60
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
 65 70 75 80
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
 85 90 95
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
 100 105 110
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
 115 120 125
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr
 130 135 140
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
 145 150 155 160
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
 165 170 175
 Ile Asp Leu Ala Gly Val Val Asp
 180

<210> 665
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 665
 acgcgtacag ttcgccgtcg aggttgaaca ccacgatcgg tgtaccggtc acttcgtcga
 60
 acacgctctt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct
 120
 cgctcacgcg gtggccccgg ccagcggcct ttccaggatc tcgaaacgca ggtcgtcgcg
 180
 cttggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cggtgcgcat
 240
 gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcactctga
 300
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa
 352

<210> 666
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 666
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp
 1 5 10 15
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg
 20 25 30
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
 35 40 45
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
 50 55 60
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Thr Ala Ala Gly
 65 70 75 80
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
 85 90 95
 Val Gln Pro Arg Arg Arg Thr Val Arg
 100 105

<210> 667
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 667
 nacgcgtacg aatcgggtgtt gcgtcgcaac ccaggggagg ccgagttcca ccaggctgtg
 60
 cgaggagatct ttgaatctct cggcccgggtg ctcgacaaga atccgcagta cgtggaggca
 120
 gccgtgttgt cgcgcatctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt
 180
 gacgacgagg gcaagatccg tatcaaccgt ggcttccgcg ttgaatattc gtcggtactg
 240
 gggccgtata aggggtggatt gcgattccac ccctcgggtg acttaggaac gattaagttc
 300
 cttgggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcaag
 360
 ggtgggtcgg actttgatcc ccatgacgcg t
 391

<210> 668
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 668
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe
 1 5 10 15
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp
 20 25 30
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35      40      45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
      50      55      60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
65      70      75      80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85      90      95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100      105      110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115      120      125
Asp Ala
      130

```

<210> 669
 <211> 707
 <212> DNA
 <213> Homo sapiens

```

<400> 669
nngagtcctg tccccgtcta agctcatcgt ggtggtgctg gcatggccgt caacaaggga
60
attgagaaca cccttgctgc cttcggccac gcggtcgagg tgggatgcac ctaccttgaa
120
actgacgttc acgcgaccag cgacggggtg ctagtggcct tccacgatcc gatactcgat
180
cgcgctcactg aatcaggcgg agtcatcgcc gccatgccgt ggcacaagggt caaacaagcc
240
aagggttggtg gcgaaccgat cccacacctta gatgagattt tcgacgcctt tcccgacgcg
300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttctttcc
360
cgtcaccggg cttggagtcg ggtttgctgc gggtcgttca gcagtaaacg catccagacc
420
ttccgtcgcc tggttcaggg acgcactgag actgcagtgg ggtcggtggg agtcnnggct
480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
540
tgccgcaccg cttgaccggg tnatgggggtg ccccttgta caccgacctt cattaaagct
600
gcccacgtc aggggagagc tggtcatgtc tggacgggta atgagatctc tgaggctcga
660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
707

```

<210> 670
 <211> 170
 <212> PRT
 <213> Homo sapiens

```

<400> 670
Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
1      5      10      15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

```

```

                20                25                30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
      35                40                45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
      50                55                60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
      65                70                75                80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
      85                90                95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
      100                105                110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
      115                120                125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
      130                135                140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
      145                150                155                160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
      165                170

```

<210> 671
 <211> 444
 <212> DNA
 <213> Homo sapiens

```

<400> 671
acgcgtgggc cttcgggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ccttggtcga ctacgcctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctcttgctc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtggt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccaccacagg tgccatttgc tgggcgcctt agggagctgc gtgggcatcc agaggagtga
360
gtcgcctcct gctctgctca gtgcccactt ccccgggcag ggcaggcggtt attaacgtag
420
agggagaaca cccatgcaca caac
444

```

<210> 672
 <211> 103
 <212> PRT
 <213> Homo sapiens

```

<400> 672
Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
1      5      10      15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
20      25      30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

          35          40          45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
   50          55          60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
  65          70          75          80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
          85          90          95
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783

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 1475 1480 1485
 His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys
 1490 1495 1500
 Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly
 1505 1510 1515 1520
 Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly Lys
 1525 1530 1535
 Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe Ala
 1540 1545 1550
 Gly His Leu Pro Arg Gly Ser Pro Val Thr Thr Arg Glu Pro Thr Pro
 1555 1560 1565
 Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp Arg
 1570 1575 1580
 Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser Thr
 1585 1590 1595 1600
 Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu
 1605 1610 1615
 Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala
 1620 1625 1630
 Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala
 1635 1640 1645
 Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His
 1650 1655 1660
 Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu
 1665 1670 1675 1680
 Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met
 1685 1690 1695
 His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg
 1700 1705 1710
 Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly
 1715 1720 1725
 Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu
 1730 1735 1740
 Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala
 1745 1750 1755 1760
 Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser
 1765 1770 1775
 Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr
 1780 1785 1790
 Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 1795 1800 1805
 Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Thr Val Glu His
 1810 1815 1820
 Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly
 1825 1830 1835 1840
 Ser Ser Gly Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser
 1845 1850 1855
 His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu
 1860 1865 1870
 Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile
 1875 1880 1885
 Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr

1890	1895	1900
Ser Ser Pro Val Arg	Pro Ala Ala Thr Phe	Pro Pro Ala Thr His Cys
1905	1910	1915
Pro Leu Gly Gly Thr	Leu Asp Gly Val Tyr	Pro Thr Leu Met Glu Pro
1925	1930	1935
Val Leu Leu Pro Lys	Glu Ala Pro Arg Val Ala Arg	Pro Glu Arg Pro
1940	1945	1950
Arg Ala Asp Thr Gly	His Ala Phe Leu Ala Lys	Pro Pro Ala Arg Ser
1955	1960	1965
Gly Leu Glu Pro Ala	Ser Ser Pro Ser Lys	Gly Ser Glu Pro Arg Pro
1970	1975	1980
Leu Val Pro Pro Val	Ser Gly His Ala Thr	Ile Ala Arg Thr Pro Ala
1985	1990	1995
Lys Asn Leu Ala Pro	His His Ala Ser Pro	Asp Pro Pro Ala Pro Pro
2005	2010	2015
Ala Ser Ala Ser Asp	Pro His Arg Glu Lys	Thr Gln Ser Lys Pro Phe
2020	2025	2030
Ser Ile Gln Glu Leu	Glu Leu Arg Ser Leu	Gly Tyr His Gly Ser Ser
2035	2040	2045
Tyr Ser Pro Glu Gly	Val Glu Pro Val Ser	Pro Val Ser Ser Pro Ser
2050	2055	2060
Leu Thr His Asp Lys	Gly Leu Pro Lys His	Leu Glu Glu Leu Asp Lys
2065	2070	2075
Ser His Leu Glu Gly	Glu Leu Arg Pro Lys	Gln Pro Gly Pro Val Lys
2085	2090	2095
Leu Gly Gly Glu Ala	Ala His Leu Pro His	Leu Arg Pro Leu Pro Glu
2100	2105	2110
Ser Gln Pro Ser Ser	Ser Pro Leu Leu Gln	Thr Ala Pro Gly Val Lys
2115	2120	2125
Gly His Gln Arg Val	Val Thr Leu Ala Gln	His Ile Ser Glu Val Ile
2130	2135	2140
Thr Gln Asp Tyr Thr	Arg His His Pro Gln	Gln Leu Ser Ala Pro Leu
2145	2150	2155
Pro Ala Pro Leu Tyr	Ser Phe Pro Gly Ala	Ser Cys Pro Val Leu Asp
2165	2170	2175
Leu Arg Arg Pro Pro	Ser Asp Leu Tyr Leu	Pro Pro Pro Asp His Gly
2180	2185	2190
Ala Pro Ala Arg Gly	Ser Pro His Ser Glu	Gly Gly Lys Arg Ser Pro
2195	2200	2205
Glu Pro Asn Lys Thr	Ser Val Leu Gly Gly	Gly Glu Asp Gly Ile Glu
2210	2215	2220
Pro Val Ser Pro Pro	Glu Gly Met Thr Glu	Pro Gly His Ser Arg Ser
2225	2230	2235
Ala Val Tyr Pro Leu	Leu Tyr Arg Asp Gly	Glu Gln Thr Glu Pro Ser
2245	2250	2255
Arg Met Gly Ser Lys	Ser Pro Gly Asn Thr	Ser Gln Pro Pro Ala Phe
2260	2265	2270
Phe Ser Lys Leu Thr	Glu Ser Asn Ser Ala	Met Val Lys Ser Lys Lys
2275	2280	2285
Gln Glu Ile Asn Lys	Lys Leu Asn Thr His	Asn Arg Asn Glu Pro Glu
2290	2295	2300
Tyr Asn Ile Ser Gln	Pro Gly Thr Glu Ile	Phe Asn Met Pro Ala Ile
2305	2310	2315
Thr Gly Thr Gly Leu	Met Thr Tyr Arg Ser	Gln Ala Val Gln Glu His

2325 2330 2335
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met
 2340 2345 2350
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
 2355 2360 2365
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
 2370 2375 2380
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly
 2385 2390 2395 2400
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys
 2405 2410 2415
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser
 2420 2425 2430
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn
 2435 2440 2445
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro
 2450 2455 2460
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro
 2465 2470 2475 2480
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His
 2485 2490 2495
 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu
 2500 2505 2510
 Thr Leu Ser Asp Ser Glu
 2515

<210> 677
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 677
 gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattggtca gttcaccctt
 60
 gagggatatag ctccggcacg ccgtgggtgtt ccacagattg aagttacttt cgatatcgat
 120
 gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggttaagga acagaagatt
 180
 cgcacgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
 240
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
 300
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn
 345

<210> 678
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 678
 Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly
 1 5 10 15
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65      70      75      80
Glu Gln Asn Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

```

<210> 679

<211> 362

<212> DNA

<213> Homo sapiens

<400> 679

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acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac ggcgagtatg atgtatctat gaatcttgag
120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcattgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

```

<210> 680

<211> 100

<212> PRT

<213> Homo sapiens

<400> 680

```

Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
 1      5      10      15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
      20      25      30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35      40      45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
      50      55      60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
65      70      75      80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85      90      95
Lys Ala Lys Asp
      100

```

<210> 681
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 681
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca
 60
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc
 120
 ggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa
 180
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta
 240
 attgcagaag gcaatatcga tacacctgaa aaggtgaaac gtgtgcttga gttaggcgcg
 300
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcacacgaa aaaattt
 357

<210> 682
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 682
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg
 1 5 10 15
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
 20 25 30
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
 35 40 45
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
 50 55 60
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
 65 70 75 80
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
 85 90 95
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
 100 105 110
 Gln Leu Ile Thr Lys Lys Phe
 115

<210> 683
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 683
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
 60
 aatattgttt tgcccgagc gtggttgcat gattgcgtca gttaccctaa aaaccatgta
 120
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
 180

aattacccca aacaatactt attagcaatt catcatgcaa tttcagcgca cagtgtcagt
 240
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
 300
 gcgctagggg caattggcgt ggctcggtgc attcaagtaa gtagccagtt acagcgccca
 360
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5					10				15		
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
		20					25				30				
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
	35					40				45					
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50				55					60					
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65					70					75				80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85					90					95		
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
		100					105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115				120						125			
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
	130					135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aaccggaac gatggatgga ttgacactat tcggcctgtt
 60
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact gggtcgtgct
 120
 gctgttcgcg gccgcttggc gctcggttcg gcctacggct tcctccaagg cgctggccg
 180
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc
 240
 gcgatgaccg catcgtccgg cttaagcccg gaaacgaaac cgaccagtgc gctgggttga
 300
 tggggcgcg gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
 360
 gtgcatgccg acgctgtcgc tcacgcgct acgctcgacc acggcgcgcg gcaatag
 417

<210> 686
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 686
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro
 1 5 10 15
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
 20 25 30
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
 35 40 45
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
 50 55 60
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
 65 70 75 80
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
 85 90 95
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
 100 105 110

<210> 687
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 687
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgca
 60
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccgtt
 120
 ctcgatgaaa ccacaggtgg tcgcacgatc gagcttcggg taccacctgc gtgcgcggtt
 180
 caattggcgg ccattgagtc gggccccaac caccaccggg gcaactccgc caatgtggcc
 240
 gagaccgacc ctgtcacctt cctgcagttg gcaactggct tctcacactg gccagaaatg
 300
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
 360
 ccagtcgttg atatggccgg ggttttccgc gacatttttg ccgacgacta ga
 412

<210> 688
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 688
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
 1 5 10 15
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
 20 25 30
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg

```

      35          40          45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
  50          55          60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
  65          70          75          80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85          90          95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100          105          110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115          120          125
Phe Arg Asp Ile Phe Ala Asp Asp
      130          135

```

<210> 689

<211> 499

<212> DNA

<213> Homo sapiens

<400> 689

```

cgcgtcgcgg tactcgacgt cgattttcat cacggaacg gcaccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg cacggcgagc cggccgtgtc ctatccctac
120
tattcgggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgcctgcagg
240
aaactccagc aattctcgcc gcaggatttg gtgatctcac tgggggtcga caccttcaag
300
gacgaccgga tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcg cttgagcatcc
480
gcccgaagac ggcgtgata
499

```

<210> 690

<211> 157

<212> PRT

<213> Homo sapiens

<400> 690

```

Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
  1          5          10          15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20          25          30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35          40          45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50          55          60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100         105         110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115         120         125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130         135         140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691
 <211> 336
 <212> DNA
 <213> Homo sapiens

```

<400> 691
ntgctgctg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggccccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgccgcacg ctgctgcgca acggctgcct ttgctggct
180
ggaggcgcgca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgctg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

```

<210> 692
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1          5          10          15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
          20          25          30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
          35          40          45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
          50          55          60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65          70          75          80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
          85          90          95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
          100         105         110

```

<210> 693
 <211> 580

<212> DNA

<213> Homo sapiens

<400> 693

```

ngggcaaccc ggaaggccg gcgtcccagc cgcctacctc gctgggaccc tggctcttgc
60
gtcccccgct ggcctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagatata ggcttggacc agagctggaa
240
atatgcggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt
300
caagtcctag cgcccttgt ggagtctccc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag
420
atcctgtcca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcaccc cgtggtcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtcctgatca
580

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<210> 694

<211> 136

<212> PRT

<213> Homo sapiens

<400> 694

```

Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
 1             5             10             15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
      20             25             30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
      35             40             45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
      50             55             60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
      65             70             75             80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
      85             90             95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
      100            105            110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
      115            120            125
Phe Thr Pro Trp Ser Arg Ser Arg
      130            135

```

<210> 695

<211> 439

<212> DNA

<213> Homo sapiens

<400> 695

ntggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtccctcgacc
60
atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccggatc
120
ggcgacaagt tcgtcccga cgtctggggc aaactcaaac tcggcaagga caacgagcac
180
accgctctgc cctggtactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag
240
gatgttggcc tcgatcccg aatcccgcg aagacgatga ccgagtacct cgacttcgcc
300
aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc
360
gcggaatggc gtgccctcgg cgtcaaggte atgaatgacg acttcaccaa gttcactttt
420
gcctcggaat ccaacgcgt
439

<210> 696

<211> 146

<212> PRT

<213> Homo sapiens

<400> 696

Xaa	Val	Thr	Gln	Ala	Ser	Asn	Gly	Thr	Met	Ala	Asp	Val	Val	Asn	Met
1				5					10					15	
Pro	Ser	Ser	Thr	Ile	Met	Ala	Leu	Ser	Arg	Ala	Asp	Tyr	Leu	Leu	Asp
			20					25					30		
Ile	Glu	Thr	Ser	Val	Pro	Gly	Ile	Gly	Asp	Lys	Phe	Val	Pro	Asp	Val
		35					40					45			
Trp	Gly	Lys	Leu	Lys	Leu	Gly	Lys	Asp	Asn	Glu	His	Thr	Ala	Leu	Pro
	50					55					60				
Trp	Tyr	Phe	Gly	Pro	Phe	Val	Val	Thr	Tyr	Asn	Lys	Asp	Ile	Phe	Lys
65					70					75				80	
Asp	Val	Gly	Leu	Asp	Pro	Glu	Ile	Pro	Pro	Lys	Thr	Met	Thr	Glu	Tyr
				85					90					95	
Leu	Asp	Phe	Ala	Lys	Lys	Ile	Thr	Ala	Ala	Gly	Lys	Gln	Ala	Val	Tyr
			100					105					110		
Gly	Asn	Thr	Ser	Trp	Tyr	Met	Leu	Ala	Glu	Trp	Arg	Ala	Leu	Gly	Val
		115					120					125			
Lys	Val	Met	Asn	Asp	Asp	Phe	Thr	Lys	Phe	Thr	Phe	Ala	Ser	Glu	Ser
	130						135				140				
Asn	Ala														
145															

<210> 697

<211> 368

<212> DNA

<213> Homo sapiens

<400> 697

nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggg
60

tgtcggtgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc
 120
 tttccaccct ggagagactc gctgccttg aaagtcttct tgccttctt gggcaactga
 180
 tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc
 240
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca
 300
 atcttgtctt cacgcagcga tacgggcccgc cgttggaat cgaacacaaa caccttgaag
 360
 gcgttgtn
 368

<210> 698
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 698
 Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser
 1 5 10 15
 His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu
 20 25 30
 Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu
 35 40 45
 Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg
 50 55 60
 Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly
 65 70 75 80
 Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala
 85 90 95
 Val Gly Ile Glu His Lys His Leu Glu Gly Val Val
 100 105

<210> 699
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 699
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 60
 cacacctcag attggcaact ggggatgact cggcactacc tgcgaagcg cggcgacgac
 120
 gacccacagg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacgtt
 180
 gcccggaagg agggctgcga gtttgtcgtc gtcgccggag atgtcttcga aaccacaaat
 240
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg
 300
 tacctgctgc ccggaaatca cgacagctta gagccggggg gtctctggga tgggccagaa
 360
 ttc
 363

<210> 700
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 700
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met
 1 5 10 15
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His
 20 25 30
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala
 35 40 45
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu
 50 55 60
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn
 65 70 75 80
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile
 85 90 95
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro
 100 105 110
 Gly Cys Leu Trp Asp Gly Pro Glu Phe
 115 120

<210> 701
 <211> 585
 <212> DNA
 <213> Homo sapiens

<400> 701
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 ttcggctacg tccattgcgc ggatgtctgc ccgctgacac tgggcaacat ggtctcggcc
 120
 ctcgatcgcc tgggctcccg ggcggacggc atcgttccga tcttcatctc cgtcgatccg
 180
 gcccgcgaca caccgcgct ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc
 240
 gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg
 300
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc
 360
 ctctctatc tgatggacgg caacaaccgc ctgttgcggt tgatggcggt cagcgccgac
 420
 gctgcctcgc tgacgcacca gctggcgccc ggctggccc gggcaagaat gagaccatga
 480
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggtcg ttcggcatca
 540
 tcctgtgtgt cggcatcgcc ggcattgtcg atttcgtcga ccggt
 585

<210> 702
 <211> 159
 <212> PRT

<213> Homo sapiens

<400> 702

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Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
      20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
      35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
      50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
      65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
      85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
      100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
      115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
      130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
      145          150          155

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<210> 703

<211> 390

<212> DNA

<213> Homo sapiens

<400> 703

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ttctctgctc catacacacc tcagcagaat ggcacgccc agcgcaagaa cataactctt
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attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgta caccatcaac cgcgtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggttaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaat ttgcaccgaa agcacatgaa
300
ggttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcgn
390

```

<210> 704

<211> 130

<212> PRT

<213> Homo sapiens

<400> 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705

<211> 513

<212> DNA

<213> Homo sapiens

<400> 705

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acgcgtatatt cgtccaaatg attcaaatac aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatgctg aataaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgacaaag ttgagaaaga ctatgcaaat tatggggatg aagctacttt cggtgccgga
240
aaatcaattc gtgatggtat ggctcaaaat cctaattgtga caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcgggtatta aaaatgggta tatttttaag attggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tgggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

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<210> 706

<211> 140

<212> PRT

<213> Homo sapiens

<400> 706

```

Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```

```

      50              55              60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile
65              70              75              80
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr
      85              90              95
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val
      100             105             110
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys
      115             120             125
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His
      130             135             140

```

<210> 707

<211> 409

<212> DNA

<213> Homo sapiens

<400> 707

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acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
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gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat tttcatggca gtgtctatgg acggctcccc ttggcatggg
180
gctgggtggc aatcctggct gtagctgcca cccctgccc ttttgcttc cctccgaggg
240
cattgtgata atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggt tccccagcct gtctggccat cccccccag ccagcccct cctgctgggt
360
gacgtgctca gtccggcccc tgctgtactg ggaggggggt aggagcata
409

```

<210> 708

<211> 136

<212> PRT

<213> Homo sapiens

<400> 708

```

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val
 1              5              10              15
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly
      20              25              30
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn
      35              40              45
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly
      50              55              60
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg
      65              70              75              80
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro
      85              90              95
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His
      100             105             110
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu

```

115 120 125
 Trp Trp Ser Glu Asp Ala Thr Arg
 130 135
 <210> 709
 <211> 771
 <212> DNA
 <213> Homo sapiens
 <400> 709
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 60
 tgaccacacc tgggccagcg acgtgtggtg cgccagcctc cccagcggat cacctcctcc
 120
 tccccctcca ggaggagagt ttctccgaag tccccatgag tgaagcaagc tcagcgaaag
 180
 aactccact ctttaggatg gagggagagg atgcccttgt gactcagtat cagagcaaag
 240
 ccagtgacca cgaaggttta ttgtctgacc ccttgagtga ccttcagttg gtctcagatt
 300
 ttaaatctcc aatcatggcc gatctgaact taagccttcc ttccattcct gaagtgcgat
 360
 cggatgatga aagaatagat cagggttgaag atgacggaga tcagggtgaa gatgatggag
 420
 agacagcaaa gtcgtcaact ctggacatag gagctttgtc cttgggcttg gtagtcccc
 480
 gtcctgagag gggaaagggg cccagtggcg aggcagatag gttggtactg ggggagggcc
 540
 tgtgtgattt caggctgcaa gcacccagg catctgtgac agtccttca gagcagacca
 600
 cagagtccgg aattcacaaa ccacatcttg gcaagagctc aagcttggat aaacagctgc
 660
 caggccccag tgggtgtgag gaagaaaaac cgatgggaaa tgggagtcca agccgcctc
 720
 ctggcacatc cctggacaat cctgtaccca gccctcccc ttctgagatc t
 771

<210> 710
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 710
 Met Ser Glu Ala Ser Ser Ala Lys Asp Thr Pro Leu Phe Arg Met Glu
 1 5 10 15
 Gly Glu Asp Ala Leu Val Thr Gln Tyr Gln Ser Lys Ala Ser Asp His
 20 25 30
 Glu Gly Leu Leu Ser Asp Pro Leu Ser Asp Leu Gln Leu Val Ser Asp
 35 40 45
 Phe Lys Ser Pro Ile Met Ala Asp Leu Asn Leu Ser Leu Pro Ser Ile
 50 55 60
 Pro Glu Val Ala Ser Asp Glu Arg Ile Asp Gln Val Glu Asp Asp
 65 70 75 80
 Gly Asp Gln Val Glu Asp Asp Gly Glu Thr Ala Lys Ser Ser Thr Leu

```

<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
 1             5             10             15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
      20             25             30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
      35             40             45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
      50             55             60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

```

<400> 714
Ile Leu Ile Ala Asn Gly Gly Met Gln Asn Pro Val Gly Ala Val Phe
  1                      5                      10                      15
Asn Pro Asp Thr Met Arg Met Glu Met Thr Asp Phe Ala Ala Val Ile
      20                      25                      30
Phe Asn Pro Val Ala Gln Ala Lys Phe Val His Thr Val Ser Ala Gly
      35                      40                      45
Tyr Val Ala Gly Ala Met Phe Val Met Ser Ile Ser Ala Trp Tyr Leu
      50                      55                      60
Leu Lys Gly Arg His Thr Asp Leu Ala Lys Arg Ser Met Ala Val Ala
65                      70                      75                      80
Ala Ser Phe Gly Leu Ala Ser Ala Leu Ser Val Val Val Leu Gly Asp
      85                      90                      95
Glu Ser Gly Tyr Leu Thr Thr Glu His Gln Lys Met Lys Ile Ala Ala
      100                      105                      110
Met Glu Ser Met Trp His Thr Glu Pro Ala Pro Ala Ser Phe Asn Leu
      115                      120                      125
Ile Ala Leu Pro Asn Gln Ala Glu Arg Lys Asn Asp Phe Ala Ile Glu
      130                      135                      140
Ile Pro Tyr Val Met Xaa Leu Ile Gly Thr Arg
145                      150                      155

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<210> 715
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 715
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 cagaccggcc tgctgcctca ggcaactggtg cgtttgcgcc aggcagcgcc gacgggtggag
 120
 tgcaagttgg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg
 180
 gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta
 240
 ctgcgcaagg agccgtttgt gttgatcgtg cccagggcgg tcgggggtga tgacccgttg
 300
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttcgtttgg cggg
 354

<210> 716
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 716
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala
 1 5 10 15
 Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu
 20 25 30
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser
 35 40 45
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile
 50 55 60
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val
 65 70 75 80
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly
 85 90 95
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp
 100 105 110
 Arg Ala Ser Phe Gly Gly
 115

<210> 717
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 717
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 ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata
 120
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca
 180

atataatcaa gctgacaata ctgatcaaac cactcgcatg aaagctacta ccgcttgacc
 240
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag
 300
 accaggtggt agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag
 360
 attcaacggc gtagcaccag cacagcaaca tagccactag t
 401

<210> 718
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 718
 Met Leu Leu Cys Trp Cys Tyr Ala Val Glu Ser His Trp Ile Ser Phe
 1 5 10 15
 His Phe Leu Glu Arg Pro Ile Phe Asn Leu Ala Thr Thr Trp Ser Ser
 20 25 30
 Phe Leu Leu Trp Thr Ile Leu Phe Leu Ser Ile Ser Leu Val Phe Ser
 35 40 45
 Ala Trp Trp Ser Ser Gly Ser Ser Phe His Ala Ser Gly Leu Ile Ser
 50 55 60
 Ile Val Ser Leu Ile Ile Leu Ser His Phe Ser Val Ser Gln His Gln
 65 70 75 80
 Phe Asp Ala Leu Leu Ser Ala Gln Leu Leu Trp Ile Trp Phe Leu
 85 90 95
 Leu Met Glu Ser His Arg Met Ala Tyr Leu Asp Asp Leu Thr Ala Leu
 100 105 110
 Pro Gly Arg Arg Ala Leu Asn Glu Lys Leu Val Gly Leu Pro Lys Arg
 115 120 125
 Tyr Ala
 130

<210> 719
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 719
 tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcggtca
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 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc
 120
 aatctccctg cgttggtaac tgggcaaaag aaagacctct gcagtccagc aacctcatcg
 180
 tgcaaagtcc gtggcgtggt caactctgac ggcttggaag ctgcagacct tgtcaaagga
 240
 cctggccga aattcaccct tgatctcttt gtcttgcca actcttgccc ctgagaatga
 300
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgct gaatcacgct
 360
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag
 480
 cataaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gaggaccgcc
 540
 atcgatcagt gtctgatact gcttgccgc gacttctttg ccgagcaatg ggtatagcgt
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 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat
 660
 gaccacgtca tcgatgggat ttgac
 685

<210> 720
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 720
 Met Ser Leu Thr Arg Arg Asn Arg Gln Gly Glu Gln Thr Thr Ala Ser
 1 5 10 15
 Thr Trp Leu Lys Thr Leu Tyr Pro Leu Leu Gly Lys Glu Val Ala Asp
 20 25 30
 Lys Gln Tyr Gln Thr Leu Ile Asp Gly Gly Thr Leu His Leu Ser Ser
 35 40 45
 Asp Phe Thr Phe Pro Val Ala Glu Tyr Leu Phe Met Leu Arg Pro Val
 50 55 60
 Glu Gln Glu Val Phe Glu Leu Gly Phe Asn Ala Lys Ser Leu Arg Ser
 65 70 75 80
 Gly Val Val Glu Gly Val Leu Ala Gly Ser Arg Ala Ala Leu Ala Gly
 85 90 95
 Leu Gln Asn Gly Asp Val Ile Gln His Phe Ser Arg Val Ser Val Ala
 100 105 110
 Leu Met Asp Ser Gln Lys Thr Val Ser Phe Ser Gly Thr Arg Val Gly
 115 120 125
 Gln Asp Lys Glu Ile Lys Gly Glu Phe Arg Pro Arg Ser Phe Asp Lys
 130 135 140
 Val Cys Ser Phe Gln Ala Val Arg Val Asp His Ala Thr Ala Phe Ala
 145 150 155 160
 Arg

<210> 721
 <211> 579
 <212> DNA
 <213> Homo sapiens

<400> 721
 aagcttgga tcagggtgtg gcagtgtggc gggagtgtgg aggtcctgcc ctgctcacgg
 60
 attgccacac ttgagcgagc ccacaagccc tacacagagg acctcaccgc ccatgtccgc
 120
 aggaacgctc tcagggtggc tgaagtctgg atggatgaat ttaaaagcca cgtctactgg
 180
 catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct
 240

ctcaggaaac agctgcagtg caagaccttc cgggtggtacc tggtcagcgt gtacccagag
 300
 atgaggatgt actccgacat cattgcctat ggagtgtctgc agaattctct gaagactgat
 360
 ttgtgtcttg accaggggcc agatacagag aatgtcccca tcatgtacat ctgccatggg
 420
 atgacgcctc agaacgtgta ctacacgagc agtcagcaga tccatgtggg cattctgagc
 480
 cccaccgtgg atgatgatga caaccgatgc ctggtggacg tcaacagccg gccccggctc
 540
 atcgaatgca gctacgcaa agccaagagg atgaagctt
 579

<210> 722

<211> 193

<212> PRT

<213> Homo sapiens

<400> 722

Lys	Leu	Gly	Ile	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Val	Glu	Val	Leu
1				5					10					15	
Pro	Cys	Ser	Arg	Ile	Ala	His	Ile	Glu	Arg	Ala	His	Lys	Pro	Tyr	Thr
			20					25					30		
Glu	Asp	Leu	Thr	Ala	His	Val	Arg	Arg	Asn	Ala	Leu	Arg	Val	Ala	Glu
		35					40					45			
Val	Trp	Met	Asp	Glu	Phe	Lys	Ser	His	Val	Tyr	Trp	His	Gly	Thr	Tyr
	50					55				60					
Gln	Glu	Asp	Ser	Gly	Ile	Asp	Ile	Gly	Asp	Ile	Thr	Ala	Arg	Lys	Ala
65					70				75					80	
Leu	Arg	Lys	Gln	Leu	Gln	Cys	Lys	Thr	Phe	Arg	Trp	Tyr	Leu	Val	Ser
			85						90				95		
Val	Tyr	Pro	Glu	Met	Arg	Met	Tyr	Ser	Asp	Ile	Ile	Ala	Tyr	Gly	Val
			100					105					110		
Leu	Gln	Asn	Ser	Leu	Lys	Thr	Asp	Leu	Cys	Leu	Asp	Gln	Gly	Pro	Asp
		115					120					125			
Thr	Glu	Asn	Val	Pro	Ile	Met	Tyr	Ile	Cys	His	Gly	Met	Thr	Pro	Gln
	130					135					140				
Asn	Val	Tyr	Tyr	Thr	Ser	Ser	Gln	Gln	Ile	His	Val	Gly	Ile	Leu	Ser
145					150				155					160	
Pro	Thr	Val	Asp	Asp	Asp	Asp	Asn	Arg	Cys	Leu	Val	Asp	Val	Asn	Ser
			165						170					175	
Arg	Pro	Arg	Leu	Ile	Glu	Cys	Ser	Tyr	Ala	Lys	Ala	Lys	Arg	Met	Lys
			180					185					190		

Leu

<210> 723

<211> 384

<212> DNA

<213> Homo sapiens

<400> 723

agcgctcctc ttacgctcag ttttgacaat gcgtgctggc agccaaccga agccgtaaaa
 60

ctcaacgaaa tgctctcgct taaaccgtgc gaaggaaccc caccgcaatg gcgcttatcc
 120
 cgcgaaagggg attaccaaatt gcgcattgat acgcgctccg gaacgcctac gctgatgctt
 180
 accgtacaaa gtgtaaccga caaacctggt acggacgtca ctcgacaatg tcctaaatgg
 240
 gacggcaagc ccctcaccct tgacgtaacg aatacattcc cggaaggctc cgtcgtacga
 300
 gacttctaca gcaagcaaac cgctatgggt cagcaaggta aaatcacact tcagcctgcc
 360
 gctaacagca atggcctgct gctg
 384

<210> 724

<211> 128

<212> PRT

<213> Homo sapiens

<400> 724

Thr	Arg	Pro	Leu	Thr	Leu	Ser	Phe	Asp	Asn	Ala	Cys	Trp	Gln	Pro	Thr
1				5					10					15	
Glu	Ala	Val	Lys	Leu	Asn	Glu	Met	Leu	Ser	Leu	Lys	Pro	Cys	Glu	Gly
			20					25					30		
Thr	Pro	Pro	Gln	Trp	Arg	Leu	Phe	Arg	Glu	Gly	Asp	Tyr	Gln	Met	Arg
			35				40					45			
Ile	Asp	Thr	Arg	Ser	Gly	Thr	Pro	Thr	Leu	Met	Leu	Thr	Val	Gln	Ser
	50					55					60				
Val	Thr	Asp	Lys	Pro	Val	Thr	Asp	Val	Thr	Arg	Gln	Cys	Pro	Lys	Trp
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Asp	Gly	Lys	Pro	Leu	Thr	Leu	Asp	Val	Thr	Asn	Thr	Phe	Pro	Glu	Gly
				85					90					95	
Ser	Val	Val	Arg	Asp	Phe	Tyr	Ser	Lys	Gln	Thr	Ala	Met	Val	Gln	Gln
			100					105					110		
Gly	Lys	Ile	Thr	Leu	Gln	Pro	Ala	Ala	Asn	Ser	Asn	Gly	Leu	Leu	Leu
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<210> 725

<211> 521

<212> DNA

<213> Homo sapiens

<400> 725

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 360

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 420
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<210> 726
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 726
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 Glu Met Ser His Arg Arg Leu Phe Leu Val His Ile Cys Pro Ser Arg
 35 40 45
 Ser Thr Pro Ser Pro Ser Ser Cys Ser Leu Pro Glu Arg Leu Cys Trp
 50 55 60
 Glu Trp Cys Ile Gly Gly Leu Gln Ala Leu Leu Gly Ser Arg Cys Ser
 65 70 75 80
 Phe Pro Gly Ser Phe Pro Ala Met Ser Leu Phe Leu Pro Pro Ser Phe
 85 90 95
 Pro Ser Gln Gln Pro Pro Ser Ser Phe His Gln Thr Trp Glu Pro Ser
 100 105 110
 Ser Gln Pro Gln Ser Pro Arg Gly Ser Ile Thr Arg
 115 120

<210> 727
 <211> 629
 <212> DNA
 <213> Homo sapiens

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<210> 728
 <211> 99
 <212> PRT
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<400> 728
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 Ser Val Glu Leu Met Leu Asn Ala Ala Asn Leu Ala Leu Val Thr Phe
 35 40 45
 Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val
 50 55 60
 Met Ile Val Ala Ala Ala Glu Val Val Val Gly Leu Ala Ile Ile Val
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 Thr Ile Phe Arg Ser Arg Arg Thr Thr Ser Val Asp Asp Thr Asn Leu
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 Leu Lys Phe

<210> 729
 <211> 4716
 <212> DNA
 <213> Homo sapiens

<400> 729
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<211> 797

<212> PRT

<213> Homo sapiens

<400> 730

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Thr	Asp	Thr	Val	Arg	Leu	Thr	Ser	Val	Val	Thr	Pro	Arg	Pro	Phe	Gly
			20					25					30		
Ser	Gln	Thr	Arg	Gly	Ile	Ser	Ser	Leu	Pro	Arg	Ser	Tyr	Thr	Met	Asp
		35					40					45			
Asp	Ala	Trp	Lys	Tyr	Asn	Gly	Asp	Val	Glu	Asp	Ile	Lys	Arg	Thr	Pro
	50					55					60				
Asn	Asn	Val	Val	Ser	Thr	Pro	Ala	Pro	Ser	Pro	Asp	Ala	Ser	Gln	Leu
65					70					75				80	
Ala	Ser	Ser	Leu	Ser	Ser	Gln	Lys	Glu	Val	Ala	Ala	Thr	Glu	Glu	Asp
			85						90				95		
Val	Thr	Arg	Leu	Pro	Ser	Pro	Thr	Ser	Pro	Phe	Ser	Ser	Leu	Ser	Gln
			100					105					110		
Asp	Gln	Ala	Ala	Thr	Ser	Lys	Ala	Thr	Leu	Ser	Ser	Thr	Ser	Gly	Leu
		115					120					125			
Asp	Leu	Met	Ser	Glu	Ser	Gly	Glu	Gly	Glu	Ile	Ser	Pro	Gln	Arg	Glu
	130					135					140				
Val	Ser	Arg	Ser	Gln	Asp	Gln	Phe	Ser	Asp	Met	Arg	Ile	Ser	Ile	Asn

145 150 155 160
 Gln Thr Pro Gly Lys Ser Leu Asp Phe Gly Phe Thr Ile Lys Trp Asp
 165 170 175
 Ile Pro Gly Ile Phe Val Ala Ser Val Glu Ala Gly Ser Pro Ala Glu
 180 185 190
 Phe Ser Gln Leu Gln Val Asp Asp Glu Ile Ile Ala Ile Asn Asn Thr
 195 200 205
 Lys Phe Ser Tyr Asn Asp Ser Lys Glu Trp Glu Glu Ala Met Ala Lys
 210 215 220
 Ala Gln Glu Thr Gly His Leu Val Met Asp Val Arg Arg Tyr Gly Lys
 225 230 235 240
 Ala Gly Ser Pro Glu Thr Lys Trp Ile Asp Ala Thr Ser Gly Ile Tyr
 245 250 255
 Asn Ser Glu Lys Ser Ser Asn Leu Ser Val Thr Thr Asp Phe Ser Glu
 260 265 270
 Ser Leu Gln Ser Ser Asn Ile Glu Ser Lys Glu Ile Asn Gly Ile His
 275 280 285
 Asp Glu Ser Asn Ala Phe Glu Ser Lys Ala Ser Glu Ser Ile Ser Leu
 290 295 300
 Lys Asn Leu Lys Arg Arg Ser Gln Phe Phe Glu Gln Gly Ser Ser Asp
 305 310 315 320
 Ser Val Val Pro Asp Leu Pro Val Pro Thr Ile Ser Ala Pro Ser Arg
 325 330 335
 Trp Val Trp Asp Gln Glu Glu Glu Arg Lys Arg Gln Glu Arg Trp Gln
 340 345 350
 Lys Glu Gln Asp Arg Leu Leu Gln Glu Lys Tyr Gln Arg Glu Gln Glu
 355 360 365
 Lys Leu Arg Glu Glu Trp Gln Arg Ala Lys Gln Glu Ala Glu Arg Glu
 370 375 380
 Asn Ser Lys Tyr Leu Asp Glu Glu Leu Met Val Leu Ser Ser Asn Ser
 385 390 395 400
 Met Ser Leu Thr Thr Arg Glu Pro Ser Leu Ala Thr Trp Glu Ala Thr
 405 410 415
 Trp Ser Glu Gly Ser Lys Ser Ser Asp Arg Glu Gly Thr Arg Ala Gly
 420 425 430
 Glu Glu Glu Arg Arg Gln Pro Gln Glu Glu Val Val His Glu Asp Gln
 435 440 445
 Gly Lys Lys Pro Gln Asp Gln Leu Val Ile Glu Arg Glu Arg Lys Trp
 450 455 460
 Glu Gln Gln Leu Gln Glu Glu Gln Glu Gln Lys Arg Leu Gln Ala Glu
 465 470 475 480
 Ala Glu Glu Gln Lys Arg Pro Ala Glu Glu Gln Lys Arg Gln Ala Glu
 485 490 495
 Ile Glu Arg Glu Thr Ser Val Arg Ile Tyr Gln Tyr Arg Arg Pro Val
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 Asp Ser Tyr Asp Ile Pro Lys Thr Glu Glu Ala Ser Ser Gly Phe Leu
 515 520 525
 Pro Gly Asp Arg Asn Lys Ser Arg Ser Thr Thr Glu Leu Asp Asp Tyr
 530 535 540
 Ser Thr Asn Lys Asn Gly Asn Asn Lys Tyr Leu Asp Gln Ile Gly Asn
 545 550 555 560
 Thr Thr Ser Ser Gln Arg Arg Ser Lys Lys Glu Gln Val Pro Ser Gly
 565 570 575
 Ala Glu Leu Glu Arg Gln Gln Ile Leu Gln Glu Met Arg Lys Arg Thr

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Pro	Leu	His	Asn	Asp	Asn	Ser	Trp	Ile	Arg	Gln	Arg	Ser	Ala	Ser	Val
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Asn	Lys	Glu	Pro	Val	Ser	Leu	Pro	Gly	Ile	Met	Arg	Arg	Gly	Glu	Ser
	610						615						620		
Leu	Asp	Asn	Leu	Asp	Ser	Pro	Arg	Ser	Asn	Ser	Trp	Arg	Gln	Pro	Pro
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Trp	Leu	Asn	Gln	Pro	Thr	Gly	Phe	Tyr	Ala	Ser	Ser	Ser	Val	Gln	Asp
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Phe	Ser	Arg	Pro	Pro	Pro	Gln	Leu	Val	Ser	Thr	Ser	Asn	Arg	Ala	Tyr
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Met	Arg	Asn	Pro	Ser	Ser	Ser	Val	Pro	Pro	Pro	Ser	Ala	Gly	Ser	Val
	675						680						685		
Lys	Thr	Ser	Thr	Thr	Gly	Val	Ala	Thr	Thr	Gln	Ser	Pro	Thr	Pro	Arg
	690					695						700			
Ser	His	Ser	Pro	Ser	Ala	Ser	Gln	Ser	Gly	Ser	Gln	Leu	Arg	Asn	Arg
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Ser	Val	Ser	Gly	Lys	Arg	Ile	Cys	Ser	Tyr	Cys	Asn	Asn	Ile	Leu	Gly
			725						730					735	
Lys	Gly	Ala	Ala	Met	Ile	Ile	Glu	Ser	Leu	Gly	Leu	Cys	Tyr	His	Leu
		740					745						750		
His	Cys	Phe	Lys	Cys	Val	Ala	Cys	Glu	Cys	Asp	Leu	Gly	Gly	Ser	Ser
	755					760						765			
Ser	Gly	Ala	Glu	Val	Arg	Ile	Arg	Asn	His	Gln	Leu	Tyr	Cys	Asn	Asp
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<210> 731

<211> 513

<212> DNA

<213> Homo sapiens

<400> 731

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 513

<210> 732

<211> 113
 <212> PRT
 <213> Homo sapiens

<400> 732
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 35 40 45
 Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln
 50 55 60
 His Met Cys Thr Cys Ser Ser Arg Lys His Phe Pro Leu Ser Phe Leu
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 Trp Pro Asp Lys Val Leu Thr Pro Ser Arg Gln Pro Glu Ser Val Phe
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 Glu

<210> 733
 <211> 4366
 <212> DNA
 <213> Homo sapiens

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 2160
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 4200
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<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

Met	Val	Val	Pro	Ser	Leu	Lys	Leu	Gln	Asp	Leu	Ile	Glu	Glu	Ile	Arg
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Gly	Ala	Lys	Thr	Gln	Ala	Gln	Glu	Arg	Glu	Val	Ile	Gln	Lys	Glu	Cys
			20					25					30		
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35				40					45				
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
	50				55					60					
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65				70					75					80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85					90						95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
	115					120					125				
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
	130					135					140				
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145				150						155				160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165					170						175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
			180					185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
	195					200					205				
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
	210					215					220				
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225				230						235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245					250						255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
			260					265					270		
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

```

      275      280      285
Val Leu Phe Glu Thr Val Leu Thr Ile Met Asp Ile Arg Ser Ala Ala
      290      295      300
Gly Leu Arg Val Leu Ala Val Asn Ile Leu Gly Arg Phe Leu Leu Asn
305      310      315      320
Ser Asp Arg Asn Ile Arg Tyr Val Ala Leu Thr Ser Leu Leu Arg Leu
      325      330      335
Val Gln Ser Asp His Ser Ala Val Gln Arg His Arg Pro Thr Val Val
      340      345      350
Glu Cys Leu Arg Glu Thr Asp Ala Ser Leu Ser Arg
      355      360

```

<210> 735
 <211> 597
 <212> DNA
 <213> Homo sapiens

```

<400> 735
gtcgactagc caaacgccc gggaaagtct tgtaccaccg atcctggttt atgcggatct
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catcgccacc atggactcgc gcaatctgga aaccgccaac cttattccag aaaaaataat
120
tgcttggtgt cctcgatccc gctctgaccg cccactggac cgctcaacc aggacatcct
180
cagtgccatc cacgacgtgg ctgcaccgct ggcaactacc atcttcgtgg tgggtgccac
240
agcgcgcgac attctgctga cacacgtgtt cggatcgcag accggacgtg ccacgctcga
300
cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
360
gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac
420
gagcgacaac acgatcgccc ggccaatcga tctcatccca ttcggcggca tcgaacagcc
480
gccagccacc atcaaatggc cgcccgacat ggctgtcatg atgaatgttg ctggctacgc
540
agatgcctgg cgggccgcag tcgaagtaga gtttgtgccc gggcgcagca tacgcgt
597

```

<210> 736
 <211> 175
 <212> PRT
 <213> Homo sapiens

```

<400> 736
Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile
1      5      10      15
Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser
20      25      30
Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
35      40      45
Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
50      55      60
His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

```

```

65          70          75          80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
          85          90          95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
          100          105          110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
          115          120          125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
          130          135          140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145          150          155          160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
          165          170          175

```

<210> 737
 <211> 497
 <212> DNA
 <213> Homo sapiens

```

<400> 737
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cgcgccggca tcgttgggta cggatacgat cccaaccctc acgccgaccg tgccgacctt
120
caccctgccc tgtcctggat cagccacgtc accttcgtta aaactgtcag tgtgggggat
180
accatcggtt acggcagaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcggttacg ccgacggact gtcccgagga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatc tgcattggacc aattcatggt cgatcttggt
360
cccgattcga acgtcacggt gggagatgag gtggtgctca ttggaacca ggaggacgaa
420
actctgaccg ctgatgacat ggccgaactc ctcggaacca ttagctacga gatcacttgc
480
gccatttcca aacgcgt
497

```

<210> 738
 <211> 165
 <212> PRT
 <213> Homo sapiens

```

<400> 738
Xaa Arg Leu Ala Asn Ser Gly Ala Ile Leu Gly His Asp Leu Gly Lys
1          5          10          15
Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
          20          25          30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
          35          40          45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
          50          55          60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

```

```

65          70          75          80
Val Gly Tyr Ala Asp Gly Leu Ser Arg Gly Leu Ser Asn Lys Gly His
          85          90          95
Val Leu Ile Arg Gly Ser Val His Pro Ile Val Gly Arg Ile Cys Met
          100          105          110
Asp Gln Phe Met Val Asp Leu Gly Pro Asp Ser Asn Val Thr Val Gly
          115          120          125
Asp Glu Val Val Leu Ile Gly Thr Gln Glu Asp Glu Thr Leu Thr Ala
          130          135          140
Asp Asp Met Ala Glu Leu Leu Gly Thr Ile Ser Tyr Glu Ile Thr Cys
145          150          155          160
Ala Ile Ser Lys Arg
          165

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<210> 739
 <211> 438
 <212> DNA
 <213> Homo sapiens

```

<400> 739
cggtcgctggg aagagcgggc gcacgcgctc aagaccaagg aaaagctggc acagaccgcc
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acggcctcat cagcagctgt gggctcaggc cccctccccg aggcggagca ggcgtggccg
120
cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
180
gccgaccagc ccccgctctg cgcccccgag gacgacgccc agctccagct ggcccttagt
240
ttgagccgag aagagcatga taaggaggag cggatccgtc gcggggatga cctgcggctg
300
cagatggcaa tcgaggagag caagaggag actgggggca aggaggagtc gtcctcatg
360
gaccttgctg acgtcttcac gccccagct cctgccccga ccacagaccc ctgggggggc
420
ccagcaccca tggctgct
438

```

<210> 740
 <211> 146
 <212> PRT
 <213> Homo sapiens

```

<400> 740
Arg Leu Arg Glu Glu Arg Ala His Ala Leu Lys Thr Lys Glu Lys Leu
1          5          10          15
Ala Gln Thr Ala Thr Ala Ser Ser Ala Ala Val Gly Ser Gly Pro Pro
          20          25          30
Pro Glu Ala Glu Gln Ala Trp Pro Gln Ser Ser Gly Glu Glu Leu
          35          40          45
Gln Leu Gln Leu Ala Leu Ala Met Ser Lys Glu Glu Ala Asp Gln Pro
          50          55          60
Pro Ser Cys Gly Pro Glu Asp Asp Ala Gln Leu Gln Leu Ala Leu Ser
65          70          75          80
Leu Ser Arg Glu Glu His Asp Lys Glu Glu Arg Ile Arg Arg Gly Asp

```

```

      85              90              95
Asp Leu Arg Leu Gln Met Ala Ile Glu Glu Ser Lys Arg Glu Thr Gly
      100              105              110
Gly Lys Glu Glu Ser Ser Leu Met Asp Leu Ala Asp Val Phe Thr Pro
      115              120              125
Pro Ala Pro Ala Pro Thr Thr Asp Pro Trp Gly Gly Pro Ala Pro Met
      130              135              140
Ala Ala
145

```

<210> 741
 <211> 726
 <212> DNA
 <213> Homo sapiens

```

<400> 741
gcctctctcc gaccgcgttg ttgtaaggat gtcgcgacgg tgcgcaaaaa tgaatatgtg
60
aatttgccgg tcattctgcct cgtcggggccc actgctagcg gaaaatcagg gctagcgggtg
120
cgagtgtgcc gccgcttgta tgcgatgag caccgcgccg aaattattaa tactgactcg
180
atggtggtgt atcgcgggat ggacattggc actgccaccc ctacactgcy cgagcagcgc
240
acggtagtgc atcacctggt gtcgattctt gatgtgactg tgccctcctc gctagtactg
300
atgcagacgc tggcccgta tgcgctcgag gattgtctgt cgcgtggtgt catccctgtc
360
ttggtgggag ggtctgcgt gtacaccaag gccatcattg acgaaatgtc catcccgcca
420
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480
ctgcatgacg agcttgcccg tcgcatccc aaggcggctg agtcaatctt gcccggcaac
540
ggcaggcgaa tcgtttcgtg ccctcgaagt ttattgaccc tgacagggtc ctttactgcc
600
accgatcccc gacgggaccc tccactggcc aagacggtgc aaatgggctt agaactgtcg
660
cgcaaagaca tagaccagcg tattgccgat cgggttgacc agatgtgggc atacggtttc
720
gtcgac
726

```

<210> 742
 <211> 242
 <212> PRT
 <213> Homo sapiens

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<400> 742
Ala Ser Leu Arg Pro Arg Cys Cys Lys Asp Val Ala Thr Val Arg Lys
  1              5              10              15
Asn Glu Tyr Val Asn Leu Pro Val Ile Cys Leu Val Gly Pro Thr Ala
      20              25              30
Ser Gly Lys Ser Gly Leu Ala Val Arg Val Cys Arg Arg Leu Tyr Val

```

35 40 45
 Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
 50 55 60
 Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
 65 70 75 80
 Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
 85 90 95
 Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
 100 105 110
 Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
 115 120 125
 Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
 130 135 140
 Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
 145 150 155 160
 Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
 165 170 175
 Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
 180 185 190
 Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
 195 200 205
 Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
 210 215 220
 Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
 225 230 235 240
 Val Asp

<210> 743
 <211> 430
 <212> DNA
 <213> Homo sapiens

<400> 743
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 120
 aagctattgg tacgagtgtg cccggcgcac gtgtactcag aggagcccga tggcactatt
 180
 tccgtggagt acgcagcgtg tctggagtgt ggcacttgct tggcggttgc tgcgccaggg
 240
 tcgcttgaat ggcactatcc cgcaggtgca atgggtatct cgttcagaga aggatgaagt
 300
 ccttgtgggc gactgtaaag cgacatggcc gtcgctcggt aggaggaatt gtggtgtccg
 360
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 420
 ctggtcgcga
 430

<210> 744
 <211> 98
 <212> PRT

<213> Homo sapiens

<400> 744

Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
 1 5 10 15
 His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
 20 25 30
 Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
 35 40 45
 Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
 50 55 60
 Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala Ala Pro Gly
 65 70 75 80
 Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
 85 90 95
 Glu Gly

<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

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 gcgtcgtggg ggcgcattgg gcggtatttc atcgccgagc ttgaacgcag cagcgagttg
 120
 tatgagcagg cggcgtttac ccgcgatctg gaaagctcgc tgatcaaggg cctgatcctc
 180
 gccacgccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
 240
 tacttgattc gcgcgcggca gtacatccac gacaacgccc gcgaagccgt gcatctggaa
 300
 gacctggaaa ccgctgccgg ggtatcgagg ttcaagttgt tcgatgcgtt tcgcaaatac
 360
 tt
 362

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1 5 10 15
 Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
 20 25 30
 Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
 35 40 45
 Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
 50 55 60
 Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```
<210> 747
<211> 416
<212> DNA
<213> Homo sapiens
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<210> 748
<211> 138
<212> PRT
<213> Homo sapiens
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<210> 749
<211> 1211

<212> DNA

<213> Homo sapiens

<400> 749

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 tcttggggcc tgctgtggcc tcccctgctg ttcaccgggc tgctcgccg acccccgggg
 120
 accatggccc agggccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac
 180
 acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc
 240
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 300
 actcctgatt acgaggagaa gtcactgctt gaggctcagc tgctgtgtca gagcggaggc
 360
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 420
 gaattcccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc
 480
 gtcacccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac
 540
 accctccagg aaatgacagc aggtgccagt gactacttct ccctgggtgag tgtaaaccgt
 600
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 660
 ctgctggtgc gggacactcc gggggagaat gtggaacca gccacactgc caccgccaca
 720
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 840
 ctgccatctc ccctcgctct gcgtcccga cccatctacg ctgaggacgg agaccgcggc
 900
 atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc
 960
 caccagact cgggcaacct caccgtggcc aggagtgtcc ccagccccat gaccttctt
 1020
 ctgctggtga agggccaaca ggccgacctt gcccgctact cagtgaacca ggtcaccgtg
 1080
 gagggctgtg gctgcggccg ggagcccgcc ccgcttcccc cagagcctgt atcgtggcac
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 1200
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 1211

<210> 750

<211> 385

<212> PRT

<213> Homo sapiens

<400> 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

1	5	10	15
Leu Val Arg Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val			
20	25	30	
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro			
35	40	45	
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala			
50	55	60	
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu			
65	70	75	80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu			
85	90	95	
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val			
100	105	110	
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr			
115	120	125	
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile			
130	135	140	
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu			
145	150	155	160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser			
165	170	175	
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp			
180	185	190	
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr			
195	200	205	
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val			
210	215	220	
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys			
225	230	235	240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala			
245	250	255	
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly			
260	265	270	
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile			
275	280	285	
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro			
290	295	300	
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr			
305	310	315	320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser			
325	330	335	
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala			
340	345	350	
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp			
355	360	365	
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu			
370	375	380	
Asp			
385			

<210> 751

<211> 345

<212> DNA

<213> Homo sapiens

<400> 751

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gcaggcggcg ggctgtcgcg caccgaggag aagctcgtcg agatgtcgaa cggctgcatc
120
tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc
180
ttcgatgcgc tggtcacga gagcaccggc gtgtccgagc cgatgccggt cgccgccacg
240
ttcgatttcc gtgaccagga cggcgtctcg ctgcgcgacg tcgcgcggct ggataccatg
300
gtcaccgtcg tcgacgcgcg gtccttcctg cgcgactacg gctcg
345

<210> 752

<211> 115

<212> PRT

<213> Homo sapiens

<400> 752

Arg Val Ala Val Ile Val Asn Asp Met Ser Glu Val Asn Ile Asp Ala
1 5 10 15
Ala Leu Val Ala Ala Gly Gly Gly Leu Ser Arg Thr Glu Glu Lys Leu
20 25 30
Val Glu Met Ser Asn Gly Cys Ile Cys Cys Thr Leu Arg Asp Asp Leu
35 40 45
Met Gln Glu Val Ala Arg Leu Ala Gly Glu Gly Arg Phe Asp Ala Leu
50 55 60
Val Ile Glu Ser Thr Gly Val Ser Glu Pro Met Pro Val Ala Ala Thr
65 70 75 80
Phe Asp Phe Arg Asp Gln Asp Gly Val Ser Leu Ala Asp Val Ala Arg
85 90 95
Leu Asp Thr Met Val Thr Val Val Asp Ala Ala Ser Phe Leu Arg Asp
100 105 110
Tyr Gly Ser
115

<210> 753

<211> 352

<212> DNA

<213> Homo sapiens

<400> 753

gcgcgccagt acgccaagac cgcccgcaag gaccgcaagg gcgaacggcg gcgtcggggc
60
gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg
120
atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg
180
cctatggtag cgcattcccc gggtaccccc ttgcacggag ccttcgcgtt ccatgtcgcg
240
cgcgccaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg
300

accgacggct atatcagccc gagctgggtac gccgacccgc agggaccaca gt
352

<210> 754
<211> 91
<212> PRT
<213> Homo sapiens

<400> 754
Met His Pro Asn Arg Ala Phe Arg Phe Ala Asp Asp Val Ser Met Leu
1 5 10 15
Asp Phe Ala Ala Lys Arg Ala Phe Ala His Ile Phe Val Ser Thr Pro
20 25 30
Glu Gly Pro Met Val Ala His Ala Pro Val Thr Pro Phe Asp Gly Ala
35 40 45
Phe Arg Phe His Val Ala Arg Gly Asn Arg Ile Ala Arg His Leu Asp
50 55 60
Gly Ala Thr Leu Leu Leu Ser Ile Ser Ala Thr Asp Gly Tyr Ile Ser
65 70 75 80
Pro Ser Trp Tyr Ala Asp Pro Gln Gly Pro Gln
85 90

<210> 755
<211> 301
<212> DNA
<213> Homo sapiens

<400> 755
tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag
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ctgtctgccca tcaaaccggg ttgccgggct ggagctcttc ccaggcccgt gtgaggaaga
120
gcaaaggccg gcaggggctc gatgggacca gtcgctcgct caggcccagg aaaaccacac
180
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca
240
ggccccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccc cctacccccg
300
g
301

<210> 756
<211> 99
<212> PRT
<213> Homo sapiens

<400> 756
Met Gln Gly Leu Ser Ser Pro Arg Ile Ser Phe Leu Glu Gly Glu Lys
1 5 10 15
Gly Pro Ser Cys Leu Pro Ser Asn Arg Val Ala Gly Leu Glu Leu Leu
20 25 30
Pro Gly Pro Cys Glu Glu Glu Gln Arg Pro Ala Gly Ala Arg Trp Asp
35 40 45
Gln Ser Leu Ala Gln Ala Gln Glu Asn His Thr Ala Gly Gly Cys Gln

50 55 60
 Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
 65 70 75 80
 His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
 85 90 95
 Tyr Pro Gly

<210> 757
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 757
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 60
 gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgcac agtccccttc
 120
 gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
 180
 acgatgcct cgctcaggcg ctccggccac ctgcccaggg ccgacgccgc cgtcaccgat
 240
 cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc
 300
 gagggacgcg t
 311

<210> 758
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 758
 Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
 1 5 10 15
 Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
 20 25 30
 Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
 35 40 45
 Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
 50 55 60
 Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp
 65 70 75 80
 Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
 85 90 95
 Phe Arg Thr Thr Glu Gly Arg
 100

<210> 759
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 759

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60
attgccgagg gcaagaccta caccgcaac tcgccgaaca tgtgggtccat gttegccgtc
120
gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agaccccgga ccagttcggg
180
ggctaccgca cgctgcgtc ggaactgcac gctgccggcc tgacagcgct ggatatcgac
240
actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg
300
ggcggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg
360
gcctcgacca agcaaggcag catctacgcg t
391

<210> 760

<211> 130

<212> PRT

<213> Homo sapiens

<400> 760

Val	His	Thr	Gly	Lys	Leu	Val	Trp	Asn	Trp	Asp	Ser	Gly	Asn	Pro	Asp
1				5					10					15	
Asp	Thr	Thr	Pro	Ile	Ala	Glu	Gly	Lys	Thr	Tyr	Thr	Arg	Asn	Ser	Pro
			20					25					30		
Asn	Met	Trp	Ser	Met	Phe	Ala	Val	Asp	Glu	Lys	Leu	Gly	Met	Leu	Tyr
	35						40					45			
Leu	Pro	Met	Gly	Asn	Gln	Thr	Pro	Asp	Gln	Phe	Gly	Gly	Tyr	Arg	Thr
	50				55						60				
Pro	Ala	Ser	Glu	Leu	His	Ala	Ala	Gly	Leu	Thr	Ala	Leu	Asp	Ile	Asp
65					70					75				80	
Thr	Gly	Lys	Val	Arg	Trp	His	Tyr	Gln	Phe	Thr	His	His	Asp	Leu	Trp
				85					90					95	
Asp	Met	Asp	Val	Gly	Gly	Gln	Pro	Ser	Leu	Ile	Asp	Ile	Lys	Thr	Ala
			100					105					110		
Ala	Gly	Val	Lys	Gln	Ala	Val	Met	Ala	Ser	Thr	Lys	Gln	Gly	Ser	Ile
		115					120						125		
Tyr	Ala														
	130														

<210> 761

<211> 324

<212> DNA

<213> Homo sapiens

<400> 761

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60
ctaggagagg ccaatccttc cctgccccac agtccttct ctgcaaagct cagggggcaa
120
tcaggtagct cctgccaag agggcccat ggttcctcgc ctaaggaagg cagggcgggg
180
cattgggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg
240

cagatttcag ggagggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt
 300
 tcctcccat ccccatcca caga
 324

<210> 762
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 762
 Met Gly Asp Gly Glu Glu Asn Phe Ala Ala Tyr Gln Asp Pro Tyr Phe
 1 5 10 15
 Pro Leu Gly Pro Pro Leu Pro Glu Ile Cys Thr Cys Ser Gln Thr Asp
 20 25 30
 Pro Ser Pro Gln Leu Ser Pro Ala Val Asn Gly Ser Gln Cys Pro Ala
 35 40 45
 Leu Pro Ser Leu Gly Glu Glu Pro Trp Gly Pro Leu Gly Gln Glu Val
 50 55 60
 Pro Asp Cys Pro Leu Ser Phe Ala Glu Lys Glu Leu Trp Gly Arg Glu
 65 70 75 80
 Gly Leu Ala Ser Pro Arg Arg Tyr Phe Leu Leu His Gln Gly Ser Lys
 85 90 95
 Lys Val Arg Pro Leu Trp Ala Tyr Leu
 100 105

<210> 763
 <211> 301
 <212> DNA
 <213> Homo sapiens

<400> 763
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 60
 tcctcggcgg tgtgctggaa gtggcggcca atatcgcatg tactcggggc gcgaccgctg
 120
 ccgcggtggc cgccaccggc tttaccgagg ccaccggcgg cctcggctgc ttcctgctgg
 180
 gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc
 240
 tgaccaagat atgcaatgcc tttaacaacg ccttatttgc gccaccgtg catgcgaaca
 300
 t
 301

<210> 764
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 764
 Met Phe Ala Cys Thr Val Gly Ala Asn Lys Ala Leu Leu Lys Ala Leu
 1 5 10 15
 His Ile Leu Val Ser Pro Val Ser Ala Pro Met Leu Leu Met Ala Arg

```

          20          25          30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
          35          40          45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Val Ala
          50          55          60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
65          70          75          80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
          85          90          95
Ala His Asn Ala
          100

```

<210> 765
 <211> 831
 <212> DNA
 <213> Homo sapiens

<400> 765
 ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca
 60
 taacattggt gttcctgtat ttaaggccct ataaacaggg agatgcgcca cctcatcagt
 120
 agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
 180
 agagaagccc agtctgacct gaacaagaca cgctgcgta gtggtagtgc cctcctgcag
 240
 tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
 300
 gacttatcct ccagtcctc agcttcaaag gcatctcagg aggatgccaa tgaaatcaag
 360
 tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
 420
 agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
 480
 aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
 540
 gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag
 600
 gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
 660
 cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc
 720
 aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
 780
 aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a
 831

<210> 766
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 766
 Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

```
<210> 767
<211> 431
<212> DNA
<213> Homo sapiens
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836

<210> 768
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 768
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser
 1 5 10 15
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala
 20 25 30
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
 35 40 45
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
 50 55 60
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
 65 70 75 80
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
 85 90 95
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser
 100 105 110

<210> 769
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 769
 tgtacacctc gtaatacatg atcgcgatac cgcccgcat gaccctaagc aactcattct
 60
 cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctggtttcc gtatgaaaga
 120
 acggtatggt ttgtatgtcg cggccctgcc actcaaact caccgtgtca cccacctcaa
 180
 aaaaatcccg ggtcggccca caaataaatc aattgcgccg ctccctccgag ttcttccatg
 240
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaaggttg
 300
 acgttgacct gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg
 360
 cccatgtcga tgatctacat cgccaccggc agcgtgtctt cgtagtcgtc atgcctgac
 420
 an
 422

<210> 770
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 770
 Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro
 1 5 10 15
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```

                20                25                30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
      35                40                45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
      50                55                60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
65                70                75                80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
      85                90                95
Pro Asp Xaa

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<210> 771
 <211> 369
 <212> DNA
 <213> Homo sapiens

```

<400> 771
gcctacgcgc aattcctcgc gggatatggcg tttaacaatg cgtctctcgg gtatgtgcat
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gcaatggcgc atcagctggg cggtttttac gatctgccgc acggcgtgtg caatgcgata
120
ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gccaggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
atgcagaga ttcgctctct ggcacgtcag gtgaatatcc cgggtgggatt gcgtgacctc
300
aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

```

<210> 772
 <211> 123
 <212> PRT
 <213> Homo sapiens

```

<400> 772
Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
1                5                10                15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
      20                25                30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
      35                40                45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
      50                55                60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65                70                75                80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
      85                90                95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
      100                105                110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

```

115

120

<210> 773
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 773
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 60
 ggttacttga tccgcgtgga gccgggcgta caaactccgg aattcaccct ggaaaacgcc
 120
 tccggttccct gccgggattc ggcggtggtg ctggtgcaac tgctgcgcaa cctgggcctg
 180
 gcggcgcgat ttgtgtctgg ctatctgac caactgaccg ccgacgtcaa agccctcgac
 240
 ggcccgtccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgtatttg
 300
 cccggcgcc
 309

<210> 774
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 774
 Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu
 1 5 10 15
 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr
 20 25 30
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala
 35 40 45
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe
 50 55 60
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp
 65 70 75 80
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys
 85 90 95
 Glu Val Tyr Leu Pro Gly Ala
 100

<210> 775
 <211> 4125
 <212> DNA
 <213> Homo sapiens

<400> 775
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 60
 atctcatctg acgtgagttc aagtacagat cacacgccca ctaaagccca gaagaatgtg
 120
 gctaccagcg aagactccga cctgagcatg cgcacactga gcacgcccag cccagccctg
 180

atatgtccac cgaatctccc aggatttcag aatggaaggg gctcgtccac ctctcgtcc
 240
 tccatcaccg gggagacggg ggccatgggt cactccccgc cccgacccg cctcacacac
 300
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 360
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 420
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 480
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 540
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 720
 aatctggagc acctggatgt gtcaggatgc tccaaagtga cctgcatcag cttgacccgg
 780
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 840
 atgacggact gcttcgtgct ggaggacgaa ggctgcaca ccatcgcggc gcactgcacg
 900
 cagctcacc acccttaact gcgccgtgc gtccgcctga ccgacgaagg cctgcgctac
 960
 ctggtgatct actgcgcctc catcaaggag ctgagcgtca gcgactgccg cttcgtcagc
 1020
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 1080
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 1140
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 1200
 aagaactgca ccaaactcaa atccctggat atcggcaaat gccctttggt atccgacacg
 1260
 ggcttgaggt gcttggccct gaactgcttc aacctcaagc ggctcagcct caagtccctg
 1320
 gagagcatca ccggccaggg cttgcagatc gtggccgcca actgctttga cctccagacg
 1380
 ctgaatgtcc aggactgcga ggtctccgtg gaggccctgc gctttgtcaa acgccactgc
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 1560
 ccgacaccca ctcaaacag ctctttcttc cggaaggtt attaggaatc tggcctttat
 1620
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 1680
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 1740
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 1800

gccctttccc tcgcacacag gccccacccc cacagttcca cgccccccc ccaaggccac
1860
accctccctc cctagagcag cagcgaggat ccatcatcag aatcacagtg ctctccagac
1920
ctcctctcta aactgcttca ttgacctaaag tcaactctctt caatcccaca cccatggaca
1980
ttcttgtaa ctcaatacca tagcactttg cataggcaaa atacttttca ggccttttta
2040
aaaaattcat tacagcaaac agctggggaa ggacatgcag tcctcccca gctctgtcaa
2100
tgactatgac cttggccaaa gcacttcact gctctgggct gcagcttcca gcactgaatc
2160
agaggccaca cagcccaaag attagcttca tgtccattat agcattgagg gagcagagat
2220
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2280
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2340
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2400
cctctccac ctctcacat cctcttttgc caggctggat gctgtcgtct ctgtacacaa
2460
atactttctg cattcccccc tccacaccat cctagcgagg caccagcaca cctaatacaca
2520
gcaaagccca gatccccca tcagttgctt ttactcagtg ttttcaaata ggagtaaagg
2580
cccttgcaat ttttaattaa caagcaaggc ccaagggaa acatgtcctc aaaagttttt
2640
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2700
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2760
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2880
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3000
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3240
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3300
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3420

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 3480
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 3540
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 3600
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 3660
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 3720
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 3780
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 3840
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 3900
 gagaccaaac caaaggtctc actaggaaat ttatctgttt taaaacattg cttccttctc
 3960
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 4020
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 4080
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 4125

<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

Tyr	Gly	Ser	Glu	Gly	Lys	Gly	Ser	Ser	Ser	Ile	Ser	Ser	Asp	Val	Ser
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Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
		35				40					45				
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55					60				
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
				85					90					95	
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100						105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
	115					120					125				
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130					135					140				
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
145					150				155					160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165					170					175		
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

```

      180      185      190
Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
      195      200      205
Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
      210      215      220
Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
      225      230      235      240
Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
      245      250      255
Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
      260      265      270
Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
      275      280      285
Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
      290      295      300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
      305      310      315      320
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
      325      330      335
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
      340      345      350
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
      355      360      365
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
      370      375      380
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
      385      390      395      400
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
      405      410      415
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
      420      425      430
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
      435      440      445
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
      450      455      460
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
      465      470      475      480
Ala Phe Phe

```

<210> 777

<211> 705

<212> DNA

<213> Homo sapiens

<400> 777

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ggtaccatcg tttttaaac taattaagat attactcatt cttgttggtg cccaattcca
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caccaatctg ctctttaatg ccagactgat ggctctaaca atccttatta actccttttt
120
gtggcttcaa ggaaaaacaa aaacctcttc tctcattcac cacctctagg ccaggagaaa
180
ttatcttttg ttcaggcttt cacagtgggg gtctgaaagt gaccagtcta gaaaaggatg
240

```

```
<400> 779
tccggacatg tgcaaacaaat tcaatgatgt ggtgcgtcga catggtgtgc atcactctgt
60
gactgtgagt gattctgagg ataccgttgc gccgtcccag ctggttcgat cccctcgtaa
120
cgccttgccct ttgaaggaac ccagtgggaa ggctagacca agtaaatatg aatcaccaaa
180
```

cgccagcaac ttcacgtca ggcattgtggc aactggcaaa gagggcactg atgatgagta
 240
 tgctaactca aactactact actegatgtc tgccaatcga ctaggagacg aggaaacgga
 300
 ggaaatgata ggtttggcta cc
 322

<210> 780
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 780
 Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His
 1 5 10 15
 Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu
 20 25 30
 Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys
 35 40 45
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val
 50 55 60
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn
 65 70 75 80
 Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu
 85 90 95
 Thr Glu Glu Met Ile Gly Leu Ala Thr
 100 105

<210> 781
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 781
 nntcgctgc ctggaatgtg tgtctgtgta tgtgtgtgta tgtatgtgtg tatggaatgt
 60
 gtgtgtatgn gaatatgtgt gtgtatngga atgtgtgtgt gtgtttggaa tgtgtgtatg
 120
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatnggaa tgtgtgtgtg tgtttggaat
 180
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg
 240
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tgngaattgtg tgtgtgt
 297

<210> 782
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 782
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val
 1 5 10 15
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```

                20                25                30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
                35                40                45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
                50                55                60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
65                70                75                80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
                85                90                95
Cys Val Cys

```

<210> 783
 <211> 612
 <212> DNA
 <213> Homo sapiens

```

<400> 783
accggtgacg taactgctcc cgctggcagc ttcgagggcg atgtcgattt gcggtgcccg
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caccgggtcg agtgagctgc ccagcagcaa gcccaccaca tcggtgacca gaccgatcac
120
tttgttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggg
180
ccgcacaaaa atcggctggg tgtcgatcaa ctgcggggtg ccaatcgag aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgctggct ttgttgaca gctgcacaaa gccctgaatc aggttgaaca
360
gttcgaggtt gacgtccagg gcgctcttgt ccgtgccgtt ttgtatattg atcaggtcgc
420
ccaggtgcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg cccagcttga gcacatcgat ggcggcctgg atcaactggc
540
cgacggtcgc gtcggtcttg agcaactggc cgtagttgcc ggcgctgacg ttgaggcgga
600
tgcccgacgc gt
612

```

<210> 784
 <211> 190
 <212> PRT
 <213> Homo sapiens

```

<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
1                5                10                15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
                20                25                30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
                35                40                45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

```

```

      50      55      60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65      70      75      80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85      90      95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100      105      110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115      120      125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130      135      140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145      150      155      160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165      170      175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180      185      190

```

<210> 785
 <211> 408
 <212> DNA
 <213> Homo sapiens

```

<400> 785
accttggaact acttcactat cgaccctcgg ctaggcgacg acgatgactt cgatcacctg
60
cttcaggcgcg ccacgcgtcg tggctgtgca gtactgctcg acggggtggt caaccacgtc
120
tcgcgtcgca accgcacgtg gcaggatgcg cagagtgtcg ggccagattc agacgccggc
180
cgtatgggttc gctgggtgtga ggggcgcctc gacgttttcg aggggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcaagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgcgggtcgcg gtgttgacgg ctggcggtcg gacgcgcgta ttccgtcaat cctgagtctt
360
gggctgcggt gctgcctccg gtgcgagaga agcgcctga cgtgagga
408

```

<210> 786
 <211> 134
 <212> PRT
 <213> Homo sapiens

```

<400> 786
Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

```

```

65              70              75              80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
      85              90              95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
      100              105              110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
      115              120              125
Glu Arg Ser Ala Leu Thr
      130

```

```

<210> 787
<211> 310
<212> DNA
<213> Homo sapiens

```

```

<400> 787
acgcgtgaag ggggaatgaaa ggggtttttcc tggatcaaaa tgatgcttgt ggcagacaca
60
gttggaaacca cagacgatgc cacgcttgtg tcagcagtgc gacactggcc cacgtggcgt
120
ccttggtctc tcctcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggctggcg gagaaagacc ggcccccttca cccacaccta
240
gacttcctgg aagggccgcc cgggtccaca acctggcccc ttaactccct gggcagctgc
300
tggggggagaa
310

```

```

<210> 788
<211> 90
<212> PRT
<213> Homo sapiens

```

```

<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1              5              10              15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
      20              25              30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
      35              40              45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
      50              55              60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65              70              75              80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
      85              90

```

```

<210> 789
<211> 369
<212> DNA
<213> Homo sapiens

```

```

<400> 789

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acgcgtgaag ttgcagcagc aagcaatctg cctcgcttct ggtgcccacc gaaaccaagg
 60
 tctgccagac agcagcgctg ggacctctcc cctccccagc aggatgggccc ggctctggaa
 120
 gcacgaggtg ttccaaagtg caaacaagct gctgttaaata aattattccc aaacgccaaa
 180
 gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg
 240
 gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt
 300
 gagtgtatgc ctgtatttcc ctgcagagct gattgccagt ccattttctt ctatcccatc
 360
 cccatttttc
 369

<210> 790

<211> 114

<212> PRT

<213> Homo sapiens

<400> 790

Met	Asp	Trp	Gln	Ser	Ala	Leu	Gln	Gly	Asn	Thr	Gly	Ile	His	Ser	Gln
1				5				10					15		
Glu	Thr	Pro	Cys	Phe	Ile	Thr	His	Asn	Lys	Lys	Lys	Thr	Lys	Cys	Gln
			20					25					30		
Tyr	Ser	Ala	Leu	Ala	Ile	Ser	Val	Arg	Gly	Lys	Lys	Arg	Lys	Lys	Gln
			35				40					45			
Ala	Ser	Lys	Pro	Ala	Arg	Ala	Leu	Ala	Phe	Gly	Asn	Asn	Tyr	Leu	Thr
		50				55				60					
Ala	Ala	Cys	Leu	His	Phe	Gly	Thr	Pro	Arg	Ala	Ser	Arg	Ala	Gly	Pro
65				70					75					80	
Ser	Cys	Trp	Gly	Gly	Glu	Arg	Ser	Gln	Arg	Cys	Cys	Leu	Ala	Asp	Leu
			85					90						95	
Gly	Phe	Gly	Gly	His	Gln	Lys	Arg	Gly	Arg	Leu	Leu	Ala	Ala	Ala	Thr
			100					105						110	
Ser	Arg														

<210> 791

<211> 420

<212> DNA

<213> Homo sapiens

<400> 791

nctctgacca aaaggaaggt atatgaaaac acaacactag gcttcattgt tgaagttgaa
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 ggtcttccag ttcttggtgt gaaatgggtat cgaaataaat ctttactaga gccagatgaa
 120
 agaatcaaaa tggaaagagt gggtaatgtg tgttctactgg aaattttctaa cattcaaaaa
 180
 ggagaagggg gagagtacat gtgtcatgct gtaaacaatca taggggaagc aaagagcttt
 240
 gcaaatgtag acataatgcc ccaggaagaa agagtgggtgg cactaccacc tccagtaaca
 300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct
 360
 caagaaattg tcctggaagt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag
 420

<210> 792
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 792
 Thr Lys Arg Lys Val Tyr Glu Asn Thr Thr Leu Gly Phe Ile Val Glu
 1 5 10 15
 Val Glu Gly Leu Pro Val Pro Gly Val Lys Trp Tyr Arg Asn Lys Ser
 20 25 30
 Leu Leu Glu Pro Asp Glu Arg Ile Lys Met Glu Arg Val Gly Asn Val
 35 40 45
 Cys Ser Leu Glu Ile Ser Asn Ile Gln Lys Gly Glu Gly Gly Glu Tyr
 50 55 60
 Met Cys His Ala Val Asn Ile Ile Gly Glu Ala Lys Ser Phe Ala Asn
 65 70 75 80
 Val Asp Ile Met Pro Gln Glu Glu Arg Val Val Ala Leu Pro Pro Pro
 85 90 95
 Val Thr His Gln His Val Met Glu Phe Asp Leu Glu His Thr Thr Ser
 100 105 110
 Ser Arg Thr Pro Ser Pro Gln Glu Ile Val Leu Glu Val Glu Leu Ser
 115 120 125
 Glu Lys Asp Val Lys Glu Phe Glu Lys Gln
 130 135

<210> 793
 <211> 479
 <212> DNA
 <213> Homo sapiens

<400> 793
 nacgcgtgcc ggttctcgga aattcattat gggaatgtgc gcgttgtgga gatgctcaga
 60
 ccgcgaacag tactgcgga acccaaacga tcatttttaa cccagacgt ccctgaacca
 120
 aagccaaagt ctacaggtca ctggggcaga ggccgccga aaccagcttc ccctcccggc
 180
 ctaggcgcg caggtccccg cccagccggg gcgatccttt ggtcggacag tgagggtggg
 240
 agcccaccgc acccaagtcc gccgcatcca cccggcgag gcgacccccg acgggcagcc
 300
 gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttcccta
 360
 gcggaggctg ggcggcgggc ttcgcgcctg cctcagtctc cccatccgtg gcccggggga
 420
 tggagccccg tcgcgcgaga ggctgcgga ggtcccagcc aggtgcctg gaacgtgga
 479

<210> 794

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 794
 Xaa Ala Cys Arg Phe Ser Glu Ile His Tyr Gly Asn Val Arg Val Val
 1 5 10 15
 Glu Met Leu Arg Pro Arg Thr Val Leu Arg Glu Pro Lys Arg Ser Phe
 20 25 30
 Leu Thr Pro Asp Val Pro Glu Pro Lys Pro Lys Ser Thr Gly His Trp
 35 40 45
 Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
 50 55 60
 Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly
 65 70 75 80
 Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro
 85 90 95
 Arg Arg Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
 100 105 110
 Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser
 115 120 125
 Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu
 130 135 140
 Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val
 145 150 155

<210> 795
 <211> 1418
 <212> DNA
 <213> Homo sapiens

<400> 795
 gccggcgccg gggaggccgg ggcctgcagg ccccggtac gacaagatcc ggactccggc
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 ccggactacg aggcgctgcc ggctggagcc actgtcacca cgcacatggt ggcaggcgcc
 120
 gtggcagggg tcttggagca ctgcgtgatg taccatcatc actgctcaa gaccgggatg
 180
 cagagtctac agcctgaccc agctgcccgc tatcgcaatg tgttggaggc cctctggagg
 240
 attataagaa cggagggcct atggaggccc atgagggggc tgaacgtcac agcaacaggc
 300
 gcagggcctg cccacgcctt ttattttgcc tgctacgaaa agttaaaaaa gacattgagt
 360
 gatgtaatcc accctggggg caatagccat attgccaatg gtgcggccgg gtgtgtggca
 420
 acattacttc atgatgcagc catgaacctt gcggaaggct gatctgctga cttggggctc
 480
 tgaatctgga tactctccat caccggttgg ctgctgtcac catttccttc ctcgttgatg
 540
 gcactactag tgggtcaagca gaggatgcag atgtacaact caccatacca ccgggtgaca
 600
 gactgtgtac gggcagtgtg gcaaaatgaa ggggccgggg ccttttaccg cagctacacc
 660

acccagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg
 720
 caggagcact ttaacccccca gagacggtac aacccaagct cccacgtcct ctctggagct
 780
 tgcgcaggag ctgtagctgc cgcagccaca accccactgg acgtttgcaa aacactgctc
 840
 aacacccagg agtccttggc tttgaactca cacattacag gacatatcac aggcatggct
 900
 agtgccttca ggacggtata tcaagtaggt ggggtgaccg cctatttccg aggggtgcag
 960
 gccagagtaa tttaccagat cccctccaca gccatcgcat ggtctgtgta tgagttcttc
 1020
 aaatacctaa tcactaaaag gcaagaagag tggagggtcg gcaagtgaag tagcactgaa
 1080
 cgaagccagg ggttcagatg aactgctgc atcctggtca cattctctgt ctctggaat
 1140
 gctccacact caagtggagt tagaaggaag gtagaggggc tctccccag gattttggtg
 1200
 ttttgactaa caccagttcc tgccaacctc tgttgccacc acctttcctt ccaggcccta
 1260
 agcactgca gcaaagcaca ccacagcacc tttgataacc tctctccatc ctgggcctga
 1320
 tgacctgctc tagactgtta tagaggata agcagtcacat tcccctgggt cctaataaaa
 1380
 agcctttaa ttaaaaaaaaa aaaaaaaaaa aaaaaaaaa
 1418

<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

Met	Ala	Leu	Leu	Val	Val	Lys	Gln	Arg	Met	Gln	Met	Tyr	Asn	Ser	Pro
1				5					10					15	
Tyr	His	Arg	Val	Thr	Asp	Cys	Val	Arg	Ala	Val	Trp	Gln	Asn	Glu	Gly
			20					25					30		
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Val
		35					40				45				
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Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
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Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser	His
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Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val	Tyr
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Gln	Val	Gly	Gly	Val	Thr	Ala	Tyr	Phe	Arg	Gly	Val	Gln	Ala	Arg	Val
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<211> 585

<212> DNA

<213> Homo sapiens

<400> 797

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<400> 798

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<213> Homo sapiens

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<213> Homo sapiens

<400> 804

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Pro	Arg	Lys	Ala	Glu	Pro	His	Ser	Phe	Arg	Glu	Lys	Val	Phe	Arg	Lys
			20					25					30		
Lys	Pro	Pro	Val	Cys	Ala	Val	Cys	Lys	Val	Thr	Ile	Asp	Gly	Thr	Gly
			35				40					45			
Val	Ser	Cys	Arg	Val	Cys	Lys	Val	Ala	Thr	His	Arg	Lys	Cys	Glu	Ala
	50				55					60					
Lys	Val	Thr	Ser	Ala	Cys	Gln	Ala	Leu	Pro	Pro	Val	Glu	Leu	Arg	Arg
65					70				75					80	
Asn	Thr	Ala	Pro	Val	Arg	Arg	Ile	Glu	His	Leu	Gly	Ser	Thr	Lys	Ser
				85					90					95	
Leu	Asn	His	Ser	Lys	Gln	Arg	Ser	Thr	Leu	Pro	Arg	Ser	Phe	Ser	Leu
			100					105					110		
Asp	Pro	Leu	Met	Glu	Arg	Arg	Trp	Asp	Leu	Asp	Leu	Thr	Tyr	Val	Thr
			115				120					125			
Glu	Arg	Ile	Leu	Ala	Ala	Ala	Phe	Pro	Ala	Arg	Pro	Asp	Glu	Gln	Arg
	130				135						140				
His	Arg	Gly	His	Leu	Arg	Glu	Leu	Ala	His	Val	Leu	Gln	Ser	Lys	His
145				150					155					160	
Arg	Asp	Lys	Tyr	Leu	Leu	Phe	Asn	Leu	Ser	Glu	Lys	Arg	His	Asp	Leu
				165				170						175	
Thr	Arg	Leu	Asn	Pro	Lys	Val	Gln	Asp	Phe	Gly	Trp	Pro	Glu	Leu	His
			180					185					190		
Ala	Pro	Pro	Leu	Asp	Lys	Leu	Cys	Ser	Ile	Cys	Lys	Ala	Met	Glu	Thr
			195				200					205			
Trp	Leu	Ser	Ala	Asp	Pro	Gln	His	Val	Val	Val	Leu	Tyr	Cys	Lys	Gly
	210					215					220				
Asn	Lys	Gly	Lys	Leu	Gly	Val	Ile	Val	Ser	Ala	Tyr	Met	His	Tyr	Ser
225				230					235					240	
Lys	Ile	Ser	Ala	Gly	Ala	Asp	Gln	Ala	Leu	Ala	Thr	Leu	Thr	Met	Arg
				245				250						255	
Lys	Phe	Cys	Glu	Asp	Lys	Val	Ala	Thr	Glu	Leu	Gln	Pro	Ser	Gln	Arg
			260					265					270		
Arg	Tyr	Ile	Ser	Tyr	Phe	Ser	Gly	Leu	Leu	Ser	Gly	Ser	Ile	Arg	Met
	275						280					285			
Asn	Ser	Ser	Pro	Leu	Phe	Leu	His	Tyr	Val	Leu	Ile	Pro	Met	Leu	Pro

290 295 300
 Ala Phe Glu Pro Gly Thr Gly Phe Gln Pro Phe Leu Lys Ile Tyr Gln
 305 310 315 320
 Ser Met Gln Leu Val Tyr Thr Ser Gly Val Tyr His Ile Ala Gly Pro
 325 330 335
 Gly Pro Gln Gln Leu Cys Ile Ser Leu Glu Pro Ala Leu Leu Lys
 340 345 350
 Gly Asp Val Met Val Thr Cys Tyr His Lys Gly Gly Arg Gly Thr Asp
 355 360 365
 Arg Thr Leu Val Phe Arg Val Gln Phe His Thr Cys Thr Ile His Gly
 370 375 380
 Pro Gln Leu Thr Phe Pro Lys Asp Gln Leu Asp Glu Ala Trp Thr Asp
 385 390 395 400
 Glu Arg Phe Pro Phe Gln Ala Ser Val Glu Phe Val Phe Ser Ser Ser
 405 410 415
 Pro Glu Lys Ile Lys Gly Ser Thr Pro Arg Asn Asp Pro Ser Val Ser
 420 425 430
 Val Asp Tyr Asn Thr Thr Glu Pro Ala Val Arg Trp Asp Ser Tyr Glu
 435 440 445
 Asn Phe Asn Gln His His Glu Asp Ser Val Asp Gly Ser Leu Thr His
 450 455 460
 Thr Arg Gly Pro Leu Asp Gly Ser Pro Tyr Ala Gln Val Gln Arg Pro
 465 470 475 480
 Pro Arg Gln Thr Pro Pro Ala Pro Ser Pro Glu Pro Pro Pro Pro
 485 490 495
 Met Leu Ser Val Ser Ser Asp Ser Gly His Ser Ser Thr Leu Thr Thr
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 Glu Pro Ala Ala Glu Ser Pro Gly Arg Pro Pro Pro Thr Ala Ala Glu
 515 520 525
 Arg Gln Glu Leu Asp Arg Leu Leu Gly Gly Cys Gly Val Ala Ser Gly
 530 535 540
 Gly Arg Gly Ala Gly Arg Glu Thr Ala Ile Leu Asp Asp Glu Glu Gln
 545 550 555 560
 Pro Thr Val Gly Gly Gly Pro His Leu Gly Val Tyr Pro Gly His Arg
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 580 585 590
 Cys Gly Val Pro Asn Gly Gly Tyr Arg Pro Glu Gly Thr Leu Glu
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 Arg Arg Arg Leu Ala Tyr Gly Gly Tyr Glu Gly Ser Pro Gln Gly Tyr
 610 615 620
 Ala Glu Ala Ser Met Glu Lys Arg Arg Leu Cys Arg Ser Leu Ser Glu
 625 630 635 640
 Gly Leu Tyr Pro Tyr Pro Pro Glu Met Gly Lys Pro Ala Thr Gly Asp
 645 650 655
 Phe Gly Tyr Arg Ala Pro Gly Tyr Arg Glu Val Val Ile Leu Glu Asp
 660 665 670
 Pro Gly Leu Pro Ala Leu Tyr Pro Cys Pro Ala Cys Glu Glu Lys Leu
 675 680 685
 Ala Leu Pro Thr Ala Ala Leu Tyr Gly Leu Arg Leu Glu Arg Glu Ala
 690 695 700
 Gly Glu Gly Trp Ala Ser Glu Ala Gly Lys Pro Leu Leu His Pro Val
 705 710 715 720
 Arg Pro Gly His Pro Leu Pro Leu Leu Leu Pro Ala Cys Gly His His

863

1155 1160 1165
 Leu Lys Val Ala Thr Pro Pro Pro Ser Ala Gln Pro Trp Lys Gly Asp
 1170 1175 1180
 Pro Val Glu Gln Leu Val Arg His Phe Leu Ile Glu Thr Gly Pro Lys
 1185 1190 1195 1200
 Gly Val Lys Ile Lys Gly Cys Pro Ser Glu Pro Tyr Phe Gly Ser Leu
 1205 1210 1215
 Ser Ala Leu Val Ser Gln His Ser Ile Ser Pro Ile Ser Leu Pro Cys
 1220 1225 1230
 Cys Leu Arg Ile Pro Ser Lys Asp Pro Leu Glu Glu Thr Pro Glu Ala
 1235 1240 1245
 Pro Val Pro Thr Asn Met Ser Thr Ala Ala Asp Leu Leu Arg Gln Gly
 1250 1255 1260
 Ala Ala Cys Ser Val Leu Tyr Leu Thr Ser Val Glu Thr Glu Ser Leu
 1265 1270 1275 1280
 Thr Gly Pro Gln Ala Val Ala Arg Ala Ser Ser Ala Ala Leu Ser Cys
 1285 1290 1295
 Ser Pro Arg Pro Thr Pro Ala Val Val His Phe Lys Val Ser Ala Gln
 1300 1305 1310
 Gly Ile Thr Leu Thr Asp Asn Gln Arg Lys Leu Phe Phe Arg Arg His
 1315 1320 1325
 Tyr Pro Val Asn Ser Ile Thr Phe Ser Ser Thr Asp Pro Gln Asp Arg
 1330 1335 1340
 Arg Trp Thr Asn Pro Asp Gly Thr Thr Ser Lys Ile Phe Gly Phe Val
 1345 1350 1355 1360
 Ala Lys Lys Pro Gly Ser Pro Trp Glu Asn Val Cys His Leu Phe Ala
 1365 1370 1375
 Glu Leu Asp Pro Asp Gln Pro Ala Gly Ala Ile Val Thr Phe Ile Thr
 1380 1385 1390
 Lys Val Leu Leu Gly Gln Arg Lys
 1395 1400

<210> 805
 <211> 550
 <212> DNA
 <213> Homo sapiens

<400> 805
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 120
 agtcatccat ttacttatca agctgttact gtgtgtgcaa gaagcgccag agagatgata
 180
 tcaaggagct cttaccatgg ctggcataga gcggctgatg agtaagtcc gtctgcacaa
 240
 agagtcccta agcattcatt cttggctgac attcttggct caggggggtct ccatggcctt
 300
 gttccccctc tcgggtcacc agttcaggtc gagggggcct atgcttggaa gggccacacc
 360
 aatggacctt gccaggacac tcagtcacag gtttcacacc caaagagaag acagcccaac
 420
 ccagaccctc aaaagagagc acctggggga agggagcgtg gaaaccagga ctcagaaaga
 480

cacaagagaa aaagaagctg tacactgggg aggcttccgg ggtacctgtg cctgccatgt
 540
 ctctgaaggc
 550

<210> 806
 <211> 118
 <212> PRT
 <213> Homo sapiens

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 20 25 30
 Met Ala Leu Phe Pro Ser Ser Gly His Gln Phe Arg Ser Arg Gly Pro
 35 40 45
 Met Leu Gly Arg Ala Thr Pro Met Asp Leu Ala Arg Thr Leu Ser His
 50 55 60
 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg
 65 70 75 80
 Glu His Leu Gly Glu Gly Ser Val Glu Thr Arg Thr Gln Lys Asp Thr
 85 90 95
 Arg Glu Lys Glu Ala Val His Trp Gly Gly Phe Arg Gly Thr Cys Ala
 100 105 110
 Cys His Val Ser Glu Gly
 115

<210> 807
 <211> 287
 <212> DNA
 <213> Homo sapiens

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 cccgaggtgg gagagcgcg cgcattggcga ccgtaaacgt atcggtgtcc gatgcatga
 120
 ccgagtgggt cgaagctcag accgggacag gccgctatac cagcgcgagc gattatatct
 180
 gcgccctgat tcgccaggac caggagcgaa gcgacggcct caggcagctt caaacgttga
 240
 tcaccgaggg gtccgacagc ggcattcagc cctcgctcgt tgatgac
 287

<210> 808
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 808
 Met Ala Val Ala Leu Pro His Trp Gln Asp Ala Lys Phe Leu Ala Met
 1 5 10 15
 Ile Ser Arg Gly Gly Arg Ala Arg Gly Met Ala Thr Val Asn Val Ser

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                20                25                30
Leu Ser Asp Ala Met Thr Glu Trp Val Glu Ala Gln Thr Gly Thr Gly
      35                40                45
Arg Tyr Thr Ser Ala Ser Asp Tyr Ile Cys Ala Leu Ile Arg Gln Asp
      50                55                60
Gln Glu Arg Ser Asp Gly Leu Arg Gln Leu Gln Thr Leu Ile Thr Glu
      65                70                75                80
Gly Phe Asp Ser Gly Ile Ser Ala Ser Ser Leu Asp Asp
                85                90

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<210> 809
 <211> 405
 <212> DNA
 <213> Homo sapiens

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<400> 809
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gggccccccc ccccccccc ccttttttttc cccggggggg tttattccca gggccaacag
120
gacgcgtggt cgcgtcaa at ggagagacga tgggtgccgc ccttgcccca cgatcctgat
180
ggccccgaga ttcctgacga tgtcaccacc ctgcaccaac aggtaatggg tctgccacgt
240
cacctgggta tccactcagc tggaatggtg ctgacgcgag aaccagtagg acgcattctgc
300
cccattgagc cggctcgaat gtttggtcgc acggggctgc agtgggacaa anaaaactgt
360
gcctggatgg ggttggggaa gtttgatctg cttgggttgg ggatg
405

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<210> 810
 <211> 135
 <212> PRT
 <213> Homo sapiens

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<400> 810
Xaa Gly Gly Gly Gly Gly Gly Val Phe Phe Pro Pro Lys Lys Lys Lys
1      5      10      15
Gly Gly Gly Gly Gly Pro Pro Pro Pro Pro Pro Leu Phe Phe Pro Arg
      20      25      30
Gly Val Tyr Ser Gln Gly Gln Gln Asp Ala Trp Ser Arg Gln Met Glu
      35      40      45
Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
      50      55      60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
      65      70      75      80
His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
      85      90      95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
      100      105      110
Leu Gln Trp Asp Lys Xaa Asn Cys Ala Trp Met Gly Leu Gly Lys Phe
      115      120      125
Asp Leu Leu Gly Leu Gly Met

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130

135

<210> 811
 <211> 642
 <212> DNA
 <213> Homo sapiens

<400> 811
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 cagtgccaat gactgccaat ggcaaagaag agctccaacc aaacaccagg tgcttcatgg
 120
 tggtagacaca ttaacaacac ccgggaagca gtactgcaa cacctagata tgagaaaaag
 180
 aaaacaggca cttaaagcga ggctaaccac ctttcaggaa tgataaaggg cagaggaccc
 240
 tgctacctct acccctgcta ctaaaggcgt ggcccacaga gcagcagcac cagcagcaca
 300
 taaaatgggg ttaaataatga caggaaaaac aaggtagacag ggaaatgggg tgaagatcaa
 360
 gtctgtggta ngctcttctt tcctagaggc ttggggcctg agctcttggg gaaagctctc
 420
 caacacctca ggggtgtgctt gttcccttgc cctgtgggga tgctcttctt acgggtggct
 480
 gactggctcc cactttcctc cgtattgttg tcttgtctct tccctcaca ccatcaaggc
 540
 tctttccctt aattctataa gacagtacct ctggcttaga aattatatgc cctcctttaa
 600
 aaaaacgaaa tgctagagga catagaactt gaggaataat tt
 642

<210> 812
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 812
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 Pro Val Ser His Pro Tyr Lys Glu His Pro His Arg Ala Gly Glu Gln
 20 25 30
 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys
 35 40 45
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe
 50 55 60
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala
 65 70 75 80
 Ala Gly Ala Ala Ala Leu Trp Ala Thr Pro Leu Val Ala Gly Val Glu
 85 90 95
 Val Thr Gly Ser Ser Ala Leu Tyr His Ser
 100 105

<210> 813
 <211> 558

<212> DNA

<213> Homo sapiens

<400> 813

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ccccggcgat agtcgctgg ggtcatggcg gatgaggggt taagagcgcg ttactgcgg
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120
gttcgctgac cagcaccggg ccgcccggct gggccgggaa accgtggaac aagggaagcg
180
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300
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420
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558

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<210> 814

<211> 151

<212> PRT

<213> Homo sapiens

<400> 814

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Met Thr Phe Ser Ala Gly Ser Leu Thr Ser Thr Gly Pro Pro Gly Trp
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 20           25           30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
 35           40           45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
 50           55           60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
 65           70           75           80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
 85           90           95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100          105          110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
115          120          125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
130          135          140
Glu Leu Val Gly Gly Tyr Ala
145          150

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<210> 815

<211> 315

<212> DNA

<213> Homo sapiens

<400> 815

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120
agctagcgca ggagaaagcc gagacctcac gtccgaagcg gattcagcaa gtgcacaacc
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240
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315

<210> 816

<211> 90

<212> PRT

<213> Homo sapiens

<400> 816

Met	Pro	Ser	Asp	Leu	Pro	Lys	Val	Asp	Asp	Glu	Lys	Ala	His	Asp	Ala
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Pro	His	Thr	Asp	Gly	Ser	Glu	Pro	Gly	Gln	Ala	Ser	Ala	Gly	Glu	Ser
			20					25					30		
Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
		35					40					45			
His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
	50					55					60				
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
65					70					75				80	
Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
				85					90						

<210> 817

<211> 321

<212> DNA

<213> Homo sapiens

<400> 817

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120
aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat
180
agtgttgagc tgctggctaa aaaaataact gaactcgggtt attcatgctt ctacattcat
240
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300
agaaaccttg tgtgcacaga t
321

<210> 818
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 818
 Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met
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 Asp Glu Leu Thr Leu Lys Gly Ile Thr Gln Tyr Tyr Ala Phe Val Glu
 20 25 30
 Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln
 35 40 45
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu
 50 55 60
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His
 65 70 75 80
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg
 85 90 95
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp
 100 105

<210> 819
 <211> 3422
 <212> DNA
 <213> Homo sapiens

<400> 819
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 420
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 720
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 3180
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 3240
 aacaggtcct ggaagtcagt ccacccccc gtgccaccca gggaccttgt gtccggaggg
 3300
 ggaggggaag cctttgccta ggtgctggg gagggccaa gcactctcac tagtcagcac
 3360
 atccatcagc tgaagacaca aaaccagat tataaataat ttcattttta attctctgta
 3420
 ca
 3422

<210> 820

<211> 494

<212> PRT

<213> Homo sapiens

<400> 820

Met	Asn	Ser	Lys	Lys	Leu	Ser	Ser	Thr	Asp	Cys	Phe	Lys	Thr	Glu	Ala
1				5					10					15	
Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25					30		
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50				55					60					
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65				70					75					80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser

<210> 821
<211> 420

<212> DNA

<213> Homo sapiens

<400> 821

acgcgtccccg tcacctgcgg tatggaccaa gtgagttgtg tgctcgacaa tgggttcgcc
60
gccatcatgg atgtgccggg tttcaactat cgcgcccata gttacaccga agcctatcgg
120
cgtttgccgc aaaatgtggg gctaggttcg gaaacgacct cgacggtgag cagccgtggg
180
gtctacaagt ttcctgttgt gctgaagtcg gatgccatct atcccgacca tcagtcgtca
240
ggctacgaca cagagtattg ttcgtggtcg aacacccccg atgtcgattt cgccttcgcc
300
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa
360
ccttcgcctt acgacaccga tgcttgcccc tctcagcctt ccctcttcgg cattgtcgac
420

<210> 822

<211> 133

<212> PRT

<213> Homo sapiens

<400> 822

Met	Asp	Gln	Val	Ser	Cys	Val	Leu	Asp	Asn	Gly	Phe	Ala	Ala	Ile	Met
1				5					10					15	
Asp	Val	Pro	Gly	Phe	Asn	Tyr	Arg	Ala	His	Arg	Tyr	Thr	Glu	Ala	Tyr
		20					25						30		
Arg	Arg	Leu	Pro	Gln	Asn	Val	Val	Leu	Gly	Ser	Glu	Thr	Thr	Ser	Thr
		35					40					45			
Val	Ser	Ser	Arg	Gly	Val	Tyr	Lys	Phe	Pro	Val	Val	Leu	Lys	Ser	Asp
	50					55					60				
Ala	Ile	Tyr	Pro	Asp	His	Gln	Ser	Ser	Gly	Tyr	Asp	Thr	Glu	Tyr	Cys
65					70					75				80	
Ser	Trp	Ser	Asn	Thr	Pro	Asp	Val	Asp	Phe	Ala	Leu	Ala	Glu	Asp	Tyr
			85					90					95		
Pro	Trp	Thr	Met	Gly	Gln	Phe	Val	Trp	Thr	Gly	Phe	Asp	Tyr	Leu	Gly
			100					105					110		
Glu	Pro	Ser	Pro	Tyr	Asp	Thr	Asp	Ala	Trp	Pro	Ser	His	Ala	Ser	Leu
			115				120					125			
Phe	Gly	Ile	Val	Asp											
			130												

<210> 823

<211> 550

<212> DNA

<213> Homo sapiens

<400> 823

tctagattct tgggcagccg agcccctctt gaattcctca gcctaccatc atgatcaaca
60
cctcccatgt tccgtccatg aatgaccgca ctgacagcac tggagagatt taatgggtca
120

ccaattgagg cagtgaaggc actcatggca ctcagagctg gaatggggct gatctgagtt
 180
 gtactgttga ctgcagtggg gatgacaacc tgcattcctt tgctggctgc atcgacaact
 240
 gctttgtaaa tggcatctac ggaagcatca cctggggccac ccacaacgag gccatccttc
 300
 acctgttgac caagagatgg gtcaatcctc ggttgcaact cacaagggtg atcttgaaaa
 360
 ggtggaagtg tagtgtttgg attctcagga agtgctgtga gcccaggctg agtgcttatt
 420
 cttttgttta ggagagctgc atcttcctgc attctcacct gaaagttctg aaacagacaa
 480
 gccatggggg tattgttagc tgggcaagga attgtggact gtccttggaa cgcctggaga
 540
 ttctggtacc
 550

<210> 824

<211> 161

<212> PRT

<213> Homo sapiens

<400> 824

Met	Ala	Cys	Leu	Phe	Gln	Asn	Phe	Gln	Val	Arg	Met	Gln	Glu	Asp	Ala
1				5					10					15	
Ala	Leu	Leu	Asn	Lys	Arg	Ile	Ser	Thr	Gln	Pro	Gly	Leu	Thr	Ala	Leu
			20					25					30		
Pro	Glu	Asn	Pro	Asn	Thr	Thr	Leu	Pro	Pro	Phe	Gln	Asp	Thr	Pro	Cys
		35					40					45			
Glu	Leu	Gln	Pro	Arg	Ile	Asp	Pro	Ser	Leu	Gly	Gln	Gln	Val	Lys	Asp
		50				55					60				
Gly	Leu	Val	Val	Gly	Gly	Pro	Gly	Asp	Ala	Ser	Val	Asp	Ala	Ile	Tyr
65					70					75				80	
Lys	Ala	Val	Val	Asp	Ala	Ala	Ser	Lys	Gly	Met	Gln	Val	Val	Ile	Thr
				85					90					95	
Thr	Ala	Val	Asn	Ser	Thr	Thr	Gln	Ile	Ser	Pro	Ile	Pro	Ala	Leu	Ser
			100					105					110		
Ala	Met	Ser	Ala	Phe	Thr	Ala	Ser	Ile	Gly	Asp	Pro	Leu	Asn	Leu	Ser
		115					120					125			
Ser	Ala	Val	Ser	Ala	Val	Ile	His	Gly	Arg	Asn	Met	Gly	Gly	Val	Asp
		130				135				140					
His	Asp	Gly	Arg	Leu	Arg	Asn	Ser	Arg	Gly	Ala	Arg	Leu	Pro	Lys	Asn
145					150					155					160
Leu															

<210> 825

<211> 327

<212> DNA

<213> Homo sapiens

<400> 825

gcgtttgcga ccggccgtaa cccgcagaat gcggcggtgt gttgcactga gggatattttg
 60

cagttgctgg atgagcgcgga gatgcgcggc gtgctcggcc acgagctgat gcacgtgtac
 120
 aaccgcgata tcctcacctc ttcgggtggcg gcgggtatcg cctccatcat cggtagcatt
 180
 gcgcagattc tttcgtttgg cgcgatgttc ggtggatcca accgcgatgg tgaacgttcc
 240
 aacccctcgc ccatgttcgt ggttgctatg ctggctccca ttgctactca ggcatccag
 300
 atggctatta gccgcacccg tgaattc
 327

<210> 826

<211> 109

<212> PRT

<213> Homo sapiens

<400> 826

Ala	Phe	Ala	Thr	Gly	Arg	Asn	Pro	Gln	Asn	Ala	Ala	Val	Cys	Cys	Thr
1				5				10					15		
Glu	Gly	Ile	Leu	Gln	Leu	Leu	Asp	Glu	Arg	Glu	Met	Arg	Gly	Val	Leu
			20					25					30		
Gly	His	Glu	Leu	Met	His	Val	Tyr	Asn	Arg	Asp	Ile	Leu	Thr	Ser	Ser
			35				40						45		
Val	Ala	Ala	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Thr	Ile	Ala	Gln	Ile	Leu
			50				55					60			
Ser	Phe	Gly	Ala	Met	Phe	Gly	Gly	Ser	Asn	Arg	Asp	Gly	Glu	Arg	Ser
65					70					75				80	
Asn	Pro	Leu	Ala	Met	Phe	Val	Val	Ala	Met	Leu	Ala	Pro	Ile	Ala	Thr
				85				90						95	
Gln	Val	Ile	Gln	Met	Ala	Ile	Ser	Arg	Thr	Arg	Glu	Phe			
			100					105							

<210> 827

<211> 534

<212> DNA

<213> Homo sapiens

<400> 827

nacgcgtacg tcaatatgca tcgtccagtc gttatcgcaa cgccgaaatc gatgctgcgc
 60
 aacaagatgg cgacctcgga tcccgaagag ttcaccaccg gtaggtggcg tcctgttcta
 120
 cccgacccat cgatcaccca cccgacggcc gttacgagga ttatcttctg ctctggcaag
 180
 gcgcgggtggg agctgggtcaa gcaacgtaag gccgccagtc ttgacggaca gctcgccatc
 240
 atcccgatgg agcgtctcta cccgctacca gtcgacgagt tggctgaggt ttttgcgcct
 300
 tacaccaacg tcacggatgt ccgctgggtc caagaagagc cagagaacca gggcgccctgg
 360
 tactacatgc tgaccacact gccccaggcc atgtcggaga agctgccagg attctttgat
 420
 ggggttagtcg gcatcacccg cccaccgtcc tcagctccgt cgggtgggaca gcacagcgtc
 480

cacatccgtg aagagcagga gttactcgag aaggctatag cctgagcgac ctga
534

<210> 828

<211> 174

<212> PRT

<213> Homo sapiens

<400> 828

Xaa	Ala	Tyr	Val	Asn	Met	His	Arg	Pro	Val	Val	Ile	Ala	Thr	Pro	Lys
1				5					10					15	
Ser	Met	Leu	Arg	Asn	Lys	Met	Ala	Thr	Ser	Asp	Pro	Glu	Glu	Phe	Thr
			20					25					30		
Thr	Gly	Arg	Trp	Arg	Pro	Val	Leu	Pro	Asp	Pro	Ser	Ile	Thr	Asp	Pro
		35				40						45			
Thr	Ala	Val	Thr	Arg	Ile	Ile	Leu	Cys	Ser	Gly	Lys	Ala	Arg	Trp	Glu
	50				55						60				
Leu	Val	Lys	Gln	Arg	Lys	Ala	Ala	Ser	Leu	Asp	Gly	Gln	Leu	Ala	Ile
65					70				75					80	
Ile	Pro	Met	Glu	Arg	Leu	Tyr	Pro	Leu	Pro	Val	Asp	Glu	Leu	Ala	Glu
			85					90					95		
Val	Phe	Ala	Pro	Tyr	Thr	Asn	Val	Thr	Asp	Val	Arg	Trp	Val	Gln	Glu
		100						105					110		
Glu	Pro	Glu	Asn	Gln	Gly	Ala	Trp	Tyr	Tyr	Met	Leu	Thr	His	Leu	Pro
		115				120						125			
Gln	Ala	Met	Ser	Glu	Lys	Leu	Pro	Gly	Phe	Phe	Asp	Gly	Leu	Val	Gly
	130					135					140				
Ile	Thr	Arg	Pro	Pro	Ser	Ser	Ala	Pro	Ser	Val	Gly	Gln	His	Ser	Val
145					150					155					160
His	Ile	Arg	Glu	Glu	Gln	Glu	Leu	Leu	Glu	Lys	Ala	Ile	Ala		
			165						170						

<210> 829

<211> 492

<212> DNA

<213> Homo sapiens

<400> 829

nagtggccgg gtggccggcg ggtgccagcc gccatggagg ccgtgccccg catgccccatg
60
atctggctgg acctgaagga ggccggtgac tttcacttcc agccagctgt gaagaagttt
120
gtcctgaaga attatggaga gaacccagaa gcctacaatg aagaactgaa gaagctggag
180
ttgctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtag tgtcctccgc
240
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag
300
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggac
360
atcaagtacg agcaggcctg tattttctcc aacnttggag cgctgcactc catgctgggg
420
gccatggaca agcgggtgtc tgaggagggc atgaaggctc cctgtacca tttccagtgc
480

gcagccggcg cc
492

<210> 830
<211> 164
<212> PRT
<213> Homo sapiens

<400> 830
Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro
1 5 10 15
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His
20 25 30
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn
35 40 45
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln
50 55 60
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg
65 70 75 80
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly
85 90 95
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser
100 105 110
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile
115 120 125
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys
130 135 140
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys
145 150 155 160
Ala Ala Gly Ala

<210> 831
<211> 303
<212> DNA
<213> Homo sapiens

<400> 831
gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgcaa tgtgcgcatc
60
gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccatggtaat
120
ggcccccagg taggtctgtt ggctctgcaa tcgacagcct acgaggaagt cggtatctat
180
ccgctggatg tcctgggagc agagtcacag gccatgatcg gctacatgat cgagcaggaa
240
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgtc
300
gac
303

<210> 832
<211> 101
<212> PRT

<213> Homo sapiens

<400> 832

```

Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1             5             10             15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
      20             25             30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
      35             40             45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
      50             55             60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
      65             70             75             80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
      85             90             95
Met Thr Val Val Asp
      100

```

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

```

nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgcagcaaa
120
cgacgccatg atcgtccagt gggatcgat ttgttctgcg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgtct
240
ctgacctatg tcatgaatct cgctcgccc gccgtcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccaagacc acccggaacc aagaagaaga gcggcgggcg agtgccgttc
360
gatgcgcgat tcggaactgg gtggatcgcc agcgagcccc cgcacgatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
466

```

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

```

Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1             5             10             15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
      20             25             30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
      35             40             45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

```

      50              55              60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys
65              70              75              80
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg
      85              90              95
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly
      100             105             110
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His
      115             120             125
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile
      130             135             140

```

<210> 835
 <211> 482
 <212> DNA
 <213> Homo sapiens

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<400> 835
acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag
60
aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgttaga gacaaaacta
180
aaagtaaaat accaagtga atcaaagcat cagcattgag cccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
420
tgaagaacaa tcccatggcc atgcaggcac tcctcccctc cacctctctg cccttcacgc
480
gt
482

```

<210> 836
 <211> 120
 <212> PRT
 <213> Homo sapiens

```

<400> 836
Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln
1              5              10              15
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys
      20              25              30
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu
      35              40              45
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser
      50              55              60
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu
65              70              75              80
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala

```

```

      85              90              95
Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu
      100              105              110
Leu Gln Ser Leu Arg Asp Val Val
      115              120

```

<210> 837
 <211> 509
 <212> DNA
 <213> Homo sapiens

<400> 837
 acgctgtggac ccccggttctg cccgcctttg cagtcacgc cctccctgaa gtcaccgctg
 60
 cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
 120
 ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggt
 180
 gcctggcggt cgagccctc ttatcctggg gaatgctggg gggcggtcct gagcagacct
 240
 gcctgctgcc cctgctggct ggcactgccc ctccccggg gaaagggttg gtggtcccc
 300
 caggggaact caaagcaggg gagcccttg agggcccaag tccctggaat atcttggcgc
 360
 tcagatggcc cccctcgaac accctcacac gggggggccg cgcggtggga ggtgaccag
 420
 cagccactct tacttgcgga agacttttct cccaatgca gcgcgggttg tatcagcctg
 480
 agccttcagg ttggtgaggc tggggtacc
 509

<210> 838
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 838
 Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
 1 5 10 15
 Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
 20 25 30
 Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
 35 40 45
 Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
 50 55 60
 Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
 65 70 75 80
 Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
 85 90 95
 Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
 100 105 110
 Gln Val Gly Glu Ala Gly Val
 115

<210> 839
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 839
 acgcgtctcg tggtcgtgcg gcacggcagg acggcggttca atgtggaggg tcgggtccag
 60
 ggccgtctcg acatgccgtt ggatgaggtg gggcgccgtc aggcactcac agtgggtcaa
 120
 gtcacgcgcg agatggaacc tgacgcgac atggcctctc cgctacaacg tgcgcgcgac
 180
 acagctcagg caatcgggtg ttgtgctgga ttgggcgtac agctggatga tcgactcatc
 240
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgatcct
 300
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn
 347

<210> 840
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 840
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu
 1 5 10 15
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg
 20 25 30
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp
 35 40 45
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala
 50 55 60
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile
 65 70 75 80
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg
 85 90 95
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr
 100 105 110
 Arg Val Gly
 115

<210> 841
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 841
 tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg
 60
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc
 120
 cgcgatgctg tcgacgatcg cgttgacggc ctcgacgctg gcgccgatga ctacatggtc
 180

aagcccttcg ccctcgacga actcctcgct cgctacgcg ccctcactcg tcgtcccggt
 240
 cccgagccag agcaaaacga ggcccctgaa caactctcct tcgctgacct cacccttgat
 300
 ccaggcaccg gcgagatcac ccgcgggaac cgtcgcatca gtttgacgcg t
 351

<210> 842
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 842
 Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg
 1 5 10 15
 Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp
 20 25 30
 Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val
 35 40 45
 Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala
 50 55 60
 Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg
 65 70 75 80
 Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp
 85 90 95
 Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg
 100 105 110
 Ile Ser Leu Thr Arg
 115

<210> 843
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 843
 ctagcccagg ctctcggtcca cgaggggctg cgcgctgtgg cctctggggc aaacccgggc
 60
 ggccctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc
 120
 tcgcgcgcca tcgacaccac ctccgacatg gccagcggtg ccaccatctc cagccgtgac
 180
 gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggttaagga cgggggttatc
 240
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc
 300
 gacaagggtt acctgtcgcc ctacatgggtc accgaccagg ttcgcatgga ggctgtgatc
 360
 gaggatcctt acatcctcat tcaactccgc aag
 393

<210> 844
 <211> 131
 <212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
 20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
 35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
 50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
 65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
 85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
 100          105          110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
 115          120          125
Ser Arg Lys
 130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

```

gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
 60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
 120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttgaggga
 180
ggcggctgcc gtgaagacag gcacccttgc tcttgagagg ggcacccaga gaaccaagac
 240
tcagcagagg gaacacaggg ctacgcccag gccccaggcc tgatatccag agtctaaatc
 300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac cccagtttcc
 360
tctgcatacg ggctccgagc cctgcactgc ctccagggta gttcccaagg tcttttccca
 420
ttacctcta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
 480
agccacagaa tcccaggcca cgcgt
 505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1           5           10           15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20           25           30
Lys Ala Pro Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35           40           45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50           55           60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65           70           75           80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85           90           95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100          105          110
Ala Pro Ala Ala Val Ala Leu Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115          120          125
Val Pro
      130

```

<210> 847

<211> 448

<212> DNA

<213> Homo sapiens

<400> 847

```

aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct cgcgatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatattgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgttagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848

<211> 149

<212> PRT

<213> Homo sapiens

<400> 848

```

Lys Leu Leu Lys Lys Glu Glu Asn Met Lys Glu Leu Val Val Asn Leu
      1           5           10           15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20           25           30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35           40           45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu

```

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100             105             110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115             120             125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130             135             140
Asp Val Arg Lys Ile
145

```

<210> 849
 <211> 463
 <212> DNA
 <213> Homo sapiens

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggatga agtgataagt
60
cttttgggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggga
180
gctgaagatg gatcatggta ttccctcctgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aacccaaacg gggaatactg gtgaacgggt caaagaatcc
300
attcaaataca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttaccgggct tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

<210> 850
 <211> 154
 <212> PRT
 <213> Homo sapiens

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1      5      10      15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20      25      30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35      40      45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50      55      60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65      70      75      80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

	85		90		95											
Phe	Lys	Glu	Ser	Ile	Gln	Ile	Asn	Ser	Gly	Leu	Leu	Ala	Leu	Gly	Asn	
		100					105						110			
Val	Ile	Ser	Ala	Leu	Gly	Asp	Pro	Arg	Arg	Lys	Ser	Ser	Ser	His	Ile	Pro
		115					120						125			
Tyr	Arg	Asp	Ala	Lys	Ile	Thr	Arg	Leu	Leu	Lys	Asp	Ser	Leu	Gly	Gly	
		130					135						140			
Ser	Ala	Lys	Thr	Val	Met	Ile	Thr	Cys	Val							
145					150											

<210> 851
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 851
 aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
 60
 gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
 120
 aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
 180
 ttgttatgct gataaggtta ttcagcttga cgatttggtc gtggtctttc aaccgttttg
 240
 cagctgggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
 300
 tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
 360
 taaccacgc gt
 372

<210> 852
 <211> 110
 <212> PRT
 <213> Homo sapiens

Met	Ser	Glu	Leu	Leu	Met	Gln	Phe	Leu	His	Ser	Leu	Ile	Asn	Ser	Phe
1			5					10					15		
Ile	Ser	His	Phe	Glu	Asn	Ser	Arg	Cys	Arg	Ile	Lys	Ala	Arg	Val	Trp
			20					25					30		
Gly	Pro	Ser	Pro	Gln	Leu	Arg	Leu	Arg	Asp	Phe	Leu	Asp	Leu	Val	Cys
			35				40					45			
Tyr	Ala	Asp	Lys	Val	Ile	Gln	Leu	Asp	Asp	Leu	Phe	Val	Val	Phe	Gln
			50			55				60					
Pro	Phe	Cys	Ser	Trp	Ser	Thr	Ile	Phe	Leu	Val	Gly	Thr	Thr	Ile	Glu
65					70				75					80	
Asp	Gln	His	Arg	Lys	Asn	Phe	Val	Asp	Ala	Glu	Gln	Thr	Pro	Thr	Asp
			85					90					95		
His	Phe	Ser	Leu	Glu	Val	Arg	Val	Ile	Leu	Ser	Asn	Pro	Arg		
			100					105					110		

<210> 853
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac
60
caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa
120
gtccaagaaa cgcatttggt agaagagctt gcaggcatag aatcagggtga tgatggcgca
180
gtggtggaag agagcgtatt agaaggcctc gataacctatt tatgtgagat aaaagaagca
240
cagattcgtc atggattgca tcgtcttggga gaattaccag aagacgataa attggccgat
300
accttggtcg ccttattgcg tttaccccggt ggcagtgaca ttaccagcaa gggaattttg
360
catgccttaa tggcagattt agagttagaa caagacgatt ttgacccaat gcaaagcacg
420
cgt
423

<210> 854

<211> 141

<212> PRT

<213> Homo sapiens

<400> 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10				15		
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
		20						25					30		
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
		35				40						45			
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
	50					55					60				
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
	65				70					75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85					90					95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
		100						105					110		
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
		115				120						125			
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
	130					135						140			

<210> 855

<211> 338

<212> DNA

<213> Homo sapiens

<400> 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga
60

tgaatgtctg tgcggatggt gctcacagca agatagtgtc tggagcgtt ggcaacttcga
 120
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag
 180
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcagtgtaa
 240
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcaactccaa
 300
 acattgctct gagcccattg gagnctctga gcagaaag
 338

<210> 856
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 856
 Met Asn Val Cys Ala Asp Val Ala His Ser Lys Ile Val Leu Gly Ala
 1 5 10 15
 Ile Gly Thr Ser Asn Lys Met Glu His Gly Ala Asp Gly Ala Leu Ser
 20 25 30
 Lys Met Glu Arg Gly Val Asp Arg Ala Trp Ser Lys Lys Glu Leu Gln
 35 40 45
 Ala Arg Trp Ser Leu Gln Gln Val Leu Leu Ser Val Arg Trp Ser Ser
 50 55 60
 Glu Lys Met Met Leu Arg Val Arg Leu Ser Ser Val Ile Gly Thr Pro
 65 70 75 80
 Asn Ile Ala Leu Ser Pro Leu Glu Xaa Leu Ser Arg Lys
 85 90

<210> 857
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 857
 ccggacagtg ggccaccagt gtttgcccc agcaatcatg tcagtgaagc ccaacctcgg
 60
 gagacacccc ggcccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc
 120
 cctggtgaca ggggtggagac ccctgtgggg gagagagccc caaccctgt ctcagcaagc
 180
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc
 240
 tctgagcagc ctccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc
 300
 agccccagg agggccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag
 360
 atttctgagg ctgccccag ggaggggtggg aagcccccta caccaccacc caagatctta
 420
 tcagagaaac tgaaa
 435

<210> 858

<211> 145
 <212> PRT
 <213> Homo sapiens

<400> 858
 Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu
 1 5 10 15
 Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro
 20 25 30
 Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro
 35 40 45
 Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser
 50 55 60
 Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly
 65 70 75 80
 Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser
 85 90 95
 Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu
 100 105 110
 Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu
 115 120 125
 Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Lys Leu
 130 135 140
 Lys
 145

<210> 859
 <211> 561
 <212> DNA
 <213> Homo sapiens

<400> 859
 nacgcgtggt gtggtaatcc gggttctggt ggcgacggct gccacccctc gtggcaagac
 60
 atgccgttgç gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctcgctggaa
 120
 ccctcgaaga ggcagggtcg gcagggtacc gtggtcggtg tacgcatcgt ttcgacgatg
 180
 aaccccatc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg
 240
 gccgctgatt ctgccgcccg cggtatccgc gacatcgaca agaaagggtc gatcgccatc
 300
 ctcagcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact
 360
 gaccctgagt tcacctggga ccaggtcgac cttgctactg tcgctgacac cggcgcgga
 420
 ttgcggctcg gcaactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgct
 480
 tccggccagg tattcggcta ccagaagttg ctgctcgta ccggccttac cccgtcgcgc
 540
 attgacgacg acggcgatgc c
 561

<210> 860

<211> 187
 <212> PRT
 <213> Homo sapiens

<400> 860
 Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro
 1 5 10 15
 Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp
 20 25 30
 Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln
 35 40 45
 Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu
 50 55 60
 Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met
 65 70 75 80
 Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly
 85 90 95
 Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro
 100 105 110
 Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln
 115 120 125
 Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly
 130 135 140
 Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala
 145 150 155 160
 Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu
 165 170 175
 Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala
 180 185

<210> 861
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 861
 ccatggggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa
 60
 gagataatgg tcatacccta tggtcactca ccatagtctg gcggtacatg gacttctcag
 120
 cccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt
 180
 gcctgaggcc tattagaggg gtctcttttc agccatcagt gttagaggcc atctgcatgg
 240
 gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttgccgt gggctttgcc
 300
 tgtttctactg ctttcagggg ggcctgccac aggggagaaa ctgggggggg ga
 352

<210> 862
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 862

Met Gly Phe Tyr Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1 5 10 15
 Tyr Leu Gln Arg Asp Asn Gly His Thr Leu Trp Ser Leu Thr Ile Val
 20 25 30
 Trp Arg Tyr Met Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
 35 40 45
 His Leu Lys Ser Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
 50 55 60
 Arg Gly Val Ser Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
 65 70 75 80
 Ser Gln Ser Leu Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
 85 90 95
 Gly Leu Cys Leu Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
 100 105 110
 Asn Trp Gly Gly
 115

<210> 863

<211> 327

<212> DNA

<213> Homo sapiens

<400> 863

tccggatcga cccggacgaa ttccacggtc cagccattga cttccaaatg ctctttgaca
 60
 tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
 120
 agtttgagct gcgagtagac gttgcggtag ttctcggtga ccgactgctc atacgagatg
 180
 tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttggttga catggccgct
 240
 tggcggaaca tggttcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
 300
 agcatttctg accggcgatg acccatn
 327

<210> 864

<211> 108

<212> PRT

<213> Homo sapiens

<400> 864

Met Gly His Arg Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1 5 10 15
 Asn Phe Lys Ser Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
 20 25 30
 Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
 35 40 45
 His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
 50 55 60
 Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
 65 70 75 80
 Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

85 90 95
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro
 100 105

<210> 865
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 865
 acgcgtcatc ctcattcaag aggccagga ggagcaccac cctccgcata ttgcgcgtgc
 60
 agctctcggt ctggctctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc
 120
 tgggtggtgtc caggatcgac acatcactgc ctccgagttc agaggtttcc tttccacct
 180
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc
 240
 tggcctccgt ctccatcgcc tctcatggc cgtcttccgc cgggtgttcc aagcccagct
 300
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat
 360
 cagaaaccat gagggtggat ctccggaggt catcgatgtg gacagactgc cacagccctc
 420
 cgtggaagcc cacataggct gttcctcttc ccaccggga cagttttgtg atgaaataga
 480
 cgaagatacg gtcctcattt tctcgtattt tgttgatttc atttataaca gaatacttag
 540
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga
 600
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gagtactcgg
 660
 tgtcaaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt
 720
 ctaaaattt
 729

<210> 866
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 866
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys
 1 5 10 15
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro
 20 25 30
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro
 35 40 45
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg
 50 55 60
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg
 65 70 75 80
 Thr Ala Gly

<210> 867
 <211> 640
 <212> DNA
 <213> Homo sapiens

<400> 867
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
 60
 tcaggtggac tctcgttggt ggccggcgtc gctggcccc tcgcacccgg tcccgtgtca
 120
 catgctccag ggccgcagctc ttgtccacct ttacctatc gaaagccttg tttttgctc
 180
 ggtaaatccc ttcattgagg gctttgatcc aggattcctt ctctccccg gtgggtgcct
 240
 ggaatttgat gtcgctgacc ttgttccttg gggatcgag caggataaag cgggtgttttc
 300
 gcttgaggag ggcacgaagg tcctggcact tctcatagct gccagctcc acagtctcca
 360
 cacacttctg atcatcctca ttctcataga ccagcagctg ggcctggcag aggagcagat
 420
 atcgggtcttt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
 480
 ccaccatctg tgctccccga ggcttctcac cggttcctt cacacctcc tcctccatgg
 540
 cgagtcggcc gaggtccgc cgctccgcca ctgcttcca gcgccgcgcg ggctctgcca
 600
 ccgcgtctac gcccgccag gcggcgactc tccgcgttct
 640

<210> 868
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 868
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
 1 5 10 15
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
 20 25 30
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
 35 40 45
 His Cys Ser Ser
 50

<210> 869
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 869
 ngggatgatgc tgctcgggc attgagcatc tttgtgtca gcgcgctgtt tatcgacaac
 60

ttcctgtcgc cgctgaatat gcgcgggctg ggcctggcga tttcgacggt gggcatcgct
 120
 gcgtgcacca tgctgttctg cctggcgctg gggcatttcg acttgctggt gggctcggtg
 180
 atcgctctgtg ccggtgtggt cgcggggatt gtgattcgtg acaccgatag cgtggcactc
 240
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgatc
 300
 gccaaactgc gcatcaacgc g
 321

<210> 870

<211> 107

<212> PRT

<213> Homo sapiens

<400> 870

Xaa	Val	Met	Leu	Leu	Ala	Ala	Leu	Ser	Ile	Phe	Val	Leu	Ser	Ala	Leu
1				5					10					15	
Phe	Ile	Asp	Asn	Phe	Leu	Ser	Pro	Leu	Asn	Met	Arg	Gly	Leu	Gly	Leu
		20						25					30		
Ala	Ile	Ser	Thr	Val	Gly	Ile	Ala	Ala	Cys	Thr	Met	Leu	Phe	Cys	Leu
		35				40						45			
Ala	Ser	Gly	His	Phe	Asp	Leu	Ser	Val	Gly	Ser	Val	Ile	Ala	Cys	Ala
	50				55					60					
Gly	Val	Val	Ala	Gly	Ile	Val	Ile	Arg	Asp	Thr	Asp	Ser	Val	Ala	Leu
65					70				75					80	
Gly	Val	Ser	Ala	Ala	Leu	Ala	Met	Gly	Leu	Val	Val	Gly	Leu	Ile	Asn
			85					90					95		
Gly	Ile	Val	Ile	Ala	Lys	Leu	Arg	Ile	Asn	Ala					
			100					105							

<210> 871

<211> 320

<212> DNA

<213> Homo sapiens

<400> 871

agatcttcag agtcctcgtc ttttaaatgg gggtaacagc agcaagtcct cagaggtgtc
 60
 ctgagcctca aaacacatcc tggtttgtaa cgtccgcagc ctcagcaggg gctaggcaca
 120
 gaacaagcat tcaggacctg gaaggtacca gcgacacctg gtcctccctt cccaggcaca
 180
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tcctcagcca
 240
 ctgccccac cactaccaca atcatactca cctctcctgg tccatacgtg acaaaggacc
 300
 tgccacggcc agggagacaa
 320

<210> 872

<211> 98

<212> PRT

<213> Homo sapiens

<400> 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1             5             10             15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
      20             25             30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
      35             40             45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
      50             55             60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
      65             70             75             80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
      85             90             95
Arg Gln

```

<210> 873

<211> 363

<212> DNA

<213> Homo sapiens

<400> 873

```

nttgtttagc atcgtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcggatg
60
catcagcatg ttttgctca cgtttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacgttta gcatcgtttt taacagatgt atcaacacgg ggttcacccg
180
ctttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcattgttcg gagagaagtg tgccaattcg gcgatacagt
360
cag
363

```

<210> 874

<211> 108

<212> PRT

<213> Homo sapiens

<400> 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1             5             10             15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
      20             25             30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
      35             40             45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
      50             55             60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```

```

65          70          75          80
Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
          85          90          95
Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
          100          105

```

<210> 875
 <211> 355
 <212> DNA
 <213> Homo sapiens

```

<400> 875
acgcgtgaag gggaccctaa ctcgtctggg ctgtaggatg cgggcgagggc ttccacaaac
60
tcaactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa
120
ccgcgaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
180
gcgctcagaa tccctgagcc ggaggccccg cgggattcag accgccagat ccccgaggag
240
tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttccagg
300
cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggctcccc cggn
355

```

<210> 876
 <211> 106
 <212> PRT
 <213> Homo sapiens

```

<400> 876
Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
1          5          10          15
Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
          20          25          30
Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
          35          40          45
Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
          50          55          60
Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
65          70          75          80
Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
          85          90          95
Pro Ala Cys His Pro Ala Ala Pro Pro Ala
          100          105

```

<210> 877
 <211> 487
 <212> DNA
 <213> Homo sapiens

```

<400> 877
acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac
60

```

caatccacct atgctaaacg tggtcagcaa gggtatctca cacgagaatt ctttggtttg
 120
 ttggccaata ccatgggaga tcaaatcctt ttagtacagg cgtacagaga aggcgaagcg
 180
 atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcgtta ttggggctgt
 240
 atggaagaag tggattgcct gcattttgaa gcttggtatt accaaggaat cgagttttgt
 300
 ctcgaaaaag ggttacagca tttcgatccg ggtacacaag gggaacacaa gattgcgcgc
 360
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcacaaagg ttttcgtgaa
 420
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc
 480
 cagcggt
 487

<210> 878
 <211> 162
 <212> PRT
 <213> Homo sapiens

<400> 878
 Thr Arg Thr Leu Gly Asn Glu Leu Thr Thr Ala Glu Ile Asp Cys Leu
 1 5 10 15
 Tyr Leu Cys Tyr Gln Ser Thr Tyr Ala Lys Arg Gly Gln Gln Gly Tyr
 20 25 30
 Leu Thr Arg Glu Phe Phe Gly Leu Leu Ala Asn Thr Met Gly Asp Gln
 35 40 45
 Ile Leu Leu Val Gln Ala Tyr Arg Glu Gly Glu Ala Ile Ala Ala Ser
 50 55 60
 Trp Cys Phe Phe Asp Asp His Ser Leu Tyr Gly Arg Tyr Trp Gly Cys
 65 70 75 80
 Met Glu Glu Val Asp Cys Leu His Phe Glu Ala Cys Tyr Tyr Gln Gly
 85 90 95
 Ile Glu Phe Cys Leu Glu Lys Gly Leu Gln His Phe Asp Pro Gly Thr
 100 105 110
 Gln Gly Glu His Lys Ile Ala Arg Gly Phe Glu Pro Val Phe Ser His
 115 120 125
 Ser Val His Tyr Ile Ala His Gln Gly Phe Arg Glu Ala Ile Gly Asn
 130 135 140
 Phe Cys Glu Glu Glu Ala Gln Ala Val Arg Glu Tyr His Gln Asp Thr
 145 150 155 160
 His Ala

<210> 879
 <211> 993
 <212> DNA
 <213> Homo sapiens

<400> 879
 nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc
 60

agccagtcca gtagggctct gaccctcct tctacagta ctgctaaaaa ttcattggga
 120
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac
 180
 gagcacaggc agctcctctc tcaccaatg caaggccctg gactccgtgc agctacctca
 240
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta
 300
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tggctctcgac
 360
 ctggtgaagg ctgtcattaa agaggaggtt ttatggccag tgttgaggtc agacgcgttc
 420
 agtggactga cggccttacc tcggagcatc cttttatttg gacctcgggg gacaggcaaa
 480
 acattatttg gcagatgcat cgctagtcag ctggggggcca catttttcaa aattgccggt
 540
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt
 600
 gtggccaggt gtcgccagcc ctcggtgatt tttgttagtg acattgacat gcttctctcc
 660
 tctcaagtga atgaggaaca tagtcagtc agtcggatga gaaccgaatt tctgatgcaa
 720
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa
 780
 ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccactt
 840
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt
 900
 ctcaatgaca aggagtgtgc actgctcgtc cagcgcacag aaggcttttc tggactagat
 960
 gtggctcatt tgtgtcagga agcagtgggtg ggc
 993

<210> 880

<211> 331

<212> PRT

<213> Homo sapiens

<400> 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5				10					15		
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25				30			
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
		35					40				45				
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
	50					55					60				
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65					70					75				80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
			85						90					95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
			100					105					110		
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

```

      115      120      125
Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr
      130      135      140
Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys
145      150      155      160
Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe
      165      170      175
Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu
      180      185      190
Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser
      195      200      205
Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser Gln Val Asn
      210      215      220
Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln
225      230      235      240
Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys
      245      250      255
Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe
      260      265      270
Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln
      275      280      285
Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys
      290      295      300
Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp
305      310      315      320
Val Ala His Leu Cys Gln Glu Ala Val Val Gly
      325      330

```

<210> 881
 <211> 313
 <212> DNA
 <213> Homo sapiens

<400> 881
 cgcgtgagcgc tgcacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt
 60
 cgtgggtttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc
 120
 gactcgcagt attatgaagg cggtttcaac gtcacggttg agattccaac atgagcggcc
 180
 aaaggatgaa catggacacg acgcgcccc aacacggtcg gggcttgccg acgatcagcc
 240
 ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc
 300
 tggcaagccg acn
 313

<210> 882
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 882
 Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

```

      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

```

<210> 883
 <211> 576
 <212> DNA
 <213> Homo sapiens

```

<400> 883
naattaagat ctggggtccc agtgtcattg gtgaaggcct tgggattcga ggcagctgag
60
tcctcactga ccaaggcaag ccattgcttct gattgcttga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac ctttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcagggtca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctcctgt ctcccagtga agacttggat ggcagccatc agggaaggct ggggtcccagc
360
tgggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgctc
420
gtgaaagagg cccaagccac catccgcatt gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttcctgg tgaacgcctt agctaagcag gtcattg
576

```

<210> 884
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 884
Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
      1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
      65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

```

100

105

<210> 885
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 885
 actagtggcg ccctcatccg ggccgctgtc ccgctctcgg agtcggctgc gttggagtcc
 60
 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc
 120
 aggcgggtgt cgcgcctcgg tgcgatcgag ttgtcgtcga ccccggtccg cccagatccg
 180
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc
 240
 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt
 300
 gatccctggc ccgatgtcag cgatgaggct ctgctagcct gcgccgagga gtggcttgac
 360
 ctcgacgcgt
 370

<210> 886
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 886
 Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala
 1 5 10 15
 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr
 20 25 30
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala
 35 40 45
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg
 50 55 60
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser
 65 70 75 80
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His
 85 90 95
 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu
 100 105 110
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala
 115 120

<210> 887
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 887
 cagggcggtg cgctcggctc cgtgctgccg atggatcatgc tcggaggctt aaccgccatc
 60

attatctccg gctgcctgaa ccagcttggg aaacgctatc cgcattctgac cggcgaaggc
 120
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt
 180
 aaagcggacg tgaccacat tgcctccggc gcgttgcctg ccgtgctgct ttacatgggtg
 240
 ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatgtt gtttgtggcg
 300
 gtgctgggtca aactgtgcaa cggcgcttct ccccgctgc tcgaaggctc gcaggtggtt
 360
 tacaaattct tccagacctc cgtcacctat ccgattctgt tcgccgttgg cgtggcgatt
 420
 acgccgtggc aggaactggg caacgcg
 447

<210> 888

<211> 149

<212> PRT

<213> Homo sapiens

<400> 888

Gln	Gly	Val	Ala	Leu	Gly	Arg	Val	Leu	Pro	Met	Val	Met	Leu	Gly	Gly
1				5				10					15		
Leu	Thr	Ala	Ile	Ile	Ile	Ser	Gly	Cys	Leu	Asn	Gln	Leu	Gly	Lys	Arg
			20					25					30		
Tyr	Pro	His	Leu	Thr	Gly	Glu	Gly	Gln	Leu	Met	Pro	Asn	Arg	Ala	Asn
		35				40						45			
Ala	Asp	Thr	Thr	Ala	Ser	Gln	Pro	Ala	Phe	Ser	Gly	Lys	Ala	Asp	Val
	50					55					60				
Thr	Thr	Ile	Ala	Ser	Gly	Ala	Leu	Leu	Ala	Val	Leu	Leu	Tyr	Met	Val
65					70					75				80	
Gly	Arg	Leu	Val	His	Lys	Leu	Ile	Gly	Leu	Pro	Ala	Pro	Val	Gly	Met
			85					90					95		
Leu	Phe	Val	Ala	Val	Leu	Val	Lys	Leu	Cys	Asn	Gly	Ala	Ser	Pro	Arg
			100					105					110		
Leu	Leu	Glu	Gly	Ser	Gln	Val	Val	Tyr	Lys	Phe	Phe	Gln	Thr	Ser	Val
		115				120						125			
Thr	Tyr	Pro	Ile	Leu	Phe	Ala	Val	Gly	Val	Ala	Ile	Thr	Pro	Trp	Gln
	130					135						140			
Glu	Leu	Val	Asn	Ala											
145															

<210> 889

<211> 450

<212> DNA

<213> Homo sapiens

<400> 889

ggtaccaccc cacacctgac aagaggtggc cagggaggaa gggagggttc ttacctcccc
 60
 atctcccctc agtaaaattc aggatgccca gtgaagtttg aatgtcagat aaacaatttg
 120
 ttagtataag gatgtaccta gcattgaaat gatgccttgt aatttactaa atctgcaact
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg
 240
 gtgctgggga gatcctgagg tcaggaaccc gtacacctct gcttctgccc tctcttcctt
 300
 gtgccggcca caaggcaatg actcctgtgt ggggtgcagag gcagaaatgg gtctggaagg
 360
 ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa
 420
 ggggagttgg cctggccgcc cttcacgcgt
 450

<210> 890
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 890
 Met Met Pro Cys Asn Leu Leu Asn Leu Gln Leu Cys Ser Leu Ile Ser
 1 5 10 15
 Trp Arg Ala Val Ala Val Ile Pro Gly Phe Arg Gly Gly Glu Gly Cys
 20 25 30
 Trp Gly Asp Pro Glu Val Arg Asn Pro Tyr Thr Ser Ala Ser Ala Leu
 35 40 45
 Ser Ser Leu Cys Arg Pro Gln Gly Asn Asp Ser Cys Val Gly Ala Glu
 50 55 60
 Ala Glu Met Gly Leu Glu Gly Asp Ser Gln Cys Leu Ala Ser Ser Gly
 65 70 75 80
 Lys Phe Cys Ile Gly Gly Ser Leu Cys Ser Lys Gly Ser Trp Pro Gly
 85 90 95
 Arg Pro Ser Arg
 100

<210> 891
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 891
 nncaccgtcc ccgtactgga tccgcgcgag gatttcgccg actgcatgca cattgacgta
 60
 ctggatccct tccacactga caacaccagt gagcacagtg acctggccac agatggccag
 120
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata
 180
 tctagccccg tcagctctag tgacgtgct aacaccaccg acagcactgc tggcaatacc
 240
 ggtgaaggta ctgccgcgaa tatgcctggt gacatggctc attcttcgac ggctaccac
 300
 ccctatgcaa gcaccggt
 318

<210> 892
 <211> 106
 <212> PRT

<213> Homo sapiens

<400> 892

```

Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1           5           10           15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
      20           25           30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
      35           40           45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
      50           55           60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
65           70           75           80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
      85           90           95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
      100           105

```

<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

```

nnggataccta tccctgaatc taaggttggt gacacatgtg tttgggatag caaggtagag
60
aagtcacaga aaaagcctgt ggaaaacagg atgaaggagg acaaaagcag catcagggaa
120
gcaatcagca aagccaagag tacagcaaata ataaagacag aacaggaagg tgaggcatct
180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctgggggaaaa gcgctatgaa
420
tgtgatgact gtggagggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
480
cacactgggt acggagagaa gacaacgcgt
510

```

<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

```

Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
      20           25           30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

```

35	40	45
Ala Asn Ile Lys Thr Glu Gln Glu Gly Glu Ala Ser Glu Lys Ser Leu		
50	55	60
His Leu Ser Pro Gln His Ile Thr His Gln Thr Met Pro Ile Gly Gln		
65	70	75
Arg Gly Ser Glu Gln Gly Lys Arg Val Glu Asn Ile Asn Gly Thr Ser		
85	90	95
Tyr Pro Ser Leu Gln Gln Lys Thr Asn Ala Val Lys Lys Leu His Lys		
100	105	110
Cys Asp Glu Cys Gly Lys Ser Phe Lys Tyr Asn Ser Arg Leu Val Gln		
115	120	125
His Lys Ile Met His Thr Gly Glu Lys Arg Tyr Glu Cys Asp Asp Cys		
130	135	140
Gly Gly Thr Phe Arg Ser Ser Ser Leu Arg Val His Lys Arg Ile		
145	150	155
His Thr Gly Tyr Gly Glu Lys Thr Thr Arg		
165	170	

<210> 895

<211> 1119

<212> DNA

<213> Homo sapiens

<400> 895

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 <212> PRT
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50 55 60
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<210> 900

<211> 734

<212> PRT

<213> Homo sapiens

<400> 900

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Leu	Gln	Leu	Leu	Tyr	Leu	Thr	Asn	Asn	Leu	Leu	Thr	Asp	Gln	Cys	Ile
		35					40					45			
Pro	Val	Leu	Val	Gly	His	Leu	His	Leu	Arg	Ile	Leu	His	Leu	Ala	Asn
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Asn	Gln	Leu	Gln	Thr	Phe	Pro	Ala	Ser	Lys	Leu	Asn	Lys	Leu	Glu	Gln
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Leu	Glu	Glu	Leu	Asn	Leu	Ser	Gly	Asn	Lys	Leu	Lys	Thr	Ile	Pro	Thr
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Thr	Ile	Ala	Asn	Cys	Lys	Arg	Leu	His	Thr	Leu	Val	Ala	His	Ser	Asn
			100					105					110		
Asn	Ile	Ser	Ile	Phe	Pro	Glu	Ile	Leu	Gln	Leu	Pro	Gln	Ile	Gln	Phe
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Val	Asp	Leu	Ser	Cys	Asn	Asp	Leu	Thr	Glu	Ile	Leu	Ile	Pro	Glu	Ala
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Leu	Pro	Ala	Thr	Leu	Gln	Asp	Leu	Asp	Leu	Thr	Gly	Asn	Thr	Asn	Leu
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Val	Leu	Glu	His	Lys	Thr	Leu	Asp	Ile	Phe	Ser	His	Ile	Thr	Thr	Leu
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Lys	Ile	Asp	Gln	Lys	Pro	Leu	Pro	Thr	Thr	Asp	Ser	Thr	Val	Thr	Ser
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Thr	Phe	Trp	Ser	His	Gly	Leu	Ala	Glu	Met	Ala	Gly	Gln	Arg	Asn	Lys

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Ala Val Tyr Gly Met Phe	Asp Gly Asp Arg Asn Glu	Glu Leu Pro Arg
225	230	235
Leu Leu Gln Cys Thr Met	Ala Asp Val Leu Leu Glu	Glu Val Gln Gln
245	250	255
Ser Thr Asn Asp Thr Val	Phe Met Ala Asn Thr Phe	Leu Val Ser His
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Arg Lys Leu Gly Met Ala	Gly Gln Lys Leu Gly Ser	Ser Ala Leu Leu
275	280	285
Cys Tyr Ile Arg Pro Asp	Thr Ala Asp Pro Ala Ser	Ser Phe Ser Leu
290	295	300
Thr Val Ala Asn Val Gly	Thr Cys Gln Ala Val Leu	Cys Arg Gly Gly
305	310	315
Lys Pro Val Pro Leu Ser	Lys Val Phe Ser Leu Glu	Gln Asp Pro Glu
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Glu Ala Gln Arg Val Lys	Asp Gln Lys Ala Ile Ile	Thr Glu Asp Asn
340	345	350
Lys Val Asn Gly Val Thr	Cys Cys Thr Arg Met Leu	Gly Cys Thr Tyr
355	360	365
Leu Tyr Pro Trp Ile Leu	Pro Lys Pro His Ile Ser	Ser Thr Pro Leu
370	375	380
Thr Ile Gln Asp Glu Leu	Leu Ile Leu Gly Asn Lys	Ala Leu Trp Glu
385	390	395
His Leu Ser Tyr Thr Glu	Ala Val Asn Ala Val Arg	His Val Gln Asp
405	410	415
Pro Leu Ala Ala Lys Lys	Leu Cys Thr Leu Ala Gln	Ser Tyr Gly
420	425	430
Cys Gln Asp Ser Val Gly	Ala Met Val Val Tyr Leu	Asn Ile Gly Glu
435	440	445
Glu Gly Cys Thr Cys Glu	Met Asn Gly Leu Thr Leu	Pro Gly Pro Val
450	455	460
Gly Phe Ala Ser Thr Thr	Thr Ile Lys Asp Ala Pro	Lys Pro Ala Thr
465	470	475
Pro Ser Ser Ser Ser Gly	Ile Ala Ser Glu Phe Ser	Ser Glu Met Ser
485	490	495
Thr Ser Glu Val Ser Ser	Glu Val Gly Ser Thr Ala	Ser Asp Glu His
500	505	510
Asn Ala Gly Gly Leu Asp	Thr Ala Leu Leu Pro Arg	Pro Glu Arg Arg
515	520	525
Cys Ser Leu His Pro Thr	Pro Thr Ser Gly Leu Phe	Gln Arg Gln Pro
530	535	540
Ser Ser Ala Thr Phe Ser	Ser Asn Gln Ser Asp Asn	Gly Leu Asp Ser
545	550	555
Asp Asp Asp Gln Pro Val	Glu Gly Val Ile Thr Asn	Gly Ser Lys Val
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Glu Val Glu Val Asp Ile	His Cys Cys Arg Gly Arg	Asp Leu Glu Asn
580	585	590
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          660          665          670
Pro Lys Arg Lys Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro
          675          680          685
Glu Asp Gln Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu
          690          695          700
Gln Met Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu
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Glu Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
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<210> 901
<211> 309
<212> DNA
<213> Homo sapiens

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<210> 902
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<212> PRT
<213> Homo sapiens

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Gly Lys Leu His Phe Leu Phe Leu Leu Met Gln Gln Gly His Pro Lys
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Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
          35          40          45
Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
          50          55          60
Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
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Asp Ala Arg Arg Ser Lys Ala Asp Ala Thr Phe Arg Ala Ala Ser Ile
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 <212> DNA
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<210> 904
 <211> 102
 <212> PRT
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 Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val
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 Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro
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 <212> DNA
 <213> Homo sapiens

<400> 905
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 ctcaacgaag acatcattat cgcggttgac cgggcagacg cgggtgattag cgtatcccag
 120
 gggctctgcy acaggctggc tggacatggc gtgacctcaa cgggtggttcc caacatcggt
 180
 gacgtcgagc tgtttgaccg tcttgatcga cgacatgagg ggacgatcgt cgtcagcgtc
 240

gccaccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc
 300
 gaggttcagt tgagaatcat cggagatgga cgcagcggc accaactgga ggccattgcc
 360
 gctgataatc cacgcgt
 377

<210> 906
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 906
 Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His
 1 5 10 15
 Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ala Gly Asp Arg Ala
 20 25 30
 Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly
 35 40 45
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu
 50 55 60
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val
 65 70 75 80
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val
 85 90 95
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln
 100 105 110
 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg
 115 120 125

<210> 907
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 907
 acgcgtagga tgatgaagtc cgtcactgga tcgttcttgg gtggcaaccg ggaagtcggt
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 gaccagttct tcaacggcga ggttcaactg aaccttgtgc cgcagggtag attcgccgag
 120
 cgcattcgtg ccggcgctgc tggattgca gcattcttca cgcctactgg ctatggtaca
 180
 gccgtgcaga aggggtgagct tgttcttaag tatgaaaaga aggacggtaa ggctgtgcca
 240
 gtcattgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa
 300
 gaggttatta aggatgaata ggatatggtg aa
 332

<210> 908
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 908

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Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
 1           5           10           15
Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
           20           25           30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
           35           40           45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
           50           55           60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65           70           75           80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
           85           90           95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
           100           105

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<210> 909

<211> 318

<212> DNA

<213> Homo sapiens

<400> 909

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acgcgtcggg catggcagct gtacagatct atcgcgtcag cagggcctac gcacacatga
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tgccgcaggg gcaccgacgc tgtcgccatc aaaagagccg cctcgcgccc gcagcgcctc
120
ccagggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
180
cccttttttt cccaccccaa caccgaaccg gcgggccatg gctgaggatt cgcaccccat
240
tcgctccggc ttgcgcacgc tcaagcgctc ctggagctcg aatgagaatg taccgccgcc
300
acaaagctcg ccgccggc
318

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<210> 910

<211> 102

<212> PRT

<213> Homo sapiens

<400> 910

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Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
 1           5           10           15
Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
           20           25           30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
           35           40           45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
           50           55           60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65           70           75           80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
           85           90           95
His Lys Ala Arg Arg Arg

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100

<210> 911
 <211> 506
 <212> DNA
 <213> Homo sapiens

<400> 911
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 caaccttatg aggctggcct tgggggaacc ctgttttagg gatgagctga acttaccggg
 120
 aggctgcatg cgaggttggt gtgaaatgca tatctggctt tgtagctggt cggctcacct
 180
 ctgggggttg cacaggggag ggggttctgc catggctaga atgcgctaag ggggtgaaac
 240
 gaagcctgct gggcccgga accacagagc agcctggcct ttgaaggaga ccctgtggca
 300
 cccctgccc accccaagt ccagccattt cacttcctcg gagatgggtgc aaagcaagaa
 360
 aaaaaaaaa atccagtgtt ctcaggctcag ccttccacca gccaggattc atcgtctgat
 420
 ctgtttgggg agagagcatg gagtgggtgga gatgggttgg gccccagtgt tttctgatta
 480
 actcgagtt cacctgaaac attttg
 506

<210> 912
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 912
 Met Phe Gln Val Asn Cys Glu Leu Ile Arg Lys His Trp Gly Pro Thr
 1 5 10 15
 His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn
 20 25 30
 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe
 35 40 45
 Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly
 50 55 60
 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val
 65 70 75 80
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser
 85 90 95
 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro
 100 105 110
 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser
 115 120 125
 Arg

<210> 913
 <211> 339

<212> DNA

<213> Homo sapiens

<400> 913

cgcttcatgg cgtggttcag gcgtacgggt ccggctactg gtgactaccg tggcacgaaa
 60
 tttttcgttc gcgagaacgg taaaaccctc gcaacctcga tgttcatggt ttgtgtcgcc
 120
 ctgggcgcca cggacctgct ttctgccctc gactcgattc cggcgtccta tggtttcacc
 180
 aacgaggggt acctatcct taccgctaac gtctttgctc tcatgggctt gcgtcagttg
 240
 tatttcctta ttggaagcct gttggaacgt ctggtgtact tgctcgtggg actggtcgtg
 300
 attttgggct ttatcgccct caagctcatt ggccacgcg
 339

<210> 914

<211> 113

<212> PRT

<213> Homo sapiens

<400> 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
1			5					10					15		
Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
		20					25					30			
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
	35					40					45				
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50				55					60					
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65				70				75				80			
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85					90				95			
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
		100					105					110			

Ala

<210> 915

<211> 663

<212> DNA

<213> Homo sapiens

<400> 915

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 gacagtgaag atcctgttgt ggacattggt gctgctaccc ctgtcatcaa tggacagtca
 120
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatggttctg
 180
 gagcagaatg gaaaatcggg acacactttg actggtgatg gtctcaatgg accatcagat
 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact
 300
 atccctttga ttaagggccc taaaggggtt gggtttgcaa ttgctgacag ccctactgga
 360
 cagaaggtga aaatgatact ggatagtcag tgggtgtcaag gccttcagaa aggagatata
 420
 attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagagggtg
 480
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtccccct
 540
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag
 600
 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga
 660
 tcc
 663

<210> 916
 <211> 221
 <212> PRT
 <213> Homo sapiens

<400> 916
 Xaa Val Pro Val Asn Gln Tyr Val Asn Leu Thr Leu Cys Arg Gly Tyr
 1 5 10 15
 Pro Leu Pro Asp Asp Ser Glu Asp Pro Val Val Asp Ile Val Ala Ala
 20 25 30
 Thr Pro Val Ile Asn Gly Gln Ser Leu Thr Lys Gly Glu Thr Cys Met
 35 40 45
 Asn Pro Gln Asp Phe Lys Pro Gly Ala Met Val Leu Glu Gln Asn Gly
 50 55 60
 Lys Ser Gly His Thr Leu Thr Gly Asp Gly Leu Asn Gly Pro Ser Asp
 65 70 75 80
 Ala Ser Glu Gln Arg Val Ser Met Ala Ser Ser Gly Ser Ser Gln Pro
 85 90 95
 Glu Leu Val Thr Ile Pro Leu Ile Lys Gly Pro Lys Gly Phe Gly Phe
 100 105 110
 Ala Ile Ala Asp Ser Pro Thr Gly Gln Lys Val Lys Met Ile Leu Asp
 115 120 125
 Ser Gln Trp Cys Gln Gly Leu Gln Lys Gly Asp Ile Ile Lys Glu Ile
 130 135 140
 Tyr His Gln Asn Val Gln Asn Leu Thr His Leu Gln Val Val Glu Val
 145 150 155 160
 Leu Lys Gln Phe Pro Val Gly Ala Asp Val Pro Leu Leu Ile Leu Arg
 165 170 175
 Gly Gly Pro Pro Ser Pro Thr Lys Ser Ala Lys Met Lys Thr Asp Lys
 180 185 190
 Lys Glu Asn Ala Gly Ser Leu Glu Ala Ile Asn Glu Pro Ile Pro Gln
 195 200 205
 Pro Met Pro Phe Pro Pro Ser Ile Ile Arg Ser Gly Ser
 210 215 220

<210> 917
 <211> 615

<212> DNA

<213> Homo sapiens

<400> 917

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 60
 ttcaaacatg accccacgtc ggccaacctc ctgcagctgg tgcgctcgtc cggagacatc
 120
 caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag
 180
 atccgcccgc acgccctcac ggtgcactcc tatcggggcg ctgccttctg tgatcactgc
 240
 ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac
 300
 taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggcccg caaacggcgc
 360
 ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtccctg
 420
 ccctgcacgg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca
 480
 tcctcttcct cctcttctgc ctcacgtat acggggccgcc ccattgagct ggacaagatg
 540
 ctgctctcca aggtcaaggt gccgcacacc ttcctcatcc acagctatac acggcccacc
 600
 gtttgccagg cttgc
 615

<210> 918

<211> 148

<212> PRT

<213> Homo sapiens

<400> 918

Ile	Val	Asp	Gln	Lys	Phe	Pro	Glu	Cys	Gly	Phe	Tyr	Gly	Leu	Tyr	Asp
1				5					10					15	
Lys	Ile	Leu	Leu	Phe	Lys	His	Asp	Pro	Thr	Ser	Ala	Asn	Leu	Leu	Gln
			20					25					30		
Leu	Val	Arg	Ser	Ser	Gly	Asp	Ile	Gln	Glu	Gly	Asp	Leu	Val	Glu	Val
		35				40						45			
Val	Leu	Ser	Ala	Ser	Ala	Thr	Phe	Glu	Asp	Phe	Gln	Ile	Arg	Pro	His
		50				55					60				
Ala	Leu	Thr	Val	His	Ser	Tyr	Arg	Ala	Pro	Ala	Phe	Cys	Asp	His	Cys
65				70					75					80	
Gly	Glu	Met	Leu	Phe	Gly	Leu	Val	Arg	Gln	Gly	Leu	Lys	Cys	Asp	Gly
			85					90						95	
Cys	Gly	Leu	Asn	Tyr	His	Lys	Arg	Cys	Ala	Phe	Ser	Ile	Pro	Asn	Asn
			100					105					110		
Cys	Ser	Gly	Ala	Arg	Lys	Arg	Arg	Leu	Ser	Ser	Thr	Ser	Leu	Ala	Ser
		115					120					125			
Gly	His	Ser	Val	Arg	Leu	Gly	Thr	Ser	Glu	Ser	Leu	Pro	Cys	Thr	Ala
	130					135					140				
Glu	Glu	Glu	Pro												
145															

<210> 919
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 919
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 acaaatgcga tcttgctcga tagcgagcgc ggtgagtacc tcgccaagat gggcccgcgc
 120
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc
 180
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatggtga agtgaagaaa
 240
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc
 294

<210> 920
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 920
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp
 1 5 10 15
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu
 20 25 30
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala
 35 40 45
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn
 50 55 60
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys
 65 70 75 80
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp
 85 90 95
 Glu Ala

<210> 921
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 921
 acgcgtttgc gcatcgcttt gaccggctctg acgatggctg agtacttccg cgatgttcag
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 aaccaggacg tgctgttggt catcgacaac atcttccggt tctcccaggc tggttctgag
 120
 gtttcaacct tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac
 180
 gagatgggccc aattgcagga gcgaatcacc tcgaccctg gtcactccat cacctcgatg
 240
 caggccgtct acgtccccgc tgacgattac accgaccggt ctccggcgac gaccttcgcc
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctcgtggcct gtacccggcc

360

gtggatccgc tggcgctcg

378

<210> 922

<211> 126

<212> PRT

<213> Homo sapiens

<400> 922

Thr	Arg	Leu	Arg	Ile	Ala	Leu	Thr	Gly	Leu	Thr	Met	Ala	Glu	Tyr	Phe
1				5					10					15	
Arg	Asp	Val	Gln	Asn	Gln	Asp	Val	Leu	Leu	Phe	Ile	Asp	Asn	Ile	Phe
			20					25					30		
Arg	Phe	Ser	Gln	Ala	Gly	Ser	Glu	Val	Ser	Thr	Leu	Leu	Gly	Arg	Met
		35					40					45			
Pro	Ser	Ala	Val	Gly	Tyr	Gln	Pro	Asn	Leu	Ala	Asp	Glu	Met	Gly	Gln
		50				55					60				
Leu	Gln	Glu	Arg	Ile	Thr	Ser	Thr	Arg	Gly	His	Ser	Ile	Thr	Ser	Met
65				70					75					80	
Gln	Ala	Val	Tyr	Val	Pro	Ala	Asp	Asp	Tyr	Thr	Asp	Pro	Ala	Pro	Ala
			85						90					95	
Thr	Thr	Phe	Ala	His	Leu	Asp	Ala	Thr	Thr	Glu	Leu	Ser	Arg	Glu	Ile
			100					105					110		
Ala	Ser	Arg	Gly	Leu	Tyr	Pro	Ala	Val	Asp	Pro	Leu	Ala	Ser		
		115					120					125			

<210> 923

<211> 571

<212> DNA

<213> Homo sapiens

<400> 923

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ctggacaccg cgctggagca cgtgcgcgga gaaatccgca ttaccctgga gcatgcacgc
120
caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac
180
cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcc
240
tggcgcgatg caatccaggc gcaatgcgcc gtgttgctgg ccctgggcaa accgctgttt
300
gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgctgc gctgttgggg
360
gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggcat taacttacc
420
ccttcgcct tgttgcaact gagtgcctaa aacgccgtgg gtatttgcac ggccgaaggc
480
ggcgctacgt ctcacgtcgc gattttggcc cgaggcaaag gcttgccgtg cgtggtcgcg
540
ctgggcgccg aagtgtcga cgtgccccaa g
571

<210> 924
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 924
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu
 1 5 10 15
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile
 20 25 30
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu
 35 40 45
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu
 50 55 60
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala
 65 70 75 80
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly
 85 90 95
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln
 100 105 110
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro
 115 120 125
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu
 130 135 140
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly
 145 150 155 160
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro
 165 170 175
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln
 180 185 190

<210> 925
 <211> 620
 <212> DNA
 <213> Homo sapiens

<400> 925
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 ncatgggtgtg tgcacgtgtg cnaactgtgta tgcacgtgtg tgcactgtgtg
 120
 gtgggtgtgta tgcacgtgtg gtgcacgtgt gcaactgtgtg tgtgtgtatg catgtgtgtg
 180
 cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg
 240
 tgtgtgcacg tgtgcactgt gtatgcatag tgtgtgcacg tgtgcactgt gtgtggatgc
 300
 atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tgggtgtgtgc acgtgtgcac
 360
 ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg
 420
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctgggc ccattctccag
 480

tgcccagcag catcacacgc actttgggtgc tttataaatg catggtcagt gaggctgcc
 540
 gcaccaagct gtccttttac cataacacct ggaatagtca cctgtgataa gctatcacat
 600
 aggaaacatt tttaaaattt
 620

<210> 926
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 926
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys
 35 40 45
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu
 50 55 60
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met
 65 70 75 80
 Cys Val His Val Cys Thr Val Tyr Ala
 85

<210> 927
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 927
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 aagaggcatt tggggtcctg ttcagatcat tccaacagca aaccgggcat ggagacccca
 120
 tctcaggtct gtgcttctct gggggccacc cagccatcct gccaccagc tcagaggcag
 180
 ggacaaagcc ctcccaagag gcagcaggca gcaagggtca gccagcgag tggggacagg
 240
 caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc
 300
 aagcacctgt aatgccggct tcccacagag gcgagccaga tcctggcact attctttaag
 360

<210> 928
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 928
 Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe
 1 5 10 15
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

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<400> 929
nnctccccag ggccgagtc tccggagtc gcagagagcc tggatggatc acaggaggat
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aagcctcggg gctcatgtgc ggagcccact ttactgata cgggaatggg ggctcacata
120
aacaacagcc ggctcaaggc caagggcgtg ggccagcacg acaacgccc gaactttggg
180
aaccagagct ttgaggagct gcgagcagcc tgtctaagaa agggggagct cttcgaggac
240
cccttattcc ctgctgaacc cagctcactg ggcttcaagg acctgggccc caactccaaa
300
aatgtgcaga acatctcctg gcagcggccc aaggatatca taaacaacc tctattcatc
360
atggatggga tttctccaac agacatctgc caggggatcc tcggggactg ctggctgctg
420
gctgccatcg gctcccttac cacctgcccc aaactgctat accgcgtggg gccagagga
480
cagagcttca agaaaaacta tgctggcatc ttccattttc agatttgga gtttggaag
540
tgggtgaacg tgggtggtaga tgaccggctg cccacaaaga atgacaagct ggtgtttgtg
600
cactcaaccg aacgcagtga gttctggagt gccctgctgg agaaggcgta tgccaagctg
660
agtgggtcct atgaagcatt gtcagggggc agtaccatgg agggccttga ggacttcaca
720
ggaggcgtag cccagagctt ccaactccag agggccctc agaacctgct caggctcctt
780
aggaaggccg tggagcgatc ctccctcatg ggttgctcca ttgaagtcac cagtgatagt
840
gaactggaat ccatgactga caagatgctg gtgagagggc acgcttactc tgtgactggc
900
cttcaggatg tccactacag aggcaaaatg gaaacactga ttcgggtccg gaatccctgg
960
ggccggattg agtggaatgg agcttgaggt gacagtgcc aaggagtgga agaggtggcc
1020
tcagacatcc agatgcagct gctgcacaag acggaggacg gggagtcttg gatgtcctac
1080

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caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc
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 1200
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 1260
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 1380
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 1500
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 1560
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 1620
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 1680
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 1740
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 1800
 aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg
 1860
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 1920
 aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc
 1980
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 2040
 gtcttggtgg ccaggatgac agatgatggc ctgatcatag actttgacag cttcatcagc
 2100
 tgtttcttga ggctaaagac catgttcaca ttctttctaa ccatggaccc caagaatact
 2160
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 2220
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 2280
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 2340

<210> 930

<211> 702

<212> PRT

<213> Homo sapiens

<400> 930

Met	Val	Ala	His	Ile	Asn	Asn	Ser	Arg	Leu	Lys	Ala	Lys	Gly	Val	Gly
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Gln	His	Asp	Asn	Ala	Gln	Asn	Phe	Gly	Asn	Gln	Ser	Phe	Glu	Leu	
			20					25				30			
Arg	Ala	Ala	Cys	Leu	Arg	Lys	Gly	Glu	Leu	Phe	Glu	Asp	Pro	Leu	Phe

```

      35      40      45
Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
  50      55      60
Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
  65      70      75      80
Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
      85      90      95
Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
      100      105      110
Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
      115      120      125
Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
      130      135      140
Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
      145      150      155      160
Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
      165      170      175
Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
      180      185      190
Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val
      195      200      205
Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu
      210      215      220
Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
      225      230      235      240
Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
      245      250      255
Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
      260      265      270
Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
      275      280      285
Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
      290      295      300
Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
      305      310      315      320
Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
      325      330      335
Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
      340      345      350
Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala
      355      360      365
Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
      370      375      380
Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
      385      390      395      400
Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp
      405      410      415
Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
      420      425      430
Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
      435      440      445
Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
      450      455      460
Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly

```

```

465          470          475          480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
          485          490          495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
          500          505          510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
          515          520          525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
          530          535          540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545          550          555          560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
          565          570          575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
          580          585          590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
          595          600          605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
          610          615          620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625          630          635          640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
          645          650          655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
          660          665          670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
          675          680          685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
          690          695          700

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<210> 931

<211> 297

<212> DNA

<213> Homo sapiens

<400> 931

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tcgcgaaggg agcctgacat gggccagaaa atcaatcccc atggtttccg tctcgggtgtg
60
acgaccgatc acaagaccgc ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttccttt acgccgctcg cccgggcatc
240
gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt
297

```

<210> 932

<211> 93

<212> PRT

<213> Homo sapiens

<400> 932

Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

```

1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
                20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
                35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
                50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
                85           90

```

<210> 933

<211> 305

<212> DNA

<213> Homo sapiens

<400> 933

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nnacgcgtcg ccaagctgtt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
60
tccgccgatc cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgcac
120
gcgctggcca tcttccgac cgaccgggat cagctggttt cggcgatcca gcaggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgcctt cgtcaacga caacacgatc
240
cgcgatctct acgtggccgg caacaaccgg gcgctcggcg aagtggcggg caaattcatg
300
ggcga
305

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<210> 934

<211> 101

<212> PRT

<213> Homo sapiens

<400> 934

```

Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
                20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
                35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
                85           90           95
Gly Lys Phe Met Gly
                100

```

<210> 935

<211> 333

<212> DNA

<213> Homo sapiens

<400> 935

acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctgggggtgga
 60
 caggctcccc tggggaagtc ctcttagaac tgagggatca acactggagg agactgcaag
 120
 gggtacggga taaatgttcc tgggtgaagga aacagcaggg gcaaaggccc tgcagcagaa
 180
 aggagcgagg ccctttggag taacagaaaag accatggtga caggagctca gaaagaccac
 240
 tgggtgtaag actataagcc agtggaggcc agattgggga atgggatggg aggggtgctt
 300
 gaagaccatg gtgaggctct cttggtcttt act
 333

<210> 936

<211> 103

<212> PRT

<213> Homo sapiens

<400> 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
1				5					10					15	
Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
		35					40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75				80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
				85					90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
															100

<210> 937

<211> 464

<212> DNA

<213> Homo sapiens

<400> 937

nnnttatctg cggagggggg ggccaccctg cccacactca tgctgcaggc ctccaccgac
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 ccggcggacg acgagctcaa ggatctgttg acggccgacc tcatggacca gcacaacctc
 120
 gaccgtgccc tggcagggtt gcgtgccagt cacgtcatcg acgaagctcg cgccgagggtg
 180
 cagcggcgtg ccgatctcgc ccgtggccat ctcgccatcc ttcccgcagg cgatgcccg
 240
 acggcggttg agaccctgtg cgacgagggt ggttcccggg cggcctgaac cccgaccctg
 300

ccagnctgcg tcccatctcc tggccgggac cgctccagcg tctgctctct gacagctcat
 360
 cgttcttccg acaccaagga gtttctcgtg gcccgtcac tcgatctcat cggcattggg
 420
 cccggcaacc cggactggat caccctggct gccgtcaagg ccan
 464

<210> 938
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 938
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln
 1 5 10 15
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala
 20 25 30
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg
 35 40 45
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala
 50 55 60
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg
 65 70 75 80
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala
 85 90 95

<210> 939
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 939
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 120
 acatggcggg ggatcgaggt tgggtggctat gaaatccatc acgggcgctct gtcgttcgct
 180
 gaggacgctg aagccttcct cgacggcgta cacgtcggtc cggtatgggg gacgatgtgg
 240
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac
 300
 gctggatcat cctggcgctcc gcactccgac gagctgggtt atcagggtcg acgcgaggcg
 360
 atgatcgaaa ccctcgccga cgcgt
 385

<210> 940
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 940
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

```

      1           5           10           15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20           25           30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35           40           45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50           55           60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
      65           70           75           80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85           90           95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100          105          110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115          120          125

```

<210> 941

<211> 348

<212> DNA

<213> Homo sapiens

<400> 941

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atcttctggg cggcgggtgat cacgctgggtg accatcggcc tgctgtttgc cggcaacttc
60
gaagccatgc aaaccatggg cgtgctggcc gggctgccgt tctcgggtgg gctgattttc
120
ttcatgttcg gtttgacaaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggctg ccgtgggttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgctga tcaagggctg gaagtgcaga ccctgctt
348

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<210> 942

<211> 116

<212> PRT

<213> Homo sapiens

<400> 942

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Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
  1           5           10           15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20           25           30
Pro Phe Ser Val Val Leu Ile Phe Phe Met Phe Gly Leu His Lys Ala
      35           40           45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
      50           55           60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
      65           70           75           80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85           90           95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

```

100 105 110
 Gln Thr Leu Leu
 115

<210> 943
 <211> 439
 <212> DNA
 <213> Homo sapiens

<400> 943
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 60
 ctcctctaataat gcatacctggg ctcctgctaa ccctgtggga aacaccgtct cttctctcct
 120
 ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccattcc agtcaatccc
 180
 ccttggttct gggatgctat ttccctggcc gcctccctct aggagtgttt agaaccctca
 240
 ctgtgggcag aaggaggga agatggctga ggtacctgga aagggacgtg tggatccccg
 300
 ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaataa gttccctaag
 360
 gaacctggct tagtgctggc ccttcacata ctgagacatg gaatccttac tactgttctc
 420
 tgaggaaaga ggctgttcc
 439

<210> 944
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 944
 Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu
 1 5 10 15
 His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp
 20 25 30
 Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu
 35 40 45
 Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly
 50 55 60
 Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr
 65 70 75 80
 Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val
 85 90 95
 Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly
 100 105 110
 Met Arg Ser Asn Val Pro
 115

<210> 945
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 945
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 gagatggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta
 120
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccctg tgtttgtctc
 180
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggctctgga
 240
 cagagtattg tgcaagttga aagtctctgg atggggctat gtatatacta ccagccaatt
 300
 tgggtgcaaa ttggatttga aggcctgcct ctgtccacn
 339

<210> 946
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 946
 Xaa Ile Arg Glu Ala Phe His Ile Phe Phe Leu Leu Ile Ile Ser Ile
 1 5 10 15
 Ala Leu Tyr Val Glu Met Val Ile Tyr Ile Tyr Thr His Thr His Ile
 20 25 30
 Tyr Val Cys Val Cys Ile Tyr Val Tyr Ile Tyr Ser Val Tyr Asn Lys
 35 40 45
 Thr Cys Thr Val Tyr Ser Ala Pro Arg Val Cys Leu Ser Asn Ser Phe
 50 55 60
 Ser Lys Glu Leu Leu Leu Phe Glu Met Glu Gly Glu Gly Gly Pro Gly
 65 70 75 80
 Gln Ser Ile Val Gln Val Glu Ser Leu Trp Met Gly Leu Cys Ile Ser
 85 90 95
 Tyr Gln Pro Ile Trp Val Gln Ile Gly Phe Glu Gly Leu Pro Leu Ser
 100 105 110
 Thr

<210> 947
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 947
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 60
 ctcgtggcat cacacctgtg cacgggggtg gggaaggagt ggacaggagt ggacaagtca
 120
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga
 180
 ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tatacactgg
 240
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc
 300

ctggataacca tgcccttctt aggctggagt tgctgccctt gtccatttac cataaaaatt
 360
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca
 420
 cgtacatccc caatgtgtac agccctactt tttctgctg atcaagttca attacttctg
 480
 ctaagatggg gactattctt gcctgctggg ccttggatgc aaggacccca atgttcaggc
 540
 agcctttggg gccttctagc atacgaatca gagcattatc tttagggtg gaataagctg
 600
 ccccaaaacc tgttgaagcc agccaggcac tgtgctccct tcacgcgt
 648

<210> 948
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 948
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 Leu Cys Thr Gly Val Gly Lys Glu Trp Thr Gly Val Asp Lys Ser Ser
 20 25 30
 Ser Ala Ala Gly Ser Ser Asp Ala Ser Ala Phe Leu Leu Cys Ala Lys
 35 40 45
 Leu Cys Arg Gly Asp Asp Ala Ser Lys Leu Ser Leu Leu Gly Met Ser
 50 55 60
 Ser Gln Ala Phe Ile His Trp Asp Ser Gln Ser Trp Ile Arg Gly Tyr
 65 70 75 80
 Ser Gly Asn Pro His Pro Trp Arg Ser Glu Pro Leu Asp Thr Met Pro
 85 90 95
 Phe Leu Gly Trp Ser Cys Cys Pro Cys Pro Phe Thr Ile Lys Ile Gly
 100 105 110
 Gln Glu Asn Thr Arg Thr His Leu Ser Phe Ser Ser Tyr Ala Lys Pro
 115 120 125
 Val Leu Pro Arg Thr Ser Pro Met Cys Thr Ala Leu Leu Phe Ser Ala
 130 135 140
 Asp Gln Val Gln Leu Leu Leu Arg Trp
 145 150

<210> 949
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 949
 acgcgtactg gttggctcat tcaactgaaaa tatgatgaca tttaaaggaa atgcaagaat
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 aagtaatgtg gaattttatc acagtgggtca agaaggcttc agggatagca cagatccaag
 120
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatattcg
 180
 aggctgtgct tttcaccatg gcttctctcc agcaattggg gtatttggga cagatggatt
 240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa
 300
 tgccaaccga gtccgagga atttgattgc actttcggtt tggccaggaa cctatcagaa
 360
 cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa
 420
 tacagtttta cagaataatg tagtggctgg atttgaaga gcaggatacc gcattgatgg
 480
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg
 540
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg
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 660
 c
 661

<210> 950

<211> 210

<212> PRT

<213> Homo sapiens

<400> 950

Met	Met	Thr	Phe	Lys	Gly	Asn	Ala	Arg	Ile	Ser	Asn	Val	Glu	Phe	Tyr
1				5					10					15	
His	Ser	Gly	Gln	Glu	Gly	Phe	Arg	Asp	Ser	Thr	Asp	Pro	Arg	Tyr	Ala
		20						25					30		
Val	Thr	Phe	Leu	Asn	Leu	Gly	Gln	Ile	Gln	Glu	His	Gly	Ser	Ser	Tyr
	35					40						45			
Ile	Arg	Gly	Cys	Ala	Phe	His	His	Gly	Phe	Ser	Pro	Ala	Ile	Gly	Val
	50					55					60				
Phe	Gly	Thr	Asp	Gly	Leu	Asp	Ile	Asp	Asp	Asn	Ile	Ile	His	Phe	Thr
65					70					75					80
Val	Gly	Glu	Gly	Ile	Arg	Ile	Trp	Gly	Asn	Ala	Asn	Arg	Val	Arg	Gly
				85					90					95	
Asn	Leu	Ile	Ala	Leu	Ser	Val	Trp	Pro	Gly	Thr	Tyr	Gln	Asn	Arg	Lys
			100					105					110		
Asp	Leu	Ser	Ser	Thr	Leu	Trp	His	Ala	Ala	Ile	Glu	Ile	Asn	Arg	Gly
	115						120						125		
Thr	Asn	Thr	Val	Leu	Gln	Asn	Asn	Val	Val	Ala	Gly	Phe	Gly	Arg	Ala
	130					135						140			
Gly	Tyr	Arg	Ile	Asp	Gly	Glu	Pro	Cys	Pro	Gly	Gln	Phe	Asn	Pro	Val
145					150					155					160
Glu	Lys	Trp	Phe	Asp	Asn	Glu	Ala	His	Gly	Gly	Leu	Tyr	Gly	Ile	Tyr
				165					170					175	
Met	Asn	Gln	Asp	Gly	Leu	Pro	Gly	Cys	Ser	Leu	Ile	Gln	Gly	Phe	Thr
			180					185					190		
Ile	Trp	Thr	Cys	Trp	Asp	Tyr	Gly	Ile	Tyr	Phe	Gln	Thr	Thr	Glu	Ser
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Val	His														
	210														

<210> 951

<211> 2615

<212> DNA

<213> Homo sapiens

<400> 951

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180
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240
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300
ctcaccagca tctcaccac tgccttctcc cgccttcgct acctggagtc gcttgacctc
360
agccacaatg gcctgacagc cctgccagcc gagagcttca ccagctcacc cctgagcgac
420
gtgaacctta gccacaacca gctccgggag gtctcagtgt ctgccttcac gacgcacagt
480
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540
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 1740
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 1920
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 1980
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 2220
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 2460
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 2520
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 2580
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 2615

<210> 952

<211> 357

<212> PRT

<213> Homo sapiens

<400> 952

Xaa	Pro	Ala	Pro	Thr	Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val
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Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu
			20				25						30		
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp
		35					40				45				
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
	50					55				60					
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu

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65          70          75          80
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu
          85          90          95
Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu
          100         105         110
Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu
          115         120         125
Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser
          130         135         140
His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser
145          150         155         160
Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro
          165         170         175
Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu
          180         185         190
Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp
          195         200         205
Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
          210         215         220
Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
225          230         235         240
Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
          245         250         255
Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
          260         265         270
Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
          275         280         285
Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
          290         295         300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
305          310         315         320
Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
          325         330         335
Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
          340         345         350
Gly Pro Thr Ile Leu
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<210> 953

<211> 347

<212> DNA

<213> Homo sapiens

<400> 953

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accacacttt ccccatccct tgatccatca ttggcgcttg aggttttccc atgtcttgac
120
tggtgtacct ggcggctctg cggagtaacc gctgcggaca cacagtagga cgggagggag
180
aagccattgc gtttcaccct ttcattggccc ttcctttccc cttccaagtg agctctttga
240
ggtagtcat ggagggcagt gtccctctgc atcctgtctg gggttgtcaa atatggccaa
300

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gtgggctcca tcggggcagc ggggtggggtg ggggggtgtct gtcagag
347

<210> 954
<211> 103
<212> PRT
<213> Homo sapiens

<400> 954
Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg
1 5 10 15
Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu
20 25 30
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser
35 40 45
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln
50 55 60
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly
65 70 75 80
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu
85 90 95
Arg Thr Gly Met Ala Ser Arg
100

<210> 955
<211> 634
<212> DNA
<213> Homo sapiens

<400> 955
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ctctgcaggt gaatggttct gcaggtgaag ggctctgcag gtgaacggtt ctgcaggtga
120
agggctctgc aggtgaacgg ttctgcaggt gagcggctct gcaggtgagc ggctctgcat
180
gtgagtgcct ctgtgactgg ctcgcaagca gcatttgtgc acacttgact ggccacaaca
240
gaatgttctt ctctgttgtc agcactgagg aggaagctcc tgcctaagcg accacagcca
300
ggcacccgct ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga
360
gctcctggaa tgcaggtga ggcagctccc acacaaaagc tatctactct ggcagttatc
420
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca
480
ggacccgctc ctgagaacac acgggtgcta gtccaagttc acagcacggc tcaagtcact
540
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt
600
caccatctca cacctggaac aagggttacg gccg
634

<210> 956

<211> 113
 <212> PRT
 <213> Homo sapiens

<400> 956

Met	Glu	Ser	Gly	Glu	Ser	Asn	Val	Ser	Met	Glu	Arg	Val	Pro	Gly	Cys
1				5				10					15		
Gly	Arg	Leu	Gly	Arg	Ser	Phe	Leu	Leu	Ser	Ala	Asp	Asn	Arg	Glu	Glu
		20					25					30			
His	Ser	Val	Val	Ala	Ser	Gln	Val	Cys	Thr	Asn	Ala	Ala	Cys	Glu	Pro
		35				40					45				
Val	Thr	Glu	Ala	Leu	Thr	Cys	Arg	Ala	Ala	His	Leu	Gln	Ser	Arg	Ser
	50				55					60					
Pro	Ala	Glu	Pro	Phe	Thr	Cys	Arg	Ala	Leu	His	Leu	Gln	Asn	Arg	Ser
65					70				75					80	
Pro	Ala	Glu	Pro	Phe	Thr	Cys	Arg	Thr	Ile	His	Leu	Gln	Ser	Arg	Ser
				85				90						95	
Pro	Ala	Glu	Pro	Phe	Thr	Cys	Arg	Ala	Ala	His	Leu	Gln	Ser	Pro	Ser
		100					105						110		

Arg

<210> 957
 <211> 823
 <212> DNA
 <213> Homo sapiens

<400> 957

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 120
 gtacctcctg gccacccagc actgcgcagc cgtggtgtcc agcctcctgg gcagccctt
 180
 gcccttgga aggtacccag ctcagactcc aggcttaggg gtccctctgg aatgatgctc
 240
 cccttggaa gatgctcccc gagccctcca cccggtctg caccctgact ttctgcatga
 300
 gttcccatgg ctgtaggcca cgtgggacag aaagtgacat ggagccaggc cccagtctct
 360
 caggtagcca cggggacctc tcctctccag gcgttttggg atcctcactg gctccggtgg
 420
 gccctgcaca gcacccccac agggaaagctg ctgtttctgc ctctctctaa ggtcccaaaa
 480
 ctgcctgggt gctctgttgg cccagggctc cagcacacac tggaggctgc cctcaccct
 540
 gtgtcttgg tccggctact ccaagccttg tcctctgcag ggcattccact gctgcctgtg
 600
 agcagacccc tgggaactgc ctgatctgag cccctcagg agcccaagga caaccttgtc
 660
 tgtaccatac atcactatgt cttcccaagc tcacacctcc cagctcccag caaagggcag
 720
 ggcgtgtcta ccaccacca gccactggg gtcccccttc ctcgcccagg cctccggagc
 780

atgggtctgc tggcccttcc tttctttgcc tcttagtctg gaa
823

<210> 958
<211> 105
<212> PRT
<213> Homo sapiens

<400> 958
Met Ala Val Gly His Val Gly Gln Lys Val Thr Trp Ser Gln Ala Pro
1 5 10 15
Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp
20 25 30
Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu
35 40 45
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val
50 55 60
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser
65 70 75 80
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu
85 90 95
Pro Val Ser Arg Pro Leu Gly Thr Ala
100 105

<210> 959
<211> 586
<212> DNA
<213> Homo sapiens

<400> 959
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acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtcagagac
120
ctggcagtgt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg
180
atcgtggact acaggaaaag gagggctcag cacgccccca ttctcattga tggggctgta
240
tgggagccag ttgagagctt caagttcctt ggtgtccaca tcaccatcga actatcatgg
300
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga
360
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta cccatcagag
420
agcatcatga ctggttgcac caccgcctgg tatggcaact gtcggcctc cgaccgcaag
480
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc
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586

<210> 960
<211> 195
<212> PRT

<213> Homo sapiens

<400> 960

Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe
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 Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
 20 25 30
 Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
 35 40 45
 Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
 50 55 60
 Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
 65 70 75 80
 Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
 85 90 95
 Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
 100 105 110
 Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
 115 120 125
 Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
 130 135 140
 Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
 145 150 155 160
 Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
 165 170 175
 Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
 180 185 190
 Leu Thr Ile
 195

<210> 961

<211> 502

<212> DNA

<213> Homo sapiens

<400> 961

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 120
 taaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa
 180
 atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc ccactcctga
 240
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 300
 ccatggccat ggagcttcaa ggaaagaaac ccctcagttt tttccgtcta gtccgccacc
 360
 tcattcccca ataagtcag ggcataatccc cagtgccatt gttcttccaa atgctaccca
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 cattgatcac cccttcacgc gt
 502

<210> 962
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 962
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 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met
 20 25 30
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu
 35 40 45
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser
 50 55 60
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp
 65 70 75 80
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys
 85 90 95
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg
 100 105

<210> 963
 <211> 1298
 <212> DNA
 <213> Homo sapiens

<400> 963
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 gcgctctaga ggagatgaat tatggatccg ccctcccga atcctggctc ggccctcccc
 120
 acgccaccca gggccagtcg ggtctgctca cagcccagag aggccgctg tccagccgcy
 180
 ggcaagagac agagcaggtc cctgtgtatc caagtccctg agcccgtag accggcccca
 240
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca
 300
 agaaagggaa gaaggggaag aaggcaccgg acccgagaa gcccaaacgg agcctgaagg
 360
 ggacgtcgcy ggtgttcatt ggcttccgcy accgaacacc caagatctac aagaagggcc
 420
 agttccgcag cgcctcgcc ttcttctggg gcctccacac cggccccac aagaccaagc
 480
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 600
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 660
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 720
 aacaggccac agtggacgcc tggctgcagc gctcgagctc ccgcatgggc tcccgcgaac
 780

tccccctccc gtcgggtgcc gagatcctgc ggcttggggg ccggctccgg aggttcccc
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 gcagccgcag catctacgcg tcaggcgagc ccctgggctt cctgcccttc gaggacgagg
 900
 cccattcca tcaactcggc tcccgcaagt cgtgtacgg gcttgagggc ttccaggacc
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 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtactcc
 1020
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 1200
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 1260
 acgagggcga ggcgcaccct tatggctact acctggat
 1298

<210> 964
 <211> 235
 <212> PRT
 <213> Homo sapiens

<400> 964
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 20 25 30
 Ser Ser Ser Arg Arg Pro Arg Ser Arg Ala Ala Asn Arg Pro Gln Trp
 35 40 45
 Thr Pro Gly Cys Ser Ala Arg Ala Pro Ala Trp Ala Pro Ala Asn Ser
 50 55 60
 Pro Ser Arg Arg Val Pro Arg Ser Cys Gly Leu Gly Ala Gly Ser Gly
 65 70 75 80
 Gly Ser Pro Ala Ala Ala Ser Thr Arg Gln Ala Ser Pro Trp Ala
 85 90 95
 Ser Cys Pro Ser Arg Thr Arg Pro His Ser Ile Thr Arg Ala Pro Ala
 100 105 110
 Ser Arg Cys Thr Gly Leu Arg Ala Ser Arg Thr Trp Ala Ser Ile Met
 115 120 125
 Thr Ile Thr Ala Thr Ala Thr Thr Thr Thr Thr Gly Ser His Ser Thr
 130 135 140
 Ala Thr Arg Ser Arg Asn Pro Thr Trp Arg Ala Ser Ala Pro Thr Ala
 145 150 155 160
 Arg Pro Gly His Pro Thr Ala Thr Thr Thr Thr Gly Thr Arg Pro Arg
 165 170 175
 Ile Pro Thr Thr Thr Thr Thr Pro Thr Ile Thr Val Ala Pro Leu Ile
 180 185 190
 Arg Gly Thr Pro Thr Ala Thr Ala Thr Thr Ile Thr Asn Pro His Met
 195 200 205
 Arg Pro Arg Arg Gly Thr Arg Leu Leu Thr Ala Thr Thr Met Gly Thr
 210 215 220
 Arg Ala Arg Arg Thr Leu Met Ala Thr Thr Trp

225

230

235

<210> 965

<211> 336

<212> DNA

<213> Homo sapiens

<400> 965

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nnngtgacca ttatgggtgg tgcccgtagc cgtgaagtgg aaggcggtga tttgttggc
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cgggtcagcg atgccgaaaa ggctgaaatc ctccggccgc ccatgtgtga tgcgcccc
120
aataccggcg gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc
180
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240
gccggcgccg tatatcgcaa tgaggatagt aatgaccttg ctctgtact caacgaggtg
300
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336

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<210> 966

<211> 112

<212> PRT

<213> Homo sapiens

<400> 966

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Asp Phe Val Gly Arg Val Ser Asp Ala Glu Lys Ala Glu Ile Leu Gly
      20           25           30
Arg Ala Asp Val Tyr Val Ala Pro Asn Thr Gly Gly Glu Ser Phe Gly
      35           40           45
Ile Val Leu Val Glu Ala Met Ala Ala Gly Ala Ala Val Val Ala Ser
      50           55           60
Asp Leu Glu Ala Phe Arg Ala Val Cys Asn Ala Asp Ser Asp Asp Val
      65           70           75           80
Ala Gly Ala Leu Tyr Arg Asn Glu Asp Ser Asn Asp Leu Ala Arg Val
      85           90           95
Leu Asn Glu Val Leu Glu Asp Pro Glu Tyr Arg Ala Arg Leu Val His
      100           105           110

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<210> 967

<211> 393

<212> DNA

<213> Homo sapiens

<400> 967

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120
tcggcctccg ctccggccgc agcctgggct gcgccagact ctgcgggagg caccttctcc
180

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<210> 968
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 968
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<210> 969
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 <212> DNA
 <213> Homo sapiens

<400> 969
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<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

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Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys
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Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu
			165					170						175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile
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Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr
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Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg
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Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg
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 <211> 337
 <212> DNA
 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

<400> 972
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 35 40 45
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu
 50 55 60
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg
 65 70 75 80
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 35 40 45
 Gly Asp Ser Ser Gly Cys Val Thr Leu Arg Thr Thr Gly Lys Val Ala
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<211> 411

<212> PRT

<213> Homo sapiens

<400> 976

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			20					25					30		
Arg	Arg	Asn	Glu	Pro	Thr	Leu	Pro	Arg	Glu	Phe	Thr	Arg	Arg	Gly	Arg
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Lys	Gln	Ile	Pro	Gln	Val	Val	Glu	Ala	Cys	Cys	Gln	Phe	Ile	Glu	Lys
			100					105					110		
His	Gly	Leu	Ser	Ala	Val	Gly	Ile	Phe	Thr	Leu	Glu	Tyr	Ser	Val	Gln
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Arg	Val	Arg	Gln	Leu	Arg	Glu	Glu	Phe	Asp	Gln	Gly	Leu	Asp	Val	Val
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			165					170					175		
Ser	Phe	Leu	Leu	Thr	Ala	Thr	Leu	Lys	Pro	Gln	Asp	Gln	Leu	Ser	Ala
		180					185						190		
Leu	Gln	Leu	Leu	Val	Tyr	Leu	Thr	Pro	Pro	Cys	His	Ser	Asp	Thr	Leu
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	210				215						220				
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Thr	Asn	Leu	Ala	Leu	Val	Phe	Gly	Ser	Ala	Leu	Leu	Lys	Lys	Gly	Lys
			245					250						255	
Phe	Gly	Lys	Arg	Glu	Ser	Arg	Lys	Thr	Lys	Leu	Gly	Ile	Asp	His	Tyr
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Val Cys Leu Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met
 50          55          60
Gly Pro Ala Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met

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<210> 979

<211> 3500

<212> DNA

<213> Homo sapiens

<400> 979

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<211> 73

<212> PRT

<213> Homo sapiens

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		20						25					30		
Cys	Phe	Gln	Val	Leu	Thr	Ala	Ser	Gly	Trp	Ser	Leu	Glu	Ala	Thr	Glu
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Glu	Arg	Asn	Ala	Trp	Leu	Arg	Ala	Ala	Glu	His	Ser	Glu	Ala	Ser	Arg
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<210> 981

<211> 404

<212> DNA

<213> Homo sapiens

<400> 981

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<210> 982

<211> 134

<212> PRT

<213> Homo sapiens

<400> 982

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 Thr Ala Pro Val Gly Trp Glu Leu Val Arg Val Glu His Val Glu Leu
 35 40 45
 Asp Asp Glu Asp Val Asp Asp Glu Asn Thr Asp Ile Thr Ala Leu Ala
 50 55 60
 Glu Ala Gly Ala Arg Gly Gly Ala Gly Asn His Arg Phe Gly Gly Asp
 65 70 75 80
 Arg Pro Gly Ser Asp Arg Val Leu Gly Arg Gln Arg Leu Gln Gln Pro
 85 90 95
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 Gly Ser Glu Pro Gly Arg
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<210> 983

<211> 579

<212> DNA

<213> Homo sapiens

<400> 983

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<213> Homo sapiens
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<213> Homo sapiens
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Ala Asn Phe Lys Ala His Asp Leu Lys Leu Val Thr Glu Ile Asn His			
	35	40	45
Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser			
	50	55	60
Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met			
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<210> 987

<211> 4224

<212> DNA

<213> Homo sapiens

<400> 987

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<210> 988
 <211> 873
 <212> PRT
 <213> Homo sapiens

<400> 988
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 Met Leu Leu Arg Gly Leu Thr Gln Ile Gln Ser Arg Ile Leu Gly Pro
 35 40 45
 Gly Arg Lys Cys Cys Ala Leu Ala Asn Leu Ala Asp Met Leu Thr Val
 50 55 60
 Phe Ala Leu Thr Glu Asp Asp Pro Gln Glu Val Ser Ala Thr Val Tyr
 65 70 75 80
 Leu Asp Lys Leu Ala Thr Val Ile Ser Val Trp Asn Ser Asp Thr Gln
 85 90 95
 Asn Pro Tyr His Gln Gln Ala Leu Ala Glu Lys Val Lys Glu Ala Glu
 100 105 110
 Arg Asp Val Ser Leu Thr Ser Leu Ala Lys Leu Pro Ser Glu Thr Ile
 115 120 125
 Phe Val Gly Cys Glu Phe Leu His His Leu Leu Arg Glu Trp Gly Glu
 130 135 140
 Glu Leu Gln Ala Val Leu Arg Ser Ser Gln Gly Thr Ser Tyr Asp Ser
 145 150 155 160
 Tyr Arg Leu Cys Asp Ser Leu Thr Ser Phe Ser Gln Asn Ala Thr Leu
 165 170 175
 Tyr Leu Asn Arg Thr Ser Leu Ser Lys Glu Asp Arg Gln Val Val Ser
 180 185 190
 Glu Leu Ala Glu Cys Val Arg Asp Phe Leu Arg Lys Thr Ser Thr Val
 195 200 205
 Leu Lys Asn Arg Ala Leu Glu Asp Ile Thr Ala Ser Ile Ala Met Ala
 210 215 220
 Val Ile Gln Gln Lys Met Asp Arg His Met Glu Val Cys Tyr Ile Phe
 225 230 235 240
 Ala Ser Glu Lys Lys Trp Ala Phe Ser Asp Glu Trp Val Ala Cys Leu
 245 250 255
 Gly Ser Asn Arg Ala Leu Phe Arg Glu Pro Asp Leu Val Leu Arg Leu
 260 265 270
 Leu Glu Thr Val Ile Asp Val Ser Thr Ala Asp Arg Ala Ile Pro Glu
 275 280 285
 Ser Gln Ile Arg Gln Val Ile His Leu Ile Leu Glu Cys Tyr Ala Asp
 290 295 300
 Leu Ser Leu Pro Gly Lys Asn Lys Val Leu Ala Gly Ile Leu Arg Ser
 305 310 315 320
 Trp Gly Arg Lys Gly Leu Ser Glu Lys Leu Leu Ala Tyr Val Glu Gly
 325 330 335
 Phe Gln Glu Asp Leu Asn Thr Thr Phe Asn Gln Leu Thr Gln Ser Ala
 340 345 350
 Ser Glu Gln Gly Leu Ala Lys Ala Val Ala Ser Val Ala Arg Leu Val
 355 360 365
 Ile Val His Pro Glu Val Thr Val Lys Lys Met Cys Ser Leu Ala Val

370	375	380
Val Asn Leu Gly Thr His Lys Phe Leu Ala Gln Ile Leu Thr Ala Phe		
385	390	395
Pro Ala Leu Arg Phe Val Glu Val Gln Gly Pro Asn Ser Ser Ala Thr		400
	405	410
Phe Met Val Ser Cys Leu Lys Glu Thr Val Trp Met Lys Phe Ser Thr		415
	420	425
Pro Lys Glu Glu Lys Gln Phe Leu Glu Leu Leu Asn Cys Leu Met Ser		430
	435	440
Pro Val Lys Pro Gln Gly Ile Pro Val Ala Ala Leu Leu Glu Pro Asp		445
	450	455
Glu Val Leu Lys Glu Phe Val Leu Pro Phe Leu Arg Leu Asp Val Glu		460
465	470	475
Glu Val Asp Leu Ser Leu Arg Ile Phe Ile Gln Thr Leu Glu Ala Asn		480
	485	490
Ala Cys Arg Glu Glu Tyr Trp Leu Gln Thr Cys Ser Pro Phe Pro Leu		495
	500	505
Leu Phe Ser Leu Cys Gln Leu Leu Asp Arg Phe Ser Lys Tyr Trp Gln		510
	515	520
Leu Pro Lys Glu Lys Arg Cys Leu Ser Leu Asp Arg Lys Asp Leu Ala		525
	530	535
Ile His Ile Leu Glu Leu Leu Cys Glu Ile Val Ser Ala Asn Ala Glu		540
545	550	555
Thr Phe Ser Pro Asp Val Trp Ile Lys Ser Leu Ser Trp Leu His Arg		560
	565	570
Lys Leu Glu Gln Leu Asp Trp Thr Val Gly Leu Arg Leu Lys Ser Phe		575
	580	585
Phe Glu Gly His Phe Lys Cys Glu Val Pro Ala Thr Leu Phe Glu Ile		590
	595	600
Cys Lys Leu Ser Glu Asp Glu Trp Thr Ser Gln Ala His Pro Gly Tyr		605
	610	615
Gly Ala Gly Thr Gly Leu Leu Ala Trp Met Glu Cys Cys Cys Val Ser		620
625	630	635
Ser Gly Ile Ser Glu Arg Met Leu Ser Leu Leu Val Val Asp Val Gly		640
	645	650
Asn Pro Glu Glu Val Arg Leu Phe Ser Lys Gly Phe Leu Val Ala Leu		655
	660	665
Val Gln Val Met Pro Trp Cys Ser Pro Gln Glu Trp Gln Arg Leu His		670
	675	680
Gln Leu Thr Arg Arg Leu Leu Glu Lys Gln Leu Leu His Val Pro Tyr		685
	690	695
Ser Leu Glu Tyr Ile Gln Phe Val Pro Leu Leu Asn Leu Lys Pro Phe		700
705	710	715
Ala Gln Glu Leu Gln Leu Ser Val Leu Phe Leu Arg Thr Phe Gln Phe		720
	725	730
Leu Cys Ser His Ser Cys Arg Asn Trp Leu Pro Leu Glu Gly Trp Asn		735
	740	745
His Val Val Lys Leu Leu Cys Gly Ser Leu Thr Arg Leu Leu Asp Ser		750
	755	760
Val Arg Ala Ile Gln Ala Ala Gly Pro Trp Val Gln Gly Pro Glu Gln		765
	770	775
Asp Leu Thr Gln Glu Ala Leu Phe Val Tyr Thr Gln Val Phe Cys His		780
785	790	795
Ala Leu His Ile Met Ala Met Leu His Pro Glu Val Cys Glu Pro Leu		800

805 810 815
 Tyr Val Leu Ala Leu Glu Thr Leu Thr Cys Tyr Glu Thr Leu Ser Lys
 820 825 830
 Thr Asn Pro Ser Val Ser Ser Leu Leu Gln Arg Ala His Glu Gln Cys
 835 840 845
 Phe Leu Lys Ser Ile Ala Glu Gly Ile Gly Pro Glu Glu Arg Arg Gln
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 Thr Leu Leu Gln Lys Met Ser Ser Phe
 865 870

<210> 989
 <211> 402
 <212> DNA
 <213> Homo sapiens

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<210> 990
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 990
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 20 25 30
 Arg Arg Val Ala Leu Cys Lys Leu Leu Ile Glu Gln Pro Asp Leu Leu
 35 40 45
 Leu Leu Asp Glu Pro Thr Asn His Leu Asp Ala Glu Ser Val Asn Trp
 50 55 60
 Leu Glu Gly His Leu Lys Ser Tyr Pro Gly Ala Val Leu Ala Val Thr
 65 70 75 80
 His Asp Arg Tyr Phe Leu Asp His Val Ala Glu Trp Ile Cys Glu Val
 85 90 95
 Asp Arg Gly Gln Leu His Pro Tyr Glu Gly Asn Tyr Ser Thr Tyr Leu
 100 105 110
 Asp Thr Lys Arg Lys Arg Leu Gln Ile Glu Gly Lys Lys Asp Ala Lys
 115 120 125
 Arg Ala Lys Ile Leu Glu

130

<210> 991
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 991
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 180
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 359

<210> 992
 <211> 119
 <212> PRT
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<400> 992
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 20 25 30
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 35 40 45
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp
 50 55 60
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val
 65 70 75 80
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser
 85 90 95
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala
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 Ser Phe Phe Lys Glu Lys Arg
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<210> 993
 <211> 450
 <212> DNA
 <213> Homo sapiens

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<210> 994
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 994
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 35 40 45
 Leu Gly Lys Phe Asp Pro Asp Asn Ile Pro Ala Asp Pro Asn Glu Leu
 50 55 60
 Phe Ala Thr Trp Phe Lys Glu Ala Val Glu Asn Glu Val Gly Asp Pro
 65 70 75 80
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 Arg Val Val Asp Leu Leu Tyr Leu Asn Ser Asp Gly Phe His
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<210> 995
 <211> 924
 <212> DNA
 <213> Homo sapiens

<400> 995
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<210> 996

<211> 308

<212> PRT

<213> Homo sapiens

<400> 996

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		20						25					30		
Leu	Met	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val	
	35					40					45				
Asn	Gln	Gly	Glu	Gly	Leu	Lys	Phe	Val	Glu	Asp	Ser	Ala	Glu	Ser	Glu
	50					55				60					
Asp	Gly	Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val
65				70					75					80	
Asp	Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Val	Leu	Arg	Glu	Thr
			85					90						95	
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met
			100					105					110		
Arg	Arg	Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala
		115					120					125			
Pro	Ala	Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val
	130					135					140				
Tyr	Phe	Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu
145				150					155					160	
Trp	Ala	Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val
			165					170					175		
Pro	Met	Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn
		180				185						190			
Asp	Val	Met	Leu	Ser	Ala	Val	Val	Met	Thr	Tyr	Trp	Thr	Asn	Phe	Ala
	195					200						205			
Lys	Thr	Gly	Asp	Pro	Asn	Gln	Pro	Val	Pro	Gln	Asp	Thr	Lys	Phe	Ile
	210				215						220				
His	Thr	Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn

```

225                230                235                240
Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
                245                250                255
Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
                260                265                270
His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
                275                280                285
Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
                290                295                300
Gly Thr Arg Arg
305

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<210> 997
<211> 320
<212> DNA
<213> Homo sapiens

```

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<400> 997
aaatttaata ccatagcctt ctcttggttg atccttctag gcatgagtta tggcattaaa
60
acgggcatcc atcttggtgt cgatatcgta cttaatgccg tgcctaaacg agtatcaaga
120
gccttgctctt tggtcggtgc ctttgccgct attatgtacg gtctcattct acttgattct
180
acctgggttag ccttactcgg tatcgatgta cgagggtggtg ccatogaata ttgggcgaag
240
atgttcaaaa taggtattgg tactgaagag cttcggttacc ctatctttat gcaagatatg
300
tttgatttgc gcccacgcgt
320

```

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<210> 998
<211> 106
<212> PRT
<213> Homo sapiens

```

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<400> 998
Lys Phe Asn Thr Ile Ala Phe Ser Trp Leu Ile Leu Leu Gly Met Ser
1                5                10                15
Tyr Gly Ile Lys Thr Gly Ile His Leu Gly Val Asp Ile Val Leu Asn
                20                25                30
Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
                35                40                45
Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
50                55                60
Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
65                70                75                80
Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe
                85                90                95
Met Gln Asp Met Phe Asp Leu Arg Pro Arg
100                105

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```

<210> 999
<211> 401

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<212> DNA

<213> Homo sapiens

<400> 999

acgcgttcag gcgggtaaca atcgcgctaa gaagctgacc aaggaaaatg tcggcatggg
 60
 acatctgagc aagagcttca tcgggtgtta tctctactca gaaggcaagt ttgtgaccag
 120
 caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
 180
 gcaaaagcct ccagcagtgg cttcagatga tctggatata ggtctcttga agagggcctt
 240
 ggatgagtgg gtggctgatg ctaagaacca cattctcaat actgaaaact tcttttagcgg
 300
 gtcaaccggg ctcaacattg acagtttcta cgtctttggg gaccaagaca tctgctggca
 360
 gttggcagct attctgaagc agagcatgaa tcgggaattg t
 401

<210> 1000

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1000

Met	Val	His	Leu	Ser	Lys	Ser	Phe	Ile	Gly	Val	Tyr	Leu	Tyr	Ser	Glu
1				5					10					15	
Gly	Lys	Phe	Val	Thr	Ser	Asn	Tyr	Leu	Asn	Arg	Gly	Tyr	Lys	Asp	Ile
			20					25					30		
Leu	Ser	Tyr	Ala	Asp	Asp	Ala	Ser	Leu	Leu	Gln	Lys	Pro	Pro	Ala	Val
		35				40					45				
Ala	Ser	Asp	Asp	Leu	Asp	Thr	Gly	Leu	Leu	Lys	Arg	Ala	Leu	Asp	Glu
		50				55					60				
Trp	Val	Ala	Asp	Ala	Lys	Asn	His	Ile	Leu	Asn	Thr	Glu	Asn	Phe	Phe
65					70					75				80	
Ser	Gly	Ser	Thr	Gly	Leu	Asn	Ile	Asp	Ser	Phe	Tyr	Val	Phe	Gly	Asp
			85					90						95	
Gln	Asp	Ile	Cys	Trp	Gln	Leu	Ala	Ala	Ile	Leu	Lys	Gln	Ser	Met	Asn
			100					105						110	
Arg	Glu	Leu													
															115

<210> 1001

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1001

cgcggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccggtactg
 60
 ttcccttatg ccctaatagc ggtgattggt ggcttctctg ccactaccgt tggttcaatt
 120
 atcggatatga ttgtcttccc gctgtttggg ctggcgatga tccttcggg tctgctaact
 180

aacttcttcg ctggtggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg
 240
 gcaattattg gcggcgtagt gcacgggctg tttatcaccc tgttaccage gatgctaacc
 300
 cccttactgg aaaccttcgg cttcaaaggc gtcaccttca gtgattccga t
 351

<210> 1002
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1002
 Arg Gly Ile Ala Met Arg Leu Val Pro Asn Ala Lys Pro Ala Leu Asp
 1 5 10 15
 Cys Pro Val Leu Phe Pro Tyr Ala Pro Asn Ala Val Ile Val Gly Phe
 20 25 30
 Leu Ala Thr Thr Val Gly Ser Ile Ile Gly Met Ile Val Phe Pro Leu
 35 40 45
 Phe Gly Leu Ala Met Ile Leu Pro Gly Leu Leu Thr Asn Phe Phe Ala
 50 55 60
 Gly Gly Ala Ala Gly Val Phe Gly Asn Ala Met Gly Gly Arg Lys Gly
 65 70 75 80
 Ala Ile Ile Gly Gly Val Val His Gly Leu Phe Ile Thr Leu Leu Pro
 85 90 95
 Ala Met Leu Ile Pro Leu Leu Glu Thr Phe Gly Phe Lys Gly Val Thr
 100 105 110
 Phe Ser Asp Ser Asp
 115

<210> 1003
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 1003
 acggtctctc ctttagtcga tcgcgaatat gataggcgaa gcgacgtgat ggtgtgacgc
 60
 acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc
 120
 acccccgcacat ggggcacact ctccggccta aagtcccgct tcgctgacgg gccacataaa
 180
 ctgcgccgtt tgttcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg
 240
 gatttgcacg tcgatttatc gaagaacctc cttaccgacg agattcgtga cgctctcctc
 300
 gaactggctg cgcagatgcg cgtcaccgag cgtcgtgacg cgatgtatgc cggtgagcac
 360
 atcaacgtca ccgaggaccg cgccgtctc cataccgcgc tgtgtcgtcc ccgactgac
 420
 gagctgcatg ttgacgggtca ggat
 444

<210> 1004

<211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1004

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Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu
 1             5             10             15
Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg
      20             25             30
Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val
      35             40             45
Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile
      50             55             60
Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg
      65             70             75             80
Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg
      85             90             95
Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His
      100            105            110
Val Asp Gly Gln Asp
      115

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<210> 1005
 <211> 299
 <212> DNA
 <213> Homo sapiens

<400> 1005

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ccatggccat tcctctggtg actgcatcca gtccgatgga tttaaaccacc cccaatgtgc
60
tgggtgactcc caagtttaca cctccagcca gggcttctct cctggggttg catacccacc
120
tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctctca
180
tttcttccca tgctgcttc tcccacactc ctccctctca catgagggca acttcctcct
240
cccagttgct caggcccaaa acctccatca gttttgactc ttctctcgca cactactcg
299

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<210> 1006
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 1006

```

Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr
 1             5             10             15
Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser
      20             25             30
Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys
      35             40             45
Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala
      50             55             60
Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

```

```
<210> 1007
<211> 389
<212> DNA
<213> Homo sapiens
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<210> 1008
<211> 105
<212> PRT
<213> Homo sapiens
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<210> 1009
<211> 324
<212> DNA
<213> Homo sapiens
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973

ngccttcacg gctgntatgc ctggcctcat ccccatccct ggcacccgtg acgatagcca
 60
 cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac
 120
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc
 180
 agaaggagga cgtagttggt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt
 240
 ctgccccgag aggaacgtgg gcattaggct gcacccgag gaagccatgt attttctgag
 300
 aaacttgccc catggtgcag atct
 324

<210> 1010
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1010
 Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro
 1 5 10 15
 Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly
 20 25 30
 Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys
 35 40 45
 Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu
 50 55 60
 Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys
 65 70 75 80
 His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu
 85 90 95
 Ala Arg His Xaa Ser His Glu Gly
 100

<210> 1011
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1011
 ctgcagaaaa ggagggggtt cccatgccaa ggcagaactg tctgggacag acgctgcccg
 60
 gatecctgag gctgcctgca ctctggacca cgagctctga gagcagcagg ttgagggccg
 120
 gtgggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cgggtgagctg
 180
 actcctgagg agggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac
 240
 ggcaccatca atgcccagga gctgggcgag ggcgtgaagg ccacgggcaa gaacctctcg
 300
 gagccccagc taaagaaact catctccgag
 330

<210> 1012

<211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1012
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
 1 5 10 15
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
 20 25 30
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
 35 40 45
 Leu Lys Lys Leu Ile Ser Glu
 50 55

<210> 1013
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 1013
 nacttgacaca tcgtggtggc gtcgctgcgt gcggcactga caatgtgact ggcgcattcg
 60
 tggcggcgctc tcctcgtcgc cgggagcggc gaggaaggat taacgatgac cagcgacgctc
 120
 cccgggattg gctcgaacgc cgccactttg gcgcggtccc aggcctgcag tgacaaggctc
 180
 gaggtgatt tggcgggtcca tcccgacaag tggcgcattc tgggggggga ccgtcctact
 240
 ggcagcctgc acatcgggtca ctacttcggg tcgctggcga atcgggtacg cgtgcagaac
 300
 aagggcattg agtctttcct tgcgctcgct gactaccagg ttatctatga ccgcgggggg
 360
 ggtggtgacc tgcaggccaa tggtatgtcg aatgtcgccg attacctggc aatcggcatt
 420
 gacccaacgc gt
 432

<210> 1014
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1014
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala
 1 5 10 15
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His
 20 25 30
 Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu
 35 40 45
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln
 50 55 60
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile
 65 70 75 80
 Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

	85		90		95							
Val	Ala	Asp	Tyr	Leu	Ala	Ile	Gly	Ile	Asp	Pro	Thr	Arg
			100				105					

<210> 1015
 <211> 467
 <212> DNA
 <213> Homo sapiens

<400> 1015
 nngaattcga tggctgtgaa aggtcgagct cttaagtgtt ttcatatccc ctgtgtgggt
 60
 gaaaaacttcc cgatgaaagc ggcacgggtt gaagagctga aagaattgga aagagtttta
 120
 cagcaaaaga agattgaagc agagtgtctt aaactacgga aggaaattgt agaggctcag
 180
 tctggagtta agttgattaa acagcgtcat gaagaggatg atgaagaaga ggaagaggaa
 240
 gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat
 300
 tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa
 360
 atcaaccaa ttatattatt gaaagatatc atttacaagg taaaaactgt tttcaataat
 420
 gagtttgacg ctgcatataa acaaaaagag tttgaaattg cacgcgt
 467

<210> 1016
 <211> 155
 <212> PRT
 <213> Homo sapiens

<400> 1016
 Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile
 1 5 10 15
 Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu
 20 25 30
 Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu
 35 40 45
 Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys
 50 55 60
 Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu
 65 70 75 80
 Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser
 85 90 95
 Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu
 100 105 110
 Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys
 115 120 125
 Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala
 130 135 140
 Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg
 145 150 155

<210> 1017
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 1017
 acgctgggt ggttgggtat gtggaacat gtgcgcgcta atgagaagga tgcgaagggg
 60
 aacattaaag tgggtcgccc cggctacttt gcgagggtca tggatttcta tgcgcattat
 120
 ctgaaggggtg cggttaccgg tttccgtccg aattttattg tgcaggataa tacggggccgt
 180
 tggcgtgttc agtcgtcgtg gccgcagccg aatcgcaactg ttacttttgc gggaccccg
 240
 ggcattgtcc gctacgttac gacgttggcg gccgcacgc atgggaatgg tcaggctatt
 300
 ccgcaggcgg atgcacagtc tcttaaccgc gagaa
 335

<210> 1018
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1018
 Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile
 1 5 10 15
 Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala
 20 25 30
 His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val
 35 40 45
 Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro
 50 55 60
 Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly
 65 70 75 80
 Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln
 85 90 95
 Ala Asp Ala Gln Ser Leu Asn Arg Glu
 100 105

<210> 1019
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 1019
 acgctgaag gggtagtcgt agtagaagtc gtccacaaac acgggccccg gcagggtccag
 60
 ctctggagcc tcctcctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg
 120
 tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtgggt
 180
 ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc aggggccacc gacagagtgg
 240

cagagagcag gtgacttcct ggcactgcgg agcgaggacc cggagaagta cttcctcaat
 300
 ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac
 360
 gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtctgg
 420
 atccagctgc tgttccagga gagcaaccct gggg
 454

<210> 1020
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1020
 Met Ala Leu Pro Met Val Pro Gly Leu Gly Asp Glu Ala Gly Glu Gly
 1 5 10 15
 Arg Gly Ala Arg Trp Cys Gly Met Lys Ser Ala Ser Leu Lys Ser Ser
 20 25 30
 Trp Leu Glu Glu Pro Leu Pro Glu Pro Ser Gly Pro Ser Val Pro Arg
 35 40 45
 Gly His Arg Gln Ser Gly Arg Glu Gln Val Thr Ser Trp His Cys Gly
 50 55 60
 Ala Arg Thr Arg Arg Ser Thr Ser Ser Met Val Ala Gly Pro Ser Ser
 65 70 75 80
 Gly Thr Gly Thr Thr Arg Trp Gln Gly Pro Pro Ser His Thr His Ala
 85 90 95
 Gly Ala Thr Gly Arg Thr Ser Arg Pro Arg Val Pro Pro Arg Ser Leu
 100 105 110
 Ser Gly Ser Ser Cys Cys Ser Arg Arg Ala Thr Leu Gly
 115 120 125

<210> 1021
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 1021
 cagctgtgtc gtgacctcct gtagaccaga gagaggtaga gcatgaaaaa tgctcattga
 60
 gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc
 120
 tgggtgaggg tcaagtgctg gggcagcagc aacaacaaac caaaaaaag ccctttgaac
 180
 tcccttaatg ttgccaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt
 240
 taaagggcac tcttgagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa
 300
 atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa
 360
 ccctgt
 366

<210> 1022

<211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1022
 Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
 1 5 10 15
 Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
 20 25 30
 Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
 35 40 45
 Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala
 50 55 60
 Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
 65 70 75 80
 Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
 85 90 95
 Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu
 100 105

<210> 1023
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1023
 gccggggttc ggggtctctga agcgatcaac ctggccgact cggatgcaga tctggacggc
 60
 ggcatcctga ccatacagca gaccaagttt ggcaagtccc gcatggtgcc gctacacccc
 120
 agcgtgatcg gtccgatggc agcctaccgg gccttgcgcc gccagtacgt gcctgcgaag
 180
 ccgcagatga cattcttcgt gggctcgcgt ggcgtgcacc ggggtgaacc gctgggagat
 240
 aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttggat cgatcgcggc
 300
 ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgccgtgag acggatgatc
 360
 ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
 420
 ggccac
 426

<210> 1024
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1024
 Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
 1 5 10 15
 Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
 20 25 30
 Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

```

      35              40              45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
  50              55              60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
65              70              75              80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
      85              90              95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
      100              105              110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
      115              120              125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
      130              135              140

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<210> 1025

<211> 518

<212> DNA

<213> Homo sapiens

<400> 1025

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naccggtggg gcgcgcaggt ggccgcgcgg tccctttgct cctgcgcaa gccggagggg
60
tgcccagaag gctaccacta gcctcagcga aggggtgcgc ctgagagccg ggtagcctcg
120
gatagcggcg ctgcgtacgc gatgatggat gagccgtggg gggaagggcg cgtcgccctcg
180
gacgtccact gcaccctgcg cgagaaggaa ctgaagctgc ccaccttccg agcccactcc
240
ccactcctga agagccgcgc gttcttcgtg gacatcctga ccctgctgag cagccactgc
300
cagctctgcc ctgcagcccc gcacctggcc gtctacctgc tggaccactt catggatcgc
360
tacaacgtca ccacctcaa gcagctctac accgtggccg tctcctgcct cctgcttgca
420
agtaagtctg aggatcggga agaccacgtc cccaagttgg agcaaataaa cagcacgagg
480
atcctgagca gccagaactt caccctcacc aagaagga
518

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<210> 1026

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1026

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Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
  1              5              10              15
Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
      20              25              30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
      35              40              45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
      50              55              60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

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65					70					75				80
Gln	Leu	Tyr	Thr	Val	Ala	Val	Ser	Cys	Leu	Leu	Leu	Ala	Ser	Lys Phe
				85					90					95
Glu	Asp	Arg	Glu	Asp	His	Val	Pro	Lys	Leu	Glu	Gln	Ile	Asn	Ser Thr
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Arg	Ile	Leu	Ser	Ser	Gln	Asn	Phe	Thr	Leu	Thr	Lys	Lys		
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 <211> 465
 <212> DNA
 <213> Homo sapiens

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 <211> 155
 <212> PRT
 <213> Homo sapiens

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Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Lys	Ala	Met Arg
			20					25					30	
Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser	Leu	Val	Asn Thr
			35				40					45		
Xaa	Pro	Glu	Ala	His	His	Xaa	Trp	Leu	Lys	Val	Ile	Thr	Ala	Asn Ile
	50					55					60			
Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp	Gln	Glu	Leu	Leu Val
65					70					75				80
Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe	Asn	Thr	Pro	Leu	Val Lys
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Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr	Glu	Ala	Gln	Ala	Thr	Ile Arg
			100					105					110	
Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro	Thr	Arg	Leu	Val	Leu	Ser	Asp Cys
		115					120					125		
Ala	Thr	Ser	His	Gly	Ser	Leu	Arg	Ile	Gln	Leu	Leu	His	Lys	Leu Ser

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 Phe Lys Leu Asn Ala Ser Ala Lys Gln Val Met
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 <213> Homo sapiens

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 tattactaac caagtgagga aaattatccc tagcaggtcc agatgaccgt gtgcatgaat
 180
 cacagggaga ccctaaagga tttcctcctg taaagctctt tccccaccta tttgctactg
 240
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 360
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 <212> PRT
 <213> Homo sapiens

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 Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser
 35 40 45
 Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe
 50 55 60
 Pro His Leu Val Ser Asn Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser
 65 70 75 80
 Cys Ser Ala Arg His Leu Trp Pro Val Leu Gly Arg Gln Tyr Leu Phe
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 Glu Pro Ser His Ser Ser Val Arg Thr Val Ser Leu His Ala
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 <211> 322
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 <213> Homo sapiens

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 180
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 322

<210> 1032

<211> 107

<212> PRT

<213> Homo sapiens

<400> 1032

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Met	Leu	Pro	Gln	Ala	Asp	Gly	Trp	Phe	Glu	Val	Glu	Val	Lys	Cys	Pro
			20					25					30		
Ala	Gly	Thr	His	Tyr	Arg	Tyr	Asn	Ile	Asp	Gly	Glu	Thr	Asp	Val	Pro
	35						40					45			
Asp	Pro	Ala	Ser	Arg	Ala	Gln	Ala	Asn	Asp	Val	His	Gly	Trp	Ser	Val
	50					55					60				
Val	Val	Asp	Pro	Leu	Ala	Tyr	Gln	Trp	Arg	His	Pro	Asn	Trp	Gln	Gly
65				70					75					80	
Arg	Pro	Trp	His	Glu	Ala	Val	Ile	Tyr	Glu	Leu	His	Val	Gly	Val	Leu
			85						90					95	
Gly	Gly	Tyr	Ala	Ala	Val	Glu	Gln	Gln	Leu	Pro					
			100					105							

<210> 1033

<211> 579

<212> DNA

<213> Homo sapiens

<400> 1033

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 120
 aattcacatt caaatccatc acttttcaca taattgctgt taatatgaac gtcattgagtc
 180
 gttgttgctc gcggttgcca gtgggactcc ccatacacgg cagcgagaca tggaggaacc
 240
 atgggactaa ggatcggttg cgccgctgat ccggcggcag tcgagtacaa ggatgtcgtc
 300
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 420

aaagccgatc gaggaatctt tttctgcggc accgggatgg gcatggccat cacggccaac
 480
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<210> 1034
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 20 25 30
 Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg
 35 40 45
 Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg
 50 55 60
 Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn
 65 70 75 80
 Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val
 85 90 95
 Glu Arg Leu Ile Met Ser Asn Asp Ala His Val Leu Cys Leu Gly Gln
 100 105 110
 Arg

<210> 1035
 <211> 363
 <212> DNA
 <213> Homo sapiens

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 360
 atn
 363

<210> 1036
 <211> 121
 <212> PRT

<213> Homo sapiens

<400> 1036

Xaa Ala Cys Asn Val Cys Val Cys Met Xaa Pro Cys Leu Cys Val Cys
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 20 25 30
 Val Cys Val Xaa Glu Ala Val Cys Ile Cys Xaa Cys Leu Cys Ala Cys
 35 40 45
 Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr
 50 55 60
 Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser
 65 70 75 80
 Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa
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 Thr Cys Ile Cys Ile Glu Ser Val Cys Ala Val Cys Met Cys Val Ser
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 Ile Glu Arg Val Gly Asp Val Val Xaa
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<210> 1037

<211> 5832

<212> DNA

<213> Homo sapiens

<400> 1037

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 120
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 240
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 780
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5700

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 5832

<210> 1038
 <211> 1485
 <212> PRT
 <213> Homo sapiens

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 Gln Gly Asn Tyr Ser Arg Pro Pro Ala Tyr Ser Gly Val Pro Ser Ala
 35 40 45
 Ser Tyr Ser Gly Pro Gly Pro Gly Met Gly Ile Ser Ala Asn Asn Gln
 50 55 60
 Met His Gly Gln Gly Pro Ser Gln Pro Cys Gly Ala Val Pro Leu Gly
 65 70 75 80
 Arg Met Pro Ser Ala Gly Met Gln Asn Arg Pro Phe Pro Gly Asn Met
 85 90 95
 Ser Ser Met Thr Pro Ser Ser Pro Gly Met Ser Gln Gln Gly Gly Pro
 100 105 110
 Gly Met Gly Pro Pro Met Pro Thr Val Asn Arg Lys Ala Gln Glu Ala
 115 120 125
 Ala Ala Ala Val Met Gln Ala Ala Ala Asn Ser Ala Gln Ser Arg Gln
 130 135 140
 Gly Ser Phe Pro Gly Met Asn Gln Ser Gly Leu Met Ala Ser Ser Ser
 145 150 155 160
 Pro Tyr Ser Gln Pro Met Asn Asn Ser Ser Ser Leu Met Asn Thr Gln
 165 170 175
 Ala Pro Pro Tyr Ser Met Ala Pro Ala Met Val Asn Ser Ser Ala Ala
 180 185 190
 Ser Val Gly Leu Ala Asp Met Met Ser Pro Gly Glu Ser Lys Leu Pro
 195 200 205
 Leu Pro Leu Lys Ala Asp Gly Lys Glu Glu Gly Thr Pro Gln Pro Glu
 210 215 220
 Ser Lys Ser Lys Asp Ser Tyr Ser Ser Gln Gly Ile Ser Gln Pro Pro
 225 230 235 240
 Thr Pro Gly Asn Leu Pro Val Pro Ser Pro Met Ser Pro Ser Ser Ala
 245 250 255
 Ser Ile Ser Ser Phe His Gly Asp Glu Ser Asp Ser Ile Ser Ser Pro
 260 265 270
 Gly Trp Pro Lys Thr Pro Ser Ser Pro Lys Ser Ser Ser Thr Thr
 275 280 285
 Thr Gly Glu Lys Ile Thr Lys Val Tyr Glu Leu Gly Asn Glu Pro Glu
 290 295 300
 Arg Lys Leu Trp Val Asp Arg Tyr Leu Thr Phe Met Glu Glu Arg Gly
 305 310 315 320
 Ser Pro Val Ser Ser Leu Pro Ala Val Gly Lys Lys Pro Leu Asp Leu

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Phe Arg Leu Tyr Val Cys Val Lys Glu Ile Gly Gly Leu Ala Gln Val
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Asn Lys Asn Lys Lys Trp Arg Glu Leu Ala Thr Asn Leu Asn Val Gly
          355          360          365
Thr Ser Ser Ser Ala Ala Ser Ser Leu Lys Lys Gln Tyr Ile Gln Tyr
          370          375          380
Leu Phe Ala Phe Glu Cys Lys Ile Glu Arg Gly Glu Glu Pro Pro Pro
385          390          395          400
Glu Val Phe Ser Thr Gly Asp Thr Lys Lys Gln Pro Lys Leu Gln Pro
          405          410          415
Pro Ser Pro Ala Asn Ser Gly Ser Leu Gln Gly Pro Gln Thr Pro Gln
          420          425          430
Ser Thr Gly Ser Asn Ser Met Ala Glu Val Pro Gly Asp Leu Lys Pro
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Pro Thr Pro Ala Ser Thr Pro His Gly Gln Met Thr Pro Met Gln Gly
          450          455          460
Gly Arg Ser Ser Thr Ile Ser Val His Asp Pro Phe Ser Asp Val Ser
465          470          475          480
Asp Ser Ser Phe Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr
          485          490          495
Gln Gln Gly Met Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu
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Pro Asn Lys Asp Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser
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Glu Pro Phe Met Thr Gln Gly Gln Met Pro Asn Ser Ser Met Gln Asp
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Met Tyr Asn Gln Ser Pro Ser Gly Ala Met Ser Asn Leu Gly Met Gly
545          550          555          560
Gln Arg Gln Gln Phe Pro Tyr Gly Ala Ser Tyr Asp Arg Arg His Glu
          565          570          575
Pro Tyr Gly Gln Gln Tyr Pro Gly Gln Gly Pro Pro Ser Gly Gln Pro
          580          585          590
Pro Tyr Gly Gly His Gln Pro Gly Leu Tyr Pro Gln Gln Pro Asn Tyr
          595          600          605
Lys Arg His Met Asp Gly Met Tyr Gly Pro Pro Ala Lys Arg His Glu
          610          615          620
Gly Asp Met Tyr Asn Met Gln Tyr Ser Ser Gln Gln Gln Glu Met Tyr
625          630          635          640
Asn Gln Tyr Gly Gly Ser Tyr Ser Gly Pro Asp Arg Arg Pro Ile Gln
          645          650          655
Gly Gln Tyr Pro Tyr Pro Tyr Ser Arg Glu Arg Met Gln Gly Pro Gly
          660          665          670
Gln Ile Gln Thr His Gly Ile Pro Leu Gln Met Met Gly Gly Pro Leu
          675          680          685
Gln Ser Ser Ser Ser Glu Gly Pro Gln Gln Asn Met Trp Ala Ala Arg
          690          695          700
Asn Asp Met Pro Tyr Pro Tyr Gln Asn Arg Gln Gly Pro Gly Gly Pro
705          710          715          720
Thr Gln Ala Pro Pro Tyr Pro Gly Met Asn Arg Thr Asp Asp Met Met
          725          730          735
Val Pro Asp Gln Arg Ile Asn His Glu Ser Gln Trp Pro Ser His Val
          740          745          750
Ser Gln Arg Gln Pro Tyr Met Ser Ser Ser Ala Ser Met Gln Pro Ile

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755					760					765					
Thr	Arg	Pro	Pro	Gln	Pro	Ser	Tyr	Gln	Thr	Pro	Pro	Ser	Leu	Pro	Asn
770					775					780					
His	Ile	Ser	Arg	Ala	Pro	Ser	Pro	Ala	Ser	Phe	Gln	Arg	Ser	Leu	Glu
785					790					795					800
Asn	Arg	Met	Ser	Pro	Ser	Lys	Ser	Pro	Phe	Leu	Pro	Ser	Met	Lys	Met
				805					810					815	
Gln	Lys	Val	Met	Pro	Thr	Val	Pro	Thr	Ser	Gln	Val	Thr	Gly	Pro	Pro
				820				825						830	
Pro	Gln	Pro	Pro	Pro	Ile	Arg	Arg	Glu	Ile	Thr	Phe	Pro	Pro	Gly	Ser
				835				840					845		
Val	Glu	Ala	Ser	Gln	Pro	Val	Leu	Lys	Gln	Arg	Arg	Lys	Ile	Thr	Ser
					850		855				860				
Lys	Asp	Ile	Val	Thr	Pro	Glu	Ala	Trp	Arg	Val	Met	Met	Ser	Leu	Lys
865					870					875					880
Ser	Gly	Leu	Leu	Ala	Glu	Ser	Thr	Trp	Ala	Leu	Asp	Thr	Ile	Asn	Ile
				885					890					895	
Leu	Leu	Tyr	Asp	Asp	Ser	Thr	Val	Ala	Thr	Phe	Asn	Leu	Ser	Gln	Leu
				900				905					910		
Ser	Gly	Phe	Leu	Glu	Leu	Leu	Val	Glu	Tyr	Phe	Arg	Lys	Cys	Leu	Ile
				915			920					925			
Asp	Ile	Phe	Gly	Ile	Leu	Met	Glu	Tyr	Glu	Val	Gly	Asp	Pro	Ser	Gln
					930		935				940				
Lys	Ala	Leu	Asp	His	Asn	Ala	Ala	Arg	Lys	Asp	Asp	Ser	Gln	Ser	Leu
945					950					955					960
Ala	Asp	Asp	Ser	Gly	Lys	Glu	Glu	Glu	Asp	Ala	Glu	Cys	Ile	Asp	Asp
				965					970					975	
Asp	Glu	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Ser	Glu	Lys	Thr	Glu
				980			985						990		
Ser	Asp	Glu	Lys	Ser	Ser	Ile	Ala	Leu	Thr	Ala	Pro	Asp	Ala	Ala	Ala
				995			1000					1005			
Asp	Pro	Lys	Glu	Lys	Pro	Lys	Gln	Ala	Ser	Lys	Phe	Asp	Lys	Leu	Pro
					1010		1015				1020				
Ile	Lys	Ile	Val	Lys	Lys	Asn	Asn	Leu	Phe	Val	Val	Asp	Arg	Ser	Asp
1025					1030					1035					1040
Lys	Leu	Gly	Arg	Val	Gln	Glu	Phe	Asn	Ser	Gly	Leu	Leu	His	Trp	Gln
				1045					1050					1055	
Leu	Gly	Gly	Gly	Asp	Thr	Thr	Glu	His	Ile	Gln	Thr	His	Phe	Glu	Ser
				1060			1065						1070		
Lys	Met	Glu	Ile	Pro	Pro	Arg	Arg	Arg	Pro	Pro	Pro	Pro	Pro	Leu	Ser
				1075			1080					1085			
Ala	Gly	Lys	Lys	Lys	Glu	Leu	Ala	Gly	Lys	Gly	Asp				

1185 1190 1195 1200
 Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly Lys Leu Ile Leu
 1205 1210 1215
 Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu
 1220 1225 1230
 Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp
 1235 1240 1245
 Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu
 1250 1255 1260
 Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile
 1265 1270 1275 1280
 Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser
 1285 1290 1295
 Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro
 1300 1305 1310
 Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln
 1315 1320 1325
 Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln
 1330 1335 1340
 Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn
 1345 1350 1355 1360
 Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln
 1365 1370 1375
 Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
 1380 1385 1390
 Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr
 1395 1400 1405
 Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu
 1410 1415 1420
 Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala
 1425 1430 1435 1440
 Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu Leu His Glu Gly
 1445 1450 1455
 Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala
 1460 1465 1470
 Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln Leu
 1475 1480 1485

<210> 1039

<211> 379

<212> DNA

<213> Homo sapiens

<400> 1039

gcaggagcca gggatgctgc tgaacatccc gcagtgcacg agacaggcct ccaccacacg
60

gaattacctt ggcctgaggt gttacgagag cacagagaga aaccaggtac agacgcgggg
120

cagaggggag agaggggagag agtgtgagag ctaagggttc gggagaagac tttgtggaaa
180

aagtcttttg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca
240

gattttgtat gtattgaagg ccctgaatac ttttttgaaa gagaatgaca tgagtacacc
300

tggtcagcca cacgtgagag gggttggagg agggaagtac cagaggcagg gagaccaggt
 360
 agaaagacct cgccatagt
 379

<210> 1040
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1040
 Met Ala Arg Ser Phe Tyr Leu Val Ser Leu Pro Leu Val Leu Pro Ser
 1 5 10 15
 Ser Asn Pro Ser His Val Trp Leu Thr Arg Cys Thr His Val Ile Leu
 20 25 30
 Phe Gln Lys Ser Ile Gln Gly Leu Gln Tyr Ile Gln Asn Leu Glu Trp
 35 40 45
 Ser Ser Pro Val Thr Glu Ser Trp Leu Cys Cys Arg Thr Gln Pro Lys
 50 55 60
 Thr Phe Ser Thr Lys Ser Ser Pro Glu Thr Leu Ala Leu Thr Leu Ser
 65 70 75 80
 Pro Ser Leu Pro Ser Ala Pro Arg Leu Tyr Leu Val Ser Leu Cys Ala
 85 90 95
 Leu Val Thr Pro Gln Ala Lys Val Ile Pro Cys Gly Gly Gly Leu Ser
 100 105 110
 Arg Ala Leu Arg Asp Val Gln Gln His Pro Trp Leu Leu
 115 120 125

<210> 1041
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 1041
 ttagtggccg tggaggccat cggctacatc gcgagtattg acaaggccga tatgtcaatc
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 gaaacggcgt acctgccgcg gctggttggt tccctggccc tgaccatccc ggtgctcgcc
 120
 ttgtcgatga tcccgccct gcacttccc cattggccgt tgtgggcgtt ggcgcttacc
 180
 accccggtgg tggtctgggg tgccctggccg ctgcaccacg ccgcgtggac caacctgcgg
 240
 caggcgcgcg ccatcatgga caccctggtg tcgctcggcg tcctcacttc gtacctctgg
 300
 tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt
 360
 cagcgcgtg atcctggccg gcaaattt
 388

<210> 1042
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1042

Leu Val Ala Val Glu Ala Ile Gly Tyr Ile Ala Ser Ile Asp Lys Ala
 1 5 10 15
 Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu
 20 25 30
 Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His
 35 40 45
 Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val
 50 55 60
 Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg
 65 70 75 80
 His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr
 85 90 95
 Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu
 100 105 110
 Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln
 115 120 125
 Ile

<210> 1043

<211> 555

<212> DNA

<213> Homo sapiens

<400> 1043

accggtgaaa ccctgatcgg ccaatcggtt tccaccgttc ccggcggcaa gggcgcaaac
 60
 caggcggtcg ctctggcgcg tcttggggcc gaagtcgcga tggtcggttg cgtgggtacc
 120
 gatgcctacg gcgcgcaatt acgcgacgca ttgttggttg aaggcatcga ttgccaggcc
 180
 gtcagcaccg tcgacggttc cagcgggttg gcgctgatcg tggtaggatga cagcagccag
 240
 aatgcgatcg ttatcgctgc cggtagcaat ggcgagctga ctccggccaa gttacagacc
 300
 tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggac
 360
 actgtcggcc atgcgcctaa gcgcgggtcg gaactgggca agacgggtgat cctcaatccg
 420
 gcgcccggca gcggcccgtt gctgaggat tggtagccg ccatcgatta cctgattccc
 480
 aacgaaagcg aagcctcggc cttgagtggc gtggtggttg attcactgga cagcgccaag
 540
 gtcgctgcta cgct
 555

<210> 1044

<211> 185

<212> PRT

<213> Homo sapiens

<400> 1044

Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

```

      1             5             10             15
Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val
      20             25             30
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg
      35             40             45
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val
      50             55             60
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln
      65             70             75             80
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala
      85             90             95
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val
      100            105            110
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg
      115            120            125
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser
      130            135            140
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro
      145            150            155            160
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu
      165            170            175
Asp Ser Ala Lys Val Ala Ala Thr Arg
      180            185

```

<210> 1045

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1045

```

ctattgccat actaccgccg cggcaacctta caggacatga tcaacgccaa cctcttcaat
60
cactccaaat tccccgagac gcaccttatg aatctatttc tcggcgctctg caaggccctg
120
cgcgccatgc acgattacca cgcaccgccg gcagagcgca tgccaattgg gcaccgaagg
180
cagaccacca cccaggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaaacgta
240
cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
300
ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaaccagg tacgtgctgc
360
aagctcctcg g
371

```

<210> 1046

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1046

```

Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
  1             5             10             15
Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu

```

```
<210> 1047
<211> 754
<212> DNA
<213> Homo sapiens
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<210> 1048
<211> 251
<212> PRT
<213> Homo sapiens
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996

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      1           5           10           15
Leu Ala Ser Leu Arg Asn Leu Asn Lys Asn Glu Val Thr Gln Val Arg
      20           25           30
Ala Met Gln Arg Pro Pro Pro Gly Val Lys Leu Val Ile Glu Ala Val
      35           40           45
Cys Ile Met Lys Gly Ile Lys Pro Lys Lys Val Pro Gly Glu Lys Pro
      50           55           60
Gly Thr Lys Val Asp Asp Tyr Trp Glu Pro Gly Lys Gly Leu Leu Gln
      65           70           75           80
Asp Pro Gly His Phe Leu Glu Ser Leu Phe Lys Phe Asp Lys Asp Asn
      85           90           95
Ile Gly Asp Val Val Ile Lys Ala Ile Gln Pro Tyr Ile Asp Asn Glu
      100          105          110
Glu Phe Gln Pro Ala Thr Ile Ala Lys Val Ser Lys Gly Cys Pro Phe
      115          120          125
Ile Trp Pro Trp Gly Gly Ala Met Pro Lys Tyr Pro Phe Val Ala Lys
      130          135          140
Ala Val Glu Pro Lys Arg Gln Ala Leu Leu Glu Ala Gln Asp Asp Leu
      145          150          155          160
Gly Val Thr Gln Arg Ile Leu Asp Glu Ala Lys Gln Arg Leu Arg Glu
      165          170          175
Val Glu Asp Gly Ile Ala Thr Met Gln Ala Lys Tyr Arg Glu Cys Ile
      180          185          190
Thr Lys Lys Glu Glu Leu Glu Leu Lys Cys Glu Gln Cys Glu Gln Arg
      195          200          205
Leu Gly His Ala Gly Lys Val Arg Thr Leu Leu Leu Gln Gly Leu Gln
      210          215          220
Ala Gly Pro Ala Gln Thr Gly Ala Arg Lys Asp Gln Gly Ala Gly Gly
      225          230          235          240
Ser Trp Gly Gly Cys Pro Thr Pro Ser Leu Ala
      245          250

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<210> 1049

<211> 558

<212> DNA

<213> Homo sapiens

<400> 1049

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cgagcaata gctgcacttg accagactgg gctttgcaat aagcgcatc cccgggctga
60
atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt
120
gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac
180
tttatggctt acataatcca gagatagatg ggctgggcat gattcccatt ttctgttggg
240
gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac
300
ctcatgtctc ccagactccc gggccccggg gctttttctc gggggcgccc cattcacatt
360
gcaattcatg gccggggcaa atgctcacc acagagatat taagcactcc aacactccat
420
ccaccaggtt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg
480

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cagctaaaga aaggttttgg catgctctgc tttattgttt cacagaagat aagaaaataa
 540
 actgcaaagt aacttaag
 558

<210> 1050
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 1050
 Met Ile Pro Ile Phe Cys Trp Gly Asn Arg Leu Thr Glu Lys Leu Arg
 1 5 10 15
 Asp Lys Tyr Lys Val Met Lys Leu Cys Thr Glu Pro His Val Ser Gln
 20 25 30
 Thr Pro Gly Ser Pro Gly Phe Phe Ser Gly Arg Pro His Ser His Cys
 35 40 45
 Asn Ser Trp Pro Gly Gln Met Leu Thr His Arg Asp Ile Lys His Ser
 50 55 60
 Asn Thr Pro Ser Thr Arg Leu Gln Pro Lys Asp Ser Glu Asp Asn Asp
 65 70 75 80
 His Ser Ile Ser Met His Tyr Ala Ala Lys Glu Arg Phe Trp His Ala
 85 90 95
 Leu Leu Tyr Cys Phe Thr Glu Asp Lys Lys Ile Asn Cys Lys Val Thr
 100 105 110

<210> 1051
 <211> 317
 <212> DNA
 <213> Homo sapiens

<400> 1051
 gcgttgagtc gggatgtcgc attcatgccc ggcgaacctt tttttgccga accggagcgt
 60
 aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaaggt
 120
 ctcaagcgcc tggctgctgt catccgtcac gcacaggctg cacaagcggc ttaaggggag
 180
 ggccatgtac aaggtttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat
 240
 gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc
 300
 gagaccccg aattttt
 317

<210> 1052
 <211> 57
 <212> PRT
 <213> Homo sapiens

<400> 1052
 Ala Leu Ser Arg Asp Val Ala Phe Met Pro Gly Glu Pro Phe Phe Ala
 1 5 10 15
 Glu Pro Glu Arg Asn Pro Gly Asn Leu Arg Leu Asn Phe Ser His Ile

20 25 30
 Ala Pro Glu Arg Leu Asp Glu Gly Leu Lys Arg Leu Ala Val Ile
 35 40 45
 Arg His Ala Gln Ala Ala Gln Ala Ala
 50 55

<210> 1053
 <211> 318
 <212> DNA
 <213> Homo sapiens

<400> 1053
 caattggcta cgcatccga acgggcgcac gggctctctat gactggcaag ccgtcgctcg
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 cggggagtg ggcctcgact atgcctacgc gatgtcgggtg aacctgacca ccgagaaccg
 120
 gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgcctcgccg aagagggtgt
 180
 cgccaaccgc cctcgttcg agcaagcgtg gctacgctac cggcaacagc cgttcacgt
 240
 cgggatcttc tcaactctga ccatcgggcg cggacgcttt caaccggcca tgcaaccggc
 300
 ggactcnnnn cccncnc
 318

<210> 1054
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 1054
 Met Gly Leu Tyr Asp Trp Gln Ala Val Ala Arg Gly Glu Trp Ala Leu
 1 5 10 15
 Asp Tyr Ala Tyr Ala Met Ser Val Asn Leu Thr Thr Glu Asn Arg Arg
 20 25 30
 Ala Trp Glu Arg Asp Leu Leu Glu Arg Tyr Leu Trp Arg Leu Ala Glu
 35 40 45
 Glu Gly Val Ala Asn Pro Pro Ser Phe Glu Gln Ala Trp Leu Arg Tyr
 50 55 60
 Arg Gln Gln Pro Phe His Val Gly Ile Phe Ser Leu Leu Thr Ile Gly
 65 70 75 80
 Ala Gly Arg Phe Gln Pro Ala Met Gln Pro Ala Asp Ser Xaa Pro Xaa
 85 90 95

<210> 1055
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 1055
 tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat
 60
 ctgcagccac tcatttaact ctctgggcta gctccacgtg ggccgtctga actctcttag
 120

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg
 180
 aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac
 240
 tgccaggggt gaagtccaag gatgggaaaa aggcctccgg ggcagagtcc tgaaatgtca
 300
 gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg
 360
 ccaaggctgc agtgcagtgg tgacaccatg g
 391

<210> 1056
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 1056
 Met Val Ser Pro Leu His Cys Ser Leu Gly Asn Arg Met Arg Pro Cys
 1 5 10 15
 Leu Ser Asn Asn Val Met Leu Phe Pro Leu Trp Cys Thr Ser Asp Ile
 20 25 30
 Ser Gly Leu Cys Pro Gly Gly Leu Phe Pro Ile Leu Gly Leu His Pro
 35 40 45
 Trp Gln Phe Ser Leu Pro Ser Gln Val Ser Gly Pro Arg Met Val Phe
 50 55 60
 Ile Arg Pro Gly Pro Leu Arg Ser Ala Glu Arg Gln Met Pro Leu Ala
 65 70 75 80
 Pro Gly Ala

<210> 1057
 <211> 341
 <212> DNA
 <213> Homo sapiens

<400> 1057
 gaattccctg cgcgtgtgac gccggtcgcc gagcaactcg gcgtgtcgct gacgctgcat
 60
 cccgatgata cgccgcgtcc gctgttcggg ttgccgcgca ttgcgtccag cgccgaggac
 120
 tatcaggcgc tggtcgatgc ggtaccgtcc aaggcgaacg gcatctgcct gtgcacgggt
 180
 tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cgccccgcgt
 240
 atcgcccttg cgcattctgc cgcgaccaag cgcgacgccg atggcctgtc gtttcatgaa
 300
 tccgaccatc tcgacggcga tgtcgacatg gtcgcgtgct c
 341

<210> 1058
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 1058

Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser
 1 5 10 15
 Leu Thr Leu His Pro Asp Asp Pro Pro Arg Pro Leu Phe Gly Leu Pro
 20 25 30
 Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val
 35 40 45
 Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val
 50 55 60
 Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg
 65 70 75 80
 Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu
 85 90 95
 Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala
 100 105 110
 Cys

<210> 1059

<211> 372

<212> DNA

<213> Homo sapiens

<400> 1059

nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa
 60
 gtcgagcggtt cgggcctgcg caccacgttc atgaacaagc tggacgtcga tgaggaagtc
 120
 gccgacatcc tgatcgacga aggtttcacc ggtatcgagg aaatcgcccta cgccccatg
 180
 caggaactgc tggagatcga ggcgttcgac gaagacacca tcaacgagtt gcgcgcccg
 240
 gcccgaatg cgctgctgac cgaggccatc gcccgaggaag agcgccctga gaccgcgcag
 300
 gatctgcttg aactcgaagg cgtgacgccg gaactggctg ccaagctggc cgagcgtcaa
 360
 gtgcgtacgc gt
 372

<210> 1060

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1060

Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val
 1 5 10 15
 Asn Arg Arg Glu Val Glu Arg Ser Gly Leu Arg Thr Thr Phe Met Asn
 20 25 30
 Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly
 35 40 45
 Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu
 50 55 60
 Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg

```

65              70              75              80
Ala Arg Asn Ala Leu Leu Thr Glu Ala Ile Ala Gln Glu Glu Arg Leu
              85              90              95
Glu Thr Ala Gln Asp Leu Leu Glu Leu Glu Gly Val Thr Pro Glu Leu
              100              105              110
Ala Ala Lys Leu Ala Glu Arg Gln Val Arg Thr Arg
              115              120

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<210> 1061
 <211> 456
 <212> DNA
 <213> Homo sapiens

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<400> 1061
tctagactcc atggcaccgg gctgagcggg taagtaagaa agataaaaag tgccttttgc
60
cccttcgagg aaaccttttt gcaggccaag caagggtctgc aagtgtttgg gagctgagag
120
gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtgg gcgggggggtt
180
gggacacgaa gggctcttcg gacctctgtg cctcttctgc cccaagggcg agaagacggg
240
cttcgcagcg accctcgggg gtccatggag ccgctgcct tcgccccctc gctcttccca
300
ggtctgaacc tggatgggga gaagaaattg aagtgccttg gagacggggg ggcttaaaac
360
actagggagc ctcatcgccc agccttgggc ccactttcct ttcgatcgtg aggattccgc
420
accccggaagc cgtcttctcg gggctccggg gcgcgc
456

```

<210> 1062
 <211> 125
 <212> PRT
 <213> Homo sapiens

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<400> 1062
Met Arg Leu Pro Ser Val Leu Ser Pro Pro Val Ser Lys Ala Leu Gln
1      5      10      15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
20     25     30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
35     40     45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
50     55     60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65     70     75     80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
85     90     95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
100    105    110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
115    120    125

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<210> 1063
<211> 3760
<212> DNA
<213> Homo sapiens

<400> 1063
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120
taaggtctta taactagtaa atatctgcat taaagaacga gttgaatgaa aattctgata
180
aattcctact taaagtgtat ccaaagaaaa cggaaaaagt ctaggagtta gtgatattag
240
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540
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1140
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1200
accatgtact cattcccttt cagcagccac agggcccaga cccattctc aggagatggc
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1380
cagggccatg tgtcaaatcg ctcagggttg ttggggacat ccctccatgg ttctccatcc
1440

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1560
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2160
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2280
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2760
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 3180
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 3480
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 3540
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 3600
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 3660
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 3760

<210> 1064

<211> 483

<212> PRT

<213> Homo sapiens

<400> 1064

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His	Gly	Ser	Pro	Ser	Cys	Thr	Leu	Arg	Arg	Ser	Ala	Val	Lys	Ser	Arg
			20					25					30		
Leu	Gly	Cys	Ala	Val	Ala	Gly	Ser	Ser	Phe	Thr	Ser	Thr	Trp	Asn	Phe
		35					40					45			
Leu	Lys	Ser	Ser	Leu	Leu	Pro	Gly	Met	Gln	His	Ala	Val	Phe	Ser	Ser
	50					55					60				
Met	Gly	Met	Phe	Ser	Ala	Ser	Ser	Leu	Val	Thr	Ala	Leu	Leu	Leu	Leu
65					70					75					80
Arg	Thr	Pro	Leu	Thr	Pro	Ser	Ser	Arg	Pro	Arg	Ala	Gly	Arg	Trp	His
				85					90					95	
Leu	Ser	Cys	Ser	Ser	Ser	Ala	Ser	Ser	Phe	Arg	Ala	Leu	Leu	Cys	Trp
			100					105					110		
Thr	Ser	Arg	Leu	Leu	Leu	Ser	Arg	Ser	Leu	Cys	Ser	Val	Ala	Arg	Ser
		115					120					125			
Ser	Ala	Ser	Ser	Arg	Leu	Ser	Tyr	Gln	Val	Lys	Leu	Gln	Met	Ala	Leu
	130					135					140				
Glu	Leu	Met	Arg	Lys	Glu	Leu	Glu	Asp	Ala	Leu	Thr	Gln	Glu	Ala	Asn
145				150						155					160
Val	Gly	Lys	Lys	Thr	Val	Ile	Trp	Lys	Glu	Lys	Val	Glu	Met	Gln	Arg
				165					170					175	
Gln	Arg	Phe	Arg	Leu	Glu	Phe	Glu	Lys	His	Arg	Gly	Phe	Leu	Ala	Gln

[illegible]

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<210> 1065
<211> 892
<212> DNA
<213> Homo sapiens
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<400> 1065
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120
ttgtccagtc tgggaagggg gaagaagaga tgaggggaag gctgtccagg ggggtgcaag
180
gccctagaga ccagcagag aagggaactt ggccactgaa ggggccctcc cattgtggct
240
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ctggttcctt agagcagctc cagcttcttg gcctcccccg tctgatgctt agctcatccc
 300
 atccccctgga gtgctgtgga gcttagatga aacagcccag tgctcactct tcaatgagcc
 360
 caccagagc agcatcaaga tgcagttggc ggggtactgg aactggcttg gcaagggctg
 420
 cgcaggcaac aggtcccagc aagagtcagc tagcctagct cagccctgca cacctggaga
 480
 cctgggggtg ctccagacac ctccggccctt taggtccctt taattgaatg tgtgtggatc
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 agtgaagggt gaggaatcat ttctctatgg cccaagacgt ttctctctgc agttgtcatg
 600
 ttagtacctg ccagcttttc ctctcttaca taaatttcat gccagagcct ggaaatgtgt
 660
 gccctttgta ggaggggcat cacaggctgg ctacacctag cagtgccagg cagagcccgt
 720
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 780
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<210> 1066

<211> 76

<212> PRT

<213> Homo sapiens

<400> 1066

Met	Cys	Ala	Leu	Cys	Arg	Arg	Gly	Ile	Thr	Gly	Trp	Leu	Thr	Ser	Ala
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Val	Pro	Gly	Arg	Ala	Arg	Pro	Ser	His	Cys	Arg	Arg	Arg	Met	Lys	Arg
			20					25				30			
Val	Trp	Asp	Arg	Ala	Val	Glu	Phe	Leu	Ala	Ser	Asn	Glu	Ser	Arg	Ile
		35					40				45				
Gln	Thr	Glu	Ser	His	Arg	Val	Ala	Gly	Glu	Asp	Met	Leu	Val	Leu	Arg
	50					55				60					
Trp	Thr	Lys	Pro	Ser	Ser	Phe	Ser	Asp	Ser	Glu	Arg				
65					70					75					

<210> 1067

<211> 418

<212> DNA

<213> Homo sapiens

<400> 1067

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 120
 ggactagaca tctggaaagc ccgagtctcc gctgacatcg aaggcgactg gactatgcac
 180
 gttgaaggct ggtcagacac ctggggcacg tggcatcaca atgccaatgc caagctcgcc
 240

gctgccatcg acgtcgaact ggtgtgccc gaaggccatg ccctcataaa cgaggcggtc
 300
 cggcacgccg agcaatccgg ggatactgac gcgatcacgg ctctgcgcga gaccgatgcc
 360
 aacctaaccc ttgaccgtgc ccccgactcg ctacaacagg tcatcaacac ctacgcgt
 418

<210> 1068
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1068
 Glu Phe Glu Val Thr Ala Asn Val Phe Arg Glu Gly His Asp Ala Val
 1 5 10 15
 Gly Ala Ser Val Val Leu Thr Asp Pro Glu Gly Asn Arg His Leu Thr
 20 25 30
 Asp Met His Gln Val Glu Pro Trp Gly Leu Asp Ile Trp Lys Ala Arg
 35 40 45
 Val Ser Ala Asp Ile Glu Gly Asp Trp Thr Met His Val Glu Gly Trp
 50 55 60
 Ser Asp Thr Trp Gly Thr Trp His His Asn Ala Asn Ala Lys Leu Ala
 65 70 75 80
 Ala Ala Ile Asp Val Glu Leu Val Cys Ala Glu Gly His Ala Leu Ile
 85 90 95
 Asn Glu Ala Val Arg His Ala Glu Gln Ser Gly Asp Thr Asp Ala Ile
 100 105 110
 Thr Ala Leu Arg Glu Thr Asp Ala Asn Leu Thr Leu Asp Arg Ala Pro
 115 120 125
 Asp Ser Leu Gln Gln Val Ile Asn Thr Tyr Ala
 130 135

<210> 1069
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 1069
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 120
 ttttctggag ctgaacatct caggtgccat gtaaggcttg gtgccagcca tgggtggagac
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 240
 tgtgagctgg tcatggcctt ggactacctg cagaaccagc gcatcattca cagggatatg
 300
 aagcctgaca atattttact tgacgaacat gggcacgtgc acatcacaga tttcaacatt
 360
 gctgcgatgc t
 371

<210> 1070

<211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1070

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Xaa Tyr Asn Phe Leu Ala Gly Ser Thr Gly Ala Asn Met Ile Arg Ser
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Pro Ala Ser Gln Gln Phe Ile Cys Arg His Ser Gln Gly Pro Pro Val
      20           25           30
Asn Ser Lys Gly Ile Ala Cys Ser Phe Ser Gly Ala Glu His Leu Arg
      35           40           45
Cys His Val Arg Leu Gly Ala Ser His Gly Gly Asp Leu Arg Tyr His
      50           55           60
Leu Gln Gln Asn Val His Phe Lys Glu Glu Thr Val Lys Leu Phe Ile
      65           70           75           80
Cys Glu Leu Val Met Ala Leu Asp Tyr Leu Gln Asn Gln Arg Ile Ile
      85           90           95
His Arg Asp Met Lys Pro Asp Asn Ile Leu Leu Asp Glu His Gly His
      100          105          110
Val His Ile Thr Asp Phe Asn Ile Ala Ala Met
      115          120

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<210> 1071
 <211> 998
 <212> DNA
 <213> Homo sapiens

<400> 1071

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120
cccacccgaa gtacgtggcc ttggagtgcc attcgcactc cacttggcca cggtttgcgt
180
tcgacctaac cagcaattgc atctcgtttg acctgctcgc gttgtcaaca tcatagcaac
240
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300
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360
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600
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660
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720
cgagattagc cacatacatg accatgtggt ccttgggtca gcacgcgaag aaaatgccaa
780

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gcgtaccctt tgggttgtgg cgcttacggt ggtgatgatg gttggcgaaa tcgtcgccgg
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900
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960
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998

<210> 1072
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1072
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Arg Ile Ala Gly Gln Ile Gln Ala Val Glu Arg Ala Leu Glu Ser Asp
20 25 30
Ala Asp Cys Ala Lys Thr Leu His Leu Val Ala Ala Thr Arg Gly Ala
35 40 45
Ile Asn Gly Leu Met Asp Glu Ile Ile Glu Asp His Ala Arg Lys His
50 55 60
Val Ala Ser Pro Thr Leu Ser Asp
65 70

<210> 1073
<211> 468
<212> DNA
<213> Homo sapiens

<400> 1073
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120
ttccccact gataaaatct tgcttctctt caaactccta ggcaaatttc tcttacttca
180
gaaagtcttg tttctccata tccttcgtaa ccaccacctg gtgcacatgc tgaaggcaga
240
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468

<210> 1074
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1074

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Met Asp Asn Phe Leu Phe Phe Lys Tyr Thr Leu Pro Met Ser Gln Leu
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Gly Cys Phe Ser Pro Thr Asp Lys Ile Leu Leu Leu Phe Lys Leu Leu
           20           25           30
Gly Lys Phe Leu Leu Leu Gln Lys Val Leu Phe Leu His Ile Leu Arg
           35           40           45
Asn His His Leu Val His Met Leu Lys Ala Glu Phe Ile Val Ser Ser
 50           55           60
Pro Ser Leu Ser Asn Ser Phe Ala Gln Thr Leu Arg Tyr Ser Phe Ile
65           70           75           80
Leu Cys Ile Ile Phe Gly Phe His Leu Phe Met Asn Ser Phe Val Phe
           85           90           95
Ser Leu Leu Ala Leu Glu Pro Arg Thr Tyr His Gly Phe Lys Val Cys
           100          105          110
Phe Asn Glu Leu Asn Gly Ile Asn Phe Val Val Leu Met Gln Ile Gln
           115          120          125
Met Pro Leu Asn Thr Asp
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<210> 1075

<211> 1633

<212> DNA

<213> Homo sapiens

<400> 1075

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180
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300
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360
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420
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720
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780
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840

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 960
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 1633

<210> 1076

<211> 87

<212> PRT

<213> Homo sapiens

<400> 1076

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Cys	Ser	Pro	Thr	Glu	Glu	Gln	Gly	Gln	Pro	Thr	Leu	Gln	Thr	Ser	Pro
			20					25					30		
Pro	Gly	Ala	Pro	Pro	Ala	Val	Trp	Pro	Thr	Ser	Ala	Pro	Pro	Ile	Ala
		35					40					45			
Thr	Ser	Thr	Ser	Trp	Lys	Cys	Pro	Thr	Pro	Arg	Pro	Pro	Pro	Gln	Trp
	50					55					60				
Ala	Gly	Pro	Ser	Ala	Ser	Ala	Leu	Asp	Ala	Asn	Pro	Pro	Ser	Ser	Ala
65					70					75					80
Leu	Thr	Arg	Ser	Lys	Ala	Thr									
						85									

<210> 1077

<211> 419

<212> DNA

<213> Homo sapiens

<400> 1077

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<210> 1078
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1078
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 20 25 30
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 35 40 45
 Phe Gly Glu Ala Glu Ala Ile Tyr Gly Tyr Asn Gly Leu His Met Asn
 50 55 60
 Leu Ala Phe Ala Ser Gly Ser Leu Val Pro Ser Leu Glu Ile Thr Tyr
 65 70 75 80
 Arg Ala Lys Asn Thr Thr Thr Ser Ala Lys Val Asp Asp Val Glu Gln
 85 90 95
 Ala Leu Arg Gly Val Leu Pro Pro Asp Val Val Thr Pro Ala Glu Leu
 100 105 110
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 115 120 125
 Arg Arg Ala Pro Arg Leu Arg Arg Thr Leu Ala
 130 135

<210> 1079
 <211> 584
 <212> DNA
 <213> Homo sapiens

<400> 1079
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<210> 1080
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1080
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 35 40 45
 Val Leu Phe Arg Ser Cys Asp Thr Thr Val Gly Lys Val Met Pro Ser
 50 55 60
 Val Thr Lys Ser Ile Tyr Pro Lys Phe Pro Gln Ala Leu Pro Phe Val
 65 70 75 80
 Cys Lys Asp Thr His Leu Phe His Cys Val Phe Cys Lys Asp Thr His
 85 90 95
 Leu Phe His Trp Gly Phe Leu Gln Arg His Pro Phe Val Ser Pro Phe
 100 105 110
 Lys Gly Phe Pro Leu His Leu Val Tyr Phe
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<210> 1081
 <211> 3077
 <212> DNA
 <213> Homo sapiens

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 240
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 300
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 360

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<210> 1082

<211> 757

<212> PRT

<213> Homo sapiens

<400> 1082

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		20					25						30		
Lys	Asn	Ile	Pro	Leu	Ala	Leu	Asn	Tyr	Ile	His	Asn	Gly	Lys	Lys	Ser
		35				40						45			
Arg	Ala	Leu	Ser	Pro	Leu	Ser	Pro	Val	Ala	Ile	Glu	Gln	Thr	Ser	Leu
		50				55					60				
Lys	Met	Met	Gln	Ala	Val	Gly	Gly	Ala	Pro	Ala	Arg	Pro	Thr	Gly	Glu
65				70					75					80	
Tyr	Ile	Cys	Asn	Gln	Cys	Gly	Ala	Lys	Tyr	Thr	Ser	Leu	Asp	Ser	Phe

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Gln	Thr	His	Leu	Lys	Thr	His	Leu	Asp	Thr	Val	Leu	Pro	Lys	Leu	Thr										
										100					105					110					
Cys	Pro	Gln	Cys	Asn	Lys	Glu	Phe	Pro	Asn	Gln	Glu	Ser	Leu	Leu	Lys										
										115					120					125					
His	Val	Thr	Ile	His	Phe	Met	Ile	Thr	Ser	Thr	Tyr	Tyr	Ile	Cys	Glu										
										130					135					140					
Ser	Cys	Asp	Lys	Gln	Phe	Thr	Ser	Val	Asp	Asp	Leu	Gln	Lys	His	Leu										
										145					150					155					
Leu	Asp	Met	His	Thr	Phe	Val	Phe	Phe	Arg	Cys	Thr	Leu	Cys	Gln	Glu										
										165					170					175					
Val	Phe	Asp	Ser	Lys	Val	Ser	Ile	Gln	Leu	His	Leu	Ala	Val	Lys	His										
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Ser	Asn	Glu	Lys	Lys	Val	Tyr	Arg	Cys	Thr	Ser	Cys	Asn	Trp	Asp	Phe										
										195					200					205					
Arg	Asn	Glu	Thr	Asp	Leu	Gln	Leu	His	Val	Lys	His	Asn	His	Leu	Glu										
										210					215					220					
Asn	Gln	Gly	Lys	Val	His	Lys	Cys	Ile	Phe	Cys	Gly	Glu	Ser	Phe	Gly										
										225					230					235					
Thr	Glu	Val	Glu	Leu	Gln	Cys	His	Ile	Thr	Thr	His	Ser	Lys	Lys	Tyr										
										245					250					255					
Asn	Cys	Lys	Phe	Cys	Ser	Lys	Ala	Phe	His	Ala	Ile	Ile	Leu	Leu	Glu										
										260					265					270					
Lys	His	Leu	Arg	Glu	Lys	His	Cys	Val	Phe	Glu	Thr	Lys	Thr	Pro	Asn										
										275					280					285					
Cys	Gly	Thr	Asn	Gly	Ala	Ser	Glu	Gln	Val	Gln	Lys	Glu	Glu	Val	Glu										
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Leu	Gln	Thr	Leu	Leu	Thr	Asn	Ser	Gln	Glu	Ser	His	Asn	Ser	His	Asp										
										305					310					315					
Gly	Ser	Glu	Glu	Asp	Val	Asp	Thr	Ser	Glu	Pro	Met	Tyr	Gly	Cys	Asp										
										325					330					335					
Ile	Cys	Gly	Ala	Ala	Tyr	Thr	Met	Glu	Thr	Leu	Leu	Gln	Asn	His	Gln										
										340					345					350					
Leu	Arg	Asp	His	Asn	Ile	Arg	Pro	Gly	Glu	Ser	Ala	Ile	Val	Lys	Lys										
										355					360					365					
Lys	Ala	Glu	Leu	Ile	Lys	Gly	Asn	Tyr	Lys	Cys	Ser	Val	Cys	Ser	Arg										
										370					375					380					
Thr	Phe	Phe	Ser	Glu	Asn	Gly	Leu	Arg	Glu	His	Met	Gln	Thr	His	Leu										
										385					390					395					
Gly	Pro	Val	Lys	His	Tyr	Met	Cys	Pro	Ile	Cys	Gly	Glu	Arg	Phe	Pro										
										405					410					415					
Ser	Leu	Leu	Thr	Leu	Thr	Glu	His	Lys	Val	Thr	His	Ser	Lys	Ser	Leu										
										420					425					430					
Asp	Thr	Gly	Asn	Cys	Arg	Ile	Cys	Lys	Met	Pro	Leu	Gln	Ser	Glu	Glu										
										435					440					445					
Glu	Phe	Leu	Glu	His	Cys	Gln	Met	His	Pro	Asp	Leu	Arg	Asn	Ser	Leu										
										450					455					460					
Thr	Gly	Phe	Arg	Cys	Val	Val	Cys	Met	Gln	Thr	Val	Thr	Ser	Thr	Leu										
										465					470					475					
Glu	Leu	Lys	Ile	His	Gly	Thr	Phe	His	Met	Gln	Lys	Thr	Gly	Asn	Gly										
										485					490					495					
Ser	Ala	Val	Gln	Thr	Thr	Gly	Arg	Gly	Gln	His	Val	Gln	Lys	Leu	Tyr										
										500					505					510					
Lys	Cys	Ala	Ser	Cys	Leu	Lys	Glu	Phe	Arg	Ser	Lys	Gln	Asp	Leu	Val										

515 520 525
 Lys Leu Asp Ile Asn Gly Leu Pro Tyr Gly Leu Cys Ala Gly Cys Val
 530 535 540
 Asn Leu Ser Lys Ser Ala Ser Pro Gly Ile Asn Val Pro Pro Gly Thr
 545 550 555 560
 Asn Arg Pro Gly Leu Gly Gln Asn Glu Asn Leu Ser Ala Ile Gly Glu
 565 570 575
 Arg Gln Gly Gly Thr Glu Thr Arg Cys Ser Ser Cys Asn Val Lys
 580 585 590
 Phe Glu Ser Glu Ser Glu Leu Gln Asn His Ile Gln Thr Ile His Arg
 595 600 605
 Glu Leu Val Pro Asp Ser Asn Ser Thr Gln Leu Lys Thr Pro Gln Val
 610 615 620
 Ser Pro Met Pro Arg Ile Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr
 625 630 635 640
 Tyr Gln Cys Ile Lys Cys Gln Met Val Phe Tyr Asn Glu Trp Asp Ile
 645 650 655
 Gln Val His Val Ala Asn His Met Ile Asp Glu Gly Leu Asn His Glu
 660 665 670
 Cys Lys Leu Cys Ser Gln Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys
 675 680 685
 His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr Phe Lys Cys
 690 695 700
 Pro Val Cys Phe Thr Val Phe Val Gln Ala Asn Lys Leu Gln Gln His
 705 710 715 720
 Ile Phe Ser Ala His Gly Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln
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<210> 1083
 <211> 516
 <212> DNA
 <213> Homo sapiens

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<210> 1084
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1084
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35 40 45
Asp Asp Val Val Ser Leu Val Lys Asp Ala Asn Leu Arg Gly Arg Gly
50 55 60
Gly Ala Gly Phe Pro Thr Gly Met Lys Trp Ser Phe Val Pro Lys Asp
65 70 75 80
Asn Pro Asn Pro Thr Tyr Leu Val Val Asn Gly Asp Glu Ser Glu Pro
85 90 95
Gly Thr Cys Lys Asp Met Pro Leu Met Met Ala Ser Pro His Thr Leu
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Val Glu Gly Val Ile Ile Ala Ser Tyr Ala Ile Lys Ala Lys Met Ala
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Phe Ile Tyr Ile Arg Gly Glu Val Leu His Val Val Arg Arg
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<210> 1085
<211> 374
<212> DNA
<213> Homo sapiens

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374

<210> 1086
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1086

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Met Ser Lys Pro Val Ile Leu Glu Ala Met Lys Gly Thr Leu Pro Glu
             20             25             30
Phe Phe Tyr Arg Asp Ile Tyr Lys Ser Asp Tyr Ser Phe Asp Leu His
             35             40             45
Gln Asp Tyr Glu Arg Ser Lys Glu Asn Phe Leu Lys Met Ile Gly Asp
             50             55             60
Ser Leu Leu Ala Glu Leu Asn Leu Val Asp Ile Asp Thr Val Arg Lys
65             70             75             80
Ile Ala Asn Ser Pro Leu Gly Ser Ser Glu Thr Leu Tyr Asp Phe Glu
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Arg Met Thr His Met Glu Val Trp Leu Arg Glu Asn Tyr Val
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<210> 1087

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1087

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423

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<210> 1088

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1088

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             20             25             30
Asp His Gly Val Ser Ile Arg Val Xaa His His Cys Ala Trp Pro Ile
             35             40             45
His Arg Ser Leu Gly Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Phe
50             55             60
Tyr Asn Thr Phe Pro Glu Val Asp Ala Leu Ala Ser Ala Val Arg Ala

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Arg Val Val Arg Met Gly Leu Gly Glu Glu Ala Leu Pro Leu Phe Phe
          35          40          45
Phe Asn Leu Ala Lys Gly Leu Leu Gly Gln Gly His Pro Ser Leu Leu
          50          55          60
Leu Gly Ala Ser Ile Phe Leu His Ser Val Lys Asn Gly Gly Val Ile
65          70          75          80
Gln Lys Tyr Pro Pro Tyr Cys Gln Gly Phe Gly Glu Gly Ser Lys Lys

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<210> 1098
 <211> 1336
 <212> PRT
 <213> Homo sapiens

<400> 1098
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 1 5 10 15
 Lys His Gly Leu Glu Lys Pro Ile Ser Phe Val Lys Asn Thr Gln Ser
 20 25 30
 Ser Ser Glu Glu Ala Arg Lys Leu Met Val Arg Leu Thr Arg His Thr
 35 40 45
 Gly Arg Lys Gln Pro Pro Val Ser Glu Ser His Trp Arg Thr Leu Leu
 50 55 60
 Gln Asp Met Leu Thr Met Gln Gln Asn Val Tyr Thr Cys Leu Asp Ser
 65 70 75 80
 Asp Ala Cys Tyr Glu Ile Phe Thr Glu Ser Leu Leu Cys Ser Ser Arg
 85 90 95
 Leu Glu Asn Ile His Leu Ala Gly Gln Met Met His Cys Ser Ala Cys
 100 105 110
 Ser Glu Asn Pro Pro Ala Gly Ile Ala His Lys Gly Lys Pro His Tyr
 115 120 125
 Arg Val Ser Tyr Glu Lys Ser Ile Asp Leu Val Leu Ala Ala Ser Arg
 130 135 140
 Glu Tyr Phe Asn Ser Ser Thr Asn Leu Thr Asp Ser Cys Met Asp Leu
 145 150 155 160
 Ala Arg Cys Cys Leu Gln Leu Ile Thr Asp Arg Pro Pro Ala Ile Gln
 165 170 175
 Glu Glu Leu Asp Leu Ile Gln Ala Val Gly Cys Leu Glu Glu Phe Gly
 180 185 190
 Val Lys Ile Leu Pro Leu Gln Val Arg Leu Cys Pro Asp Arg Ile Ser
 195 200 205
 Leu Ile Lys Glu Cys Ile Ser Gln Ser Pro Thr Cys Tyr Lys Gln Ser
 210 215 220
 Thr Lys Leu Leu Gly Leu Ala Glu Leu Leu Arg Val Ala Gly Glu Asn
 225 230 235 240
 Pro Glu Glu Arg Arg Gly Gln Val Leu Ile Leu Leu Val Glu Gln Ala
 245 250 255
 Leu Arg Phe His Asp Tyr Lys Ala Ala Ser Met His Cys Gln Glu Leu
 260 265 270
 Met Ala Thr Gly Tyr Pro Lys Ser Trp Asp Val Cys Ser Gln Leu Gly

1029

705 710 715 720
 His Glu Arg Leu Gln Tyr Tyr Phe Thr Leu Leu Glu Asn Cys Gly Cys
 725 730 735
 Ala Asp Leu Gly Asn Cys Ala Ile Lys Pro Glu Thr His Ile Arg Leu
 740 745 750
 Leu Lys Lys Phe Lys Val Val Ala Ser Gly Leu Asn Tyr Lys Lys Leu
 755 760 765
 Thr Asp Glu Asn Met Ser Pro Leu Glu Ala Leu Glu Pro Val Leu Ser
 770 775 780
 Ser Gln Asn Ile Leu Ser Ile Ser Lys Leu Val Pro Lys Ile Pro Glu
 785 790 795 800
 Lys Asp Gly Gln Met Leu Ser Pro Ser Ser Leu Tyr Thr Ile Trp Leu
 805 810 815
 Gln Lys Leu Phe Trp Thr Gly Asp Pro His Leu Ile Lys Gln Val Pro
 820 825 830
 Gly Ser Ser Pro Glu Trp Leu His Ala Tyr Asp Val Cys Met Lys Tyr
 835 840 845
 Phe Asp Arg Leu His Pro Gly Asp Leu Ile Thr Val Val Asp Ala Val
 850 855 860
 Thr Phe Ser Pro Lys Ala Val Thr Lys Leu Ser Val Glu Ala Arg Lys
 865 870 875 880
 Glu Met Thr Arg Lys Ala Ile Lys Thr Val Lys His Phe Ile Glu Lys
 885 890 895
 Pro Arg Lys Arg Asn Ser Glu Asp Glu Ala Gln Glu Ala Lys Asp Ser
 900 905 910
 Lys Val Thr Tyr Ala Asp Thr Leu Asn His Leu Glu Lys Ser Leu Ala
 915 920 925
 His Leu Glu Thr Leu Ser His Ser Phe Ile Leu Ser Leu Lys Asn Ser
 930 935 940
 Glu Gln Glu Thr Leu Gln Lys Tyr Ser His Leu Tyr Asp Leu Ser Arg
 945 950 955 960
 Ser Glu Lys Glu Lys Leu His Asp Glu Ala Val Ala Ile Cys Leu Asp
 965 970 975
 Gly Gln Pro Leu Ala Met Ile Gln Gln Leu Leu Glu Val Ala Val Gly
 980 985 990
 Pro Leu Asp Ile Ser Pro Lys Asp Ile Val Gln Ser Ala Ile Met Lys
 995 1000 1005
 Ile Ile Ser Ala Leu Ser Gly Gly Ser Ala Asp Leu Gly Gly Pro Arg
 1010 1015 1020
 Asp Pro Leu Lys Val Leu Glu Gly Val Val Ala Ala Val His Thr Ser
 1025 1030 1035 1040
 Val Asp Lys Gly Glu Glu Leu Val Ser Pro Glu Asp Leu Leu Glu Trp
 1045 1050 1055
 Leu Arg Pro Phe Cys Ala Asp Asp Ala Trp Pro Val Arg Pro Arg Ile
 1060 1065 1070
 His Val Leu Gln Ile Leu Gly Gln Ser Phe His Leu Thr Glu Glu Asp
 1075 1080 1085
 Ser Lys Leu Leu Val Phe Phe Arg Thr Glu Ala Ile Leu Lys Ala Ser
 1090 1095 1100
 Trp Pro Gln Arg Gln Val Asp Ile Ala Asp Ile Glu Asn Glu Glu Asn
 1105 1110 1115 1120
 Arg Tyr Cys Leu Phe Met Glu Leu Leu Glu Ser Ser His His Glu Ala
 1125 1130 1135
 Glu Phe Gln His Leu Val Leu Leu Leu Gln Ala Trp Pro Pro Met Lys

```

          1140          1145          1150
Ser Glu Tyr Val Ile Thr Asn Asn Pro Trp Val Arg Leu Ala Thr Val
          1155          1160          1165
Met Leu Thr Arg Cys Thr Met Glu Asn Lys Glu Gly Leu Gly Asn Glu
          1170          1175          1180
Val Leu Lys Met Cys Arg Ser Leu Tyr Asn Thr Lys Gln Met Leu Pro
1185          1190          1195          1200
Ala Glu Gly Val Lys Glu Leu Cys Leu Leu Leu Leu Asn Gln Ser Leu
          1205          1210          1215
Leu Leu Pro Ser Leu Lys Leu Leu Leu Glu Ser Arg Asp Glu His Leu
          1220          1225          1230
His Glu Met Ala Leu Glu Gln Ile Thr Ala Val Thr Thr Val Asn Asp
          1235          1240          1245
Ser Asn Cys Asp Gln Glu Leu Leu Ser Leu Leu Leu Asp Ala Lys Leu
          1250          1255          1260
Leu Val Lys Cys Val Ser Thr Pro Phe Tyr Pro Arg Ile Val Asp His
1265          1270          1275          1280
Leu Leu Ala Ser Leu Gln Gln Gly Arg Trp Asp Ala Glu Glu Leu Gly
          1285          1290          1295
Arg His Leu Arg Glu Ala Gly His Glu Ala Glu Ala Gly Ser Leu Leu
          1300          1305          1310
Leu Ala Val Arg Gly Thr His Gln Ala Phe Arg Thr Phe Ser Thr Ala
          1315          1320          1325
Leu Arg Ala Ala Gln His Trp Val
          1330          1335

```

<210> 1099

<211> 309

<212> DNA

<213> Homo sapiens

<400> 1099

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acgcgtgctc tctcccgctt ggcaatcagc atggcctttt cgagctcggc ggtgcgcaat
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tgaaccattt cttccagttg cgatttttca gaaagcagcg tcgattgacc ttcggtcagc
120
ttgcgcacat agcgcttggt gcggtctggca aggatatagg cgagtatcaa tgcacctgcy
180
agggcgagga tgcaggcaat ggtcagccag aagcgcaact tgtccatggc tatgttgcyg
240
gcgattagcc gacgatcttc ttcacccagg aaactgttga tggttttcct gacgtcatcc
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atctggcca
309

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<210> 1100

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1100

```

Met Asp Asp Val Arg Lys Thr Ile Asn Ser Phe Leu Gly Glu Glu Asp
1      5      10      15
Arg Arg Leu Ile Ala Arg Asn Ile Ala Met Asp Lys Leu Arg Phe Trp

```

```

      20      25      30
Leu Thr Ile Ala Ser Ile Leu Ala Leu Ala Gly Ala Leu Ile Leu Ala
      35      40      45
Tyr Ile Leu Ala Ser Arg Thr Lys Arg Tyr Val Arg Lys Leu Thr Glu
      50      55      60
Gly Gln Ser Thr Leu Leu Ser Glu Lys Ser Gln Leu Glu Glu Met Val
      65      70      75      80
Gln Leu Arg Thr Ala Glu Leu Glu Lys Ala Met Leu Ile Ala Lys Arg
      85      90      95
Glu Arg Ala Arg
      100

```

<210> 1101
 <211> 540
 <212> DNA
 <213> Homo sapiens

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<400> 1101
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gacaacgtca gcgggacgat tgtggtccgt aagggccacg agggtagaca tctattgacc
120
ctcgcagaca ccgatcgac cctcgatcct gacgatctag tcatcgccga cgactcggga
180
gccattggcc tggctggcgt catgggtggt gcggccaccg aagtgactgc tgagacgacg
240
tcaatcatcc tcgagggcgc tcaattcgac ccgatgacgg gcgctcgtgc ttaccgacgc
300
cacaagctcg gttcggaggc ctcccgcgc tttgagcggg gcgttgatcc gatttgcgcc
360
cataccgcag ccgttcgcgc agcggaattg ctgcgccagt acggcgggtgc caccgtcggt
420
gagccaccg tcgttggtga ggtccccgag atgccacgtc aaacgatcaa cgctgattta
480
cctaaccgga ttctcggcac gaaggtgcc actgaagagg tcatcgagat cttgacgcgt
540

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<210> 1102
 <211> 180
 <212> PRT
 <213> Homo sapiens

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<400> 1102
Val Asp Val Thr Asn Tyr Val Met Leu Glu Ser Gly Gln Pro Leu His
1      5      10      15
Ala Tyr Asp Ala Asp Asn Val Ser Gly Thr Ile Val Val Arg Lys Ala
      20      25      30
His Glu Gly Glu His Leu Leu Thr Leu Asp Asp Thr Asp Arg Thr Leu
      35      40      45
Asp Pro Asp Asp Leu Val Ile Ala Asp Asp Ser Gly Ala Ile Gly Leu
      50      55      60
Ala Gly Val Met Gly Gly Ala Ala Thr Glu Val Thr Ala Glu Thr Thr
      65      70      75      80
Ser Ile Ile Leu Glu Gly Ala His Phe Asp Pro Met Thr Gly Ala Arg

```

				85					90					95					
Ala	Tyr	Arg	Arg	His	Lys	Leu	Gly	Ser	Glu	Ala	Ser	Arg	Arg	Phe	Glu				
			100					105					110						
Arg	Gly	Val	Asp	Pro	Ile	Cys	Ala	His	Thr	Ala	Ala	Val	Arg	Ala	Ala				
		115					120					125							
Glu	Leu	Leu	Ala	Gln	Tyr	Gly	Gly	Ala	Thr	Val	Gly	Glu	Pro	Thr	Val				
	130					135					140								
Val	Gly	Glu	Val	Pro	Glu	Met	Pro	Arg	Gln	Thr	Ile	Asn	Ala	Asp	Leu				
145				150					155				160						
Pro	Asn	Arg	Ile	Leu	Gly	Thr	Lys	Val	Pro	Thr	Glu	Glu	Val	Ile	Glu				
			165					170					175						
Ile	Leu	Thr	Arg																
			180																

<210> 1103

<211> 537

<212> DNA

<213> Homo sapiens

<400> 1103

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cctttctctcc aaccaggcgc tgcggcgccg gcacttgccc gacgttataa aacaattcaa
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cgtcagggttt accatcgctg tactcaacca aatggtagcc gtatccacct tccccaccga
120
tcgcgaccca ggtgatcttt ccctcgcat agattgacgt ggcattctcg tcggagtga
180
tcaagcagcg cttaggcagc tgctgggccc gcggttcgc ctagctcgcc ggagcacacg
240
aacccttccc gaagataacc gcccaaggcct ggcacacctt ctgctgcacc cattccggct
300
tgacgccgac cgccaccgca ctggtgaaca tagccgcaat aaggagaatt gcgatgtatt
360
ccggcgccgc ggcaccccga tcgtcccttg tccgcatggg tctcccctcc actacctacc
420
caatacaggg gagagcataa aaagaaaccc atagccgcac ctgagcccat ggccccaaac
480
cgggggcccaa gccgggccc aaccatggga tcaaccgat gtccgtacat caccgct
537

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<210> 1104

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1104

Met	Tyr	Gly	His	Pro	Val	Asp	Pro	Met	Val	Trp	Ala	Arg	Leu	Gly	Pro				
1				5				10					15						
Arg	Phe	Gly	Ala	Met	Gly	Ser	Gly	Ala	Ala	Met	Gly	Phe	Phe	Leu	Cys				
		20					25				30								
Ser	Pro	Leu	Tyr	Trp	Val	Gly	Ser	Gly	Gly	Glu	Thr	His	Ala	Asp	Lys				
	35					40					45								
Gly	Arg	Ser	Gly	Cys	Arg	Arg	Ala	Gly	Ile	His	Arg	Asn	Ser	Pro	Tyr				
50				55						60									
Cys	Gly	Tyr	Val	His	Gln	Cys	Gly	Gly	Gly	Arg	Arg	Gln	Ala	Gly	Met				

145

<210> 1107
 <211> 618
 <212> DNA
 <213> Homo sapiens

<400> 1107
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 120
 agaacctcga agagcgcgtc gccacgcgca cacaggcgct ggctgaagcc aaccaacgcc
 180
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 240
 atggaagccg gggggccagct caccggcggc atcgcccatg atttcaacaa catgctgacc
 300
 gggattatcg gcagcctgga cttgatgcag cgctacatcn aggccggggc cagcgacgaa
 360
 atcggccgnc ttactgacgc cgccgtatcg tccgcccacg gcgcggccgc cctcacccat
 420
 cggtgctggt cggttctcgc cgccagtcg ctggccccc gcccgctgga cccaaccag
 480
 ctggtagcgt ccctggagga tctgttccag cgaaccaaag gcgcgcatat cagctcaaa
 540
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 600
 ctgctcaacc tggcgatc
 618

<210> 1108
 <211> 182
 <212> PRT
 <213> Homo sapiens

<400> 1108
 Met Arg Pro Asn Ala Asn Ser Pro Lys Arg Pro Cys Ala Thr Ser Thr
 1 5 10 15
 Arg Thr Ser Lys Ser Ala Ser Pro Ser Ala His Arg Arg Trp Leu Lys
 20 25 30
 Pro Thr Asn Ala Trp Gln Asn Lys Met Phe Lys Arg Lys Arg Ala Glu
 35 40 45
 Asp Ala Leu Arg His Ala Gln Lys Met Glu Ala Gly Gly Gln Leu Thr
 50 55 60
 Gly Gly Ile Ala His Asp Phe Asn Asn Met Leu Thr Gly Ile Ile Gly
 65 70 75 80
 Ser Leu Asp Leu Met Gln Arg Tyr Ile Xaa Ala Gly Arg Ser Asp Glu
 85 90 95
 Ile Gly Arg Leu Thr Asp Ala Ala Val Ser Ser Ala His Arg Ala Ala
 100 105 110
 Ala Leu Thr His Arg Leu Leu Ala Phe Ser Arg Arg Gln Ser Leu Ala
 115 120 125
 Pro Arg Pro Leu Asp Pro Asn Gln Leu Val Ala Ser Leu Glu Asp Leu

130	135	140
Phe Gln Arg Thr Lys Gly Ala His Ile Thr Leu Lys Val Gln Leu Gly		
145	150	155
Arg Asp Ile Trp Pro Val Asn Thr Asp Ala Ser Gln Leu Glu Asn Ala		160
	165	170
Leu Leu Asn Leu Ala Ile		175
	180	

<210> 1109
 <211> 325
 <212> DNA
 <213> Homo sapiens

<400> 1109
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 agcctcaaga tcgtcgcacc gctggggggc atcctcgtgc ccttggatca ggtgcccgat
 120
 cccgttttctg cccagaagat ggtgggagac gggatctccc tggaccccat ctcaaacgaa
 180
 ttgctggcgc cggtcgccgg caccgtgacc cagctccaca acgcccacca cgcgctcacg
 240
 atcacgaccc cggaaggcat cgaggttctg gtccatatcg gactggatac cgtgatgctg
 300
 cgcggcgaca gctatcccc ccccn
 325

<210> 1110
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1110
Thr Gly Glu His Gln Gly Gly Thr Met Gln Thr Thr Leu Pro Ser Ser
1 5 10 15
Leu Lys Pro Ser Ser Leu Lys Ile Val Ala Pro Leu Gly Gly Ile Leu
20 25 30
Val Pro Leu Asp Gln Val Pro Asp Pro Val Phe Ala Gln Lys Met Val
35 40 45
Gly Asp Gly Ile Ser Leu Asp Pro Ile Ser Asn Glu Leu Leu Ala Pro
50 55 60
Val Ala Gly Thr Val Thr Gln Leu His Asn Ala His His Ala Leu Thr
65 70 75 80
Ile Thr Thr Pro Glu Gly Ile Glu Val Leu Val His Ile Gly Leu Asp
85 90 95
Thr Val Met Leu Arg Gly Asp Ser Tyr Pro Pro Pro
100 105

<210> 1111
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 1111

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 actgaactcg tcaacgccgc ctatagccgg gttgacatgg tggaaacgccg tggcgaattc
 120
 gcagtacgtg gcggcatcgt cgacgtcttc ccaccggtgc tagaacaccc ggtccgtatc
 180
 gatttttttg gtgacgagat cgaggaaatg acctccttcg cggtagccga ccagcgatcc
 240
 accgacgaga ctcaccaaga actgatctgc gctccttgcc gtgagctcat cctcaccgac
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 360
 gagcggatcg gcaacgggtca agctt
 385

<210> 1112
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1112
 Xaa Arg Val Ala Pro Val Arg Leu Ala Val Gly Glu Glu His Asp Leu
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 Thr Glu Leu Ala Thr Glu Leu Val Asn Ala Ala Tyr Ser Arg Val Asp
 20 25 30
 Met Val Glu Arg Arg Gly Glu Phe Ala Val Arg Gly Gly Ile Val Asp
 35 40 45
 Val Phe Pro Pro Val Leu Glu His Pro Val Arg Ile Asp Phe Phe Gly
 50 55 60
 Asp Glu Ile Glu Glu Met Thr Ser Phe Ala Val Ala Asp Gln Arg Ser
 65 70 75 80
 Thr Asp Glu Thr His Gln Glu Leu Ile Cys Ala Pro Cys Arg Glu Leu
 85 90 95
 Ile Leu Thr Asp Glu Val Arg Ser Arg Ala Lys Ala Leu Leu Thr Asp
 100 105 110
 His Pro Glu Leu Ala Asp Met Leu Glu Arg Ile Gly Asn Gly Gln Ala
 115 120 125

<210> 1113
 <211> 400
 <212> DNA
 <213> Homo sapiens

<400> 1113
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 cactcgggact tctcggggac cggcggagtc gatcagaccg accgttctac caatatcgac
 120
 gagcacacca tcgaggagat gcatcagatc gcctcgcgtt accccgactc ccgttcggcg
 180
 ttgctgccga tcctgcacct ggttcagtcg gtggacggac gcatctcgcc ggctcggtatt
 240
 gagactgcgg ctgaagtgtc cggcattacc accgcccagg tatccggggg ggcgaccttc
 300

tacaccatgt ataagaagca ccctgcgggc cagcatcaca tcggtgtctg caccacggcg
 360
 ctgtgcgccg tcatgggtgg cgaggaggtg cttgcccgtn
 400

<210> 1114
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 1114
 Xaa Arg Pro Met Ser Asp Arg Glu Pro Val Asn Leu Gly Tyr Pro Tyr
 1 5 10 15
 Val Glu Ser Phe His Ser Asp Phe Ser Gly Thr Gly Gly Val Asp Gln
 20 25 30
 Thr Asp Arg Ser Thr Asn Ile Asp Glu His Thr Ile Glu Glu Met His
 35 40 45
 Gln Ile Ala Ser Arg Tyr Pro Asp Ser Arg Ser Ala Leu Leu Pro Ile
 50 55 60
 Leu His Leu Val Gln Ser Val Asp Gly Arg Ile Ser Pro Val Gly Ile
 65 70 75 80
 Glu Thr Ala Ala Glu Val Leu Gly Ile Thr Thr Ala Gln Val Ser Gly
 85 90 95
 Val Ala Thr Phe Tyr Thr Met Tyr Lys Lys His Pro Ala Gly Gln His
 100 105 110
 His Ile Gly Val Cys Thr Thr Ala Leu Cys Ala Val Met Gly Gly Glu
 115 120 125
 Glu Val Leu Ala Arg
 130

<210> 1115
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 1115
 tctccgactg cacagattag agaaaggact gcgatgacca ttcgcaccac tcatgttggt
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 tccctgcccc gcacccccga gctgatcgag gcgaatcgtg cgcgcctga gggttcgctc
 120
 ggcgaggctg acttcacgtc gctgctgcag gatcagggtg acggcgttgt gaagcgtcag
 180
 gctgagattg gcctggatat cgtcaatgac ggcgagtacg gtcacgcgat gcttgacacg
 240
 gttgattacg gcgcgtgggtg gacgtattcc atctctcgtt tcggcgggct gtcctttgag
 300
 gacgtgcagc gttttgatgt gcgtcccccg gctggccgtg acggtcgcct gtctttctcg
 360
 tcgttcgctg agcgcgcga ctggcagcgt ttccggacgc gt
 402

<210> 1116
 <211> 134
 <212> PRT

<213> Homo sapiens

<400> 1116

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Ser Pro Thr Ala Gln Ile Arg Glu Arg Thr Ala Met Thr Ile Arg Thr
 1           5           10           15
Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Ile Glu Ala Asn
      20           25           30
Arg Ala Arg Arg Glu Gly Ser Leu Gly Glu Ala Asp Phe Thr Ser Leu
      35           40           45
Leu Gln Asp Gln Val Asp Gly Val Val Lys Arg Gln Ala Glu Ile Gly
      50           55           60
Leu Asp Ile Val Asn Asp Gly Glu Tyr Gly His Ala Met Leu Asp Thr
      65           70           75           80
Val Asp Tyr Gly Ala Trp Trp Thr Tyr Ser Ile Ser Arg Phe Gly Gly
      85           90           95
Leu Ser Phe Glu Asp Val Gln Arg Phe Asp Val Arg Pro Pro Ala Gly
      100          105          110
Arg Asp Gly Arg Leu Ser Phe Ser Ser Phe Ala Glu Arg Arg Asp Trp
      115          120          125
Gln Arg Phe Arg Thr Arg
      130

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<210> 1117

<211> 307

<212> DNA

<213> Homo sapiens

<400> 1117

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ggcgccgggtc ttgccttggc tgggaagtggc atgcagacct tgggtgcggaa cccgctggct
60
gacctctacc tgctaggtgt atcggctggc gcaagtgtgg gagcaaccgc agtcacgct
120
ttggggatgt tcacttcgtg gggaactcac cgactcactc ttgggtgccct tgtaggggcc
180
ttggcggcag ctgcattggt ctatctcatt tccatggcgc aaggaggcat gacgccgctt
240
cggttggtgc tgtcgggcgt ggtgttgctc tcggcgcttct cgcgttggcg agtttccctg
300
tctttcg
307

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<210> 1118

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1118

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Gly Ala Gly Leu Ala Leu Ala Gly Ser Gly Met Gln Thr Leu Val Arg
 1           5           10           15
Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ala Ser
      20           25           30
Val Gly Ala Thr Ala Val Ile Ala Leu Gly Met Phe Thr Ser Trp Gly
      35           40           45
Thr His Arg Leu Thr Leu Gly Ala Leu Val Gly Ala Leu Ala Ala Ala

```

50 55 60
 Ala Leu Val Tyr Leu Ile Ser Met Ala Gln Gly Gly Met Thr Pro Leu
 65 70 75 80
 Arg Leu Val Leu Ser Gly Val Val Leu Ser Ser Ala Phe Ser Arg Trp
 85 90 95
 Arg Val Ser Ser Ser Phe
 100

<210> 1119
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 1119
 cgcgctccttg agatgcttga gcaggctcggg attgaggatc cagccagggt gatggattcc
 60
 tatccgcctc aactgtccgg tggccagcgt caacggggtc tgcttgccat ggcgttggtg
 120
 aactcgccgg atctgctcat ttgtgacgag ccgacgaccg ccttgacgt caccgtgcag
 180
 tctcaggtac tggcgactat cgatgaggtg cttgactcgg ttggtgccgc atgcctattt
 240
 attaccacg atttggcggg tgtctgcac atctgccggg agcttatcgt gatgacgtcg
 300
 ggcaagggtc ttgaagccgg atcagcgcgt gatgtgttat ctcaccctga tca
 353

<210> 1120
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1120
 Arg Val Leu Glu Met Leu Glu Gln Val Gly Ile Glu Asp Pro Ala Arg
 1 5 10 15
 Val Met Asp Ser Tyr Pro His Gln Leu Ser Gly Gly Gln Arg Gln Arg
 20 25 30
 Val Leu Leu Ala Met Ala Leu Val Asn Ser Pro Asp Leu Leu Ile Cys
 35 40 45
 Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Val Gln Ser Gln Val Leu
 50 55 60
 Ala Thr Ile Asp Glu Val Leu Asp Ser Val Gly Ala Ala Cys Leu Phe
 65 70 75 80
 Ile Thr His Asp Leu Ala Val Val Ser His Ile Cys Arg Glu Leu Ile
 85 90 95
 Val Met Thr Ser Gly Lys Val Val Glu Ala Gly Ser Ala Arg Asp Val
 100 105 110
 Leu Ser His Pro Asp
 115

<210> 1121
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 1121

tgatcaccca tgctccactc gaccgcgcgc tcgacgatgc gacggctgag acgatgctcg
 60
 cccagggcac ggtgttcac cgcacctga cgatgatgaa aggcgtcgcc gcgaatctca
 120
 ccgcagcggg cgttcccggg gtgagctatg cacacgcca cgagagcacg cgcgcgatgc
 180
 atgccgcggg cgttccggc ctggccggca ccgacgccta catcgggtcc ttcacacggg
 240
 catcgccgcc atacggcgag agcatgcacg acgaagacgc ctacatcggg ctcctcgaac
 300
 gggcaatgcc gccatacggc gagagcatgc acgacgaact cgctctgctc gtggacgcc
 360
 gcctgtcaac agccgaagcg ctgcgcgctg ccacctcgac gggcgc
 406

<210> 1122

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1122

Met	Leu	Ala	Gln	Gly	Thr	Val	Phe	Ile	Pro	Thr	Leu	Thr	Met	Met	Lys
1				5					10					15	
Gly	Val	Ala	Ala	Asn	Leu	Thr	Ala	Ala	Gly	Val	Pro	Gly	Val	Ser	Tyr
			20					25					30		
Ala	His	Ala	His	Glu	Ser	Thr	Arg	Ala	Met	His	Ala	Ala	Gly	Val	Pro
		35					40					45			
Val	Leu	Ala	Gly	Thr	Asp	Ala	Tyr	Ile	Gly	Ser	Phe	Thr	Arg	Ala	Ser
	50				55						60				
Pro	Pro	Tyr	Gly	Glu	Ser	Met	His	Asp	Glu	Asp	Ala	Tyr	Ile	Gly	Leu
65				70					75					80	
Leu	Glu	Arg	Ala	Met	Pro	Pro	Tyr	Gly	Glu	Ser	Met	His	Asp	Glu	Leu
			85					90					95		
Ala	Leu	Leu	Val	Asp	Ala	Gly	Leu	Ser	Thr	Ala	Glu	Ala	Leu	Arg	Ala
			100				105						110		
Ala	Thr	Ser	Thr	Gly											
			115												

<210> 1123

<211> 337

<212> DNA

<213> Homo sapiens

<400> 1123

gccggcgatg cggttcattaa ggcctaagat gcgccgacgc cccccgctt tcctcgccct
 60
 cgcctccacc gcccttgccg cagcggggat ggtgggggtgc tcgtccgagg gggcatcgcc
 120
 aagcgaatgc tccccgttg atattgccgc agtgcgcgag gccctgccgc attcgctcgc
 180
 taaggcgaag ctgcacccgc actccaccaa cgaggatgaa cactcctttt ccattgctcta
 240

ccgcgcgcaa gataaggagc aggtcagctt gctggggacg aagtatgagg ccgacggtgc
 300
 acccgtctgc cccgatgacc ccaatgaggc agcgcgc
 337

<210> 1124
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1124
 Met Arg Ser Leu Arg Pro Lys Met Arg Arg Arg Leu Pro Ala Phe Leu
 1 5 10 15
 Ala Leu Ala Ser Thr Ala Leu Ala Ala Gly Met Val Gly Cys Ser
 20 25 30
 Ser Glu Gly Ala Ser Pro Ser Glu Cys Ser Pro Val Asp Ile Ala Ala
 35 40 45
 Val Arg Glu Ala Leu Pro His Ser Leu Ala Lys Ala Lys Leu Asp Pro
 50 55 60
 His Ser Thr Asn Glu Asp Glu His Ser Phe Ser Met Leu Tyr Arg Ala
 65 70 75 80
 Gln Asp Lys Glu Gln Val Ser Leu Leu Gly Thr Lys Tyr Glu Ala Asp
 85 90 95
 Gly Ala Pro Val Cys Pro Asp Asp Pro Asn Glu Ala Ala Arg
 100 105 110

<210> 1125
 <211> 555
 <212> DNA
 <213> Homo sapiens

<400> 1125
 nncttgaatc gaatcggcat tgcgtctaaa catgacgttg agacactctc tgctaagctc
 60
 gaagagctga cggcattgct agaacgtgtc gcgcgtaaac actaaggaga catcgggatg
 120
 gctgttaaaa agactactca gaaagaaggc agctcgtgga tcggggaagt tgaaaaatat
 180
 tcccgtaaaa tctggcttgc tggtttaggc gtgtactcga aggttagcag tgacggcggc
 240
 aaatacttcg agacgttggc caaggacggc gagaaggccg agaagttgac caagagccca
 300
 gtcggtaaaa aagtagaggc ggcaaaagcg agcgccggtt ctgcgaaatc gagcatttcg
 360
 gatacctggg gcaagttgga agagactttc gacaagcgtc tcaacagtgc tatttcgcga
 420
 ttgggcgtgc ccagcaaagc ggaactgaag acgctgcaca gcaaggtcga taccctgacc
 480
 aagcaaatcg aaaaactcac cgggtgcaaaa gtggccccgg ctaaaacggc agccgctaaa
 540
 cctgctgcca agctt
 555

<210> 1126

<211> 146
 <212> PRT
 <213> Homo sapiens

<400> 1126
 Met Ala Val Lys Lys Thr Thr Gln Lys Glu Gly Ser Ser Trp Ile Gly
 1 5 10 15
 Glu Val Glu Lys Tyr Ser Arg Lys Ile Trp Leu Ala Gly Leu Gly Val
 20 25 30
 Tyr Ser Lys Val Ser Ser Asp Gly Gly Lys Tyr Phe Glu Thr Leu Val
 35 40 45
 Lys Asp Gly Glu Lys Ala Glu Lys Leu Thr Lys Ser Pro Val Gly Lys
 50 55 60
 Lys Val Glu Ala Ala Lys Ala Ser Ala Gly Ser Ala Lys Ser Ser Ile
 65 70 75 80
 Ser Asp Thr Trp Gly Lys Leu Glu Glu Thr Phe Asp Lys Arg Leu Asn
 85 90 95
 Ser Ala Ile Ser Arg Leu Gly Val Pro Ser Lys Ala Glu Leu Lys Thr
 100 105 110
 Leu His Ser Lys Val Asp Thr Leu Thr Lys Gln Ile Glu Lys Leu Thr
 115 120 125
 Gly Ala Lys Val Ala Pro Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala
 130 135 140
 Lys Leu
 145

<210> 1127
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 1127
 cccgaccgcg tactcgtggt cgggtgccgga gtgatgggtg cagcacacgc acacgcgctc
 60
 cgcggtgccc tccaggcagt cgtgtgcggc gtggtcgacc tgcaggagcg agcagcgcaa
 120
 tcactcgctt cggaagtggg cgtacccggg ttcaccgacc tggatgaaggc gatcgagtcg
 180
 accgctccgg acgcccgggt catcgccacg ccggactcgg ctcaccgcca accgggtgag
 240
 accgccatcg acgcccgcct tgccgtcctg gtcgagaaac cgctcgccac gaccgtcgat
 300
 gacgccgaag cgatcgtgct ccgcgtgaa cgggcccggc tccgtctcat ga
 352

<210> 1128
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1128
 Pro Asp Arg Val Leu Val Val Gly Ala Gly Val Met Gly Ala Ala His
 1 5 10 15
 Ala His Ala Leu Arg Gly Ser Leu Gln Ala Val Val Cys Gly Val Val

```

      20      25      30
Asp Leu Gln Glu Arg Ala Ala Gln Ser Leu Ala Ser Glu Val Gly Val
      35      40      45
Pro Gly Phe Thr Asp Leu Val Lys Ala Ile Glu Ser Thr Ala Pro Asp
      50      55      60
Ala Ala Val Ile Ala Thr Pro Asp Ser Ala His Arg Gln Pro Ala Glu
65      70      75      80
Thr Ala Ile Asp Ala Gly Leu Ala Val Leu Val Glu Lys Pro Leu Ala
      85      90      95
Thr Thr Val Asp Asp Ala Glu Ala Ile Val Leu Arg Ala Glu Arg Ala
      100      105      110
Gly Val Arg Leu Met
      115

```

<210> 1129

<211> 336

<212> DNA

<213> Homo sapiens

<400> 1129

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ntggcagccc tggaggagcc gatggtggac ctggacggcg agctgccttt cgtgcggccc
60
ctgccccaca ttgccgtgct ccaggacgag ctgccgcaac tcttcagga tgacgacgtc
120
ggggccgatg aggaagaggc agagttgcgg ggccaacaca cgctcacaga gaagtttgtc
180
tgcctggatg actcctttgg ccatgactgc agcttgacct gtgatgactg caggaacgga
240
gggacctgcc tcctgggcct ggatggctgg gattgccccg agggctggac tgggctcatc
300
tgcaatgaga cttggtcctc gggctgcatg gatatt
336

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<210> 1130

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1130

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Xaa Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
1      5      10      15
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
      20      25      30
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu
      35      40      45
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
      50      55      60
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65      70      75      80
Gly Thr Cys Leu Leu Gly Leu Asp Gly Trp Asp Cys Pro Glu Gly Trp
      85      90      95
Thr Gly Leu Ile Cys Asn Glu Thr Trp Ser Ser Gly Cys Met Asp Ile
      100      105      110

```

<210> 1131
 <211> 672
 <212> DNA
 <213> Homo sapiens

<400> 1131
 gcgttggtgg tgctcatggc ccgggaaaat ccgctggatc aatacctctt tgagcacccc
 60
 gaattattgt tctcgtccctc ggtggaatcg actgtgttgc acccgataa cccgtatgtg
 120
 ctcggcccg cgcgtggccgc ggccgcccag gaggcatacc tctcccctgc ggacgaagag
 180
 ttttacgggt cggcctttgc cgggatatgc aaaacgctga caggccagaa cgtactgcga
 240
 cgtcgcggaa atcggctggt ctggactcgt ccggaacggg ctgtcgacgc catcgacctg
 300
 cgatcggcgg caggcaaagg gattgacatt atcgacgtgt ccaccgggag ggtcatcggg
 360
 gtagtcgacg aagccgcccgc agaccgtacc gtgcatccag gcgcggtgta cctgcatcag
 420
 ggggatcagt ggctggtcga cgaatacaac ccggtcgagc accacgccct ggtgcaccag
 480
 gacctgccgg gatattggac tcaaccgcag tcagcgtcga cggtgagaat ccttcgggag
 540
 gagagacgtc gcgcttgtgg tcccggatat gtggcgtgcg ggcaggtgga actgacagag
 600
 caagttgttg ggtatctgcg tcgcgacgaa ttcaccaatg atgtgtggta ctcgctggcc
 660
 ctcgagatgc cc
 672

<210> 1132
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 1132
 Ala Leu Val Val Leu Met Ala Arg Glu Asn Pro Leu Asp Gln Tyr Leu
 1 5 10 15
 Phe Glu His Pro Glu Leu Leu Phe Ser Ser Ser Val Glu Ser Thr Val
 20 25 30
 Leu His Pro Asp Asn Pro Tyr Val Leu Gly Pro His Val Ala Ala Ala
 35 40 45
 Ala Gln Glu Ala Tyr Leu Ser Pro Ala Asp Glu Glu Phe Tyr Gly Ser
 50 55 60
 Ala Phe Ala Gly Ile Cys Lys Thr Leu Thr Gly Gln Asn Val Leu Arg
 65 70 75 80
 Arg Arg Gly Asn Arg Leu Phe Trp Thr Arg Pro Glu Arg Ala Val Asp
 85 90 95
 Ala Ile Asp Leu Arg Ser Ala Ala Gly Lys Gly Ile Asp Ile Ile Asp
 100 105 110
 Val Ser Thr Gly Arg Val Ile Gly Val Val Asp Glu Ala Ala Ala Asp
 115 120 125
 Arg Thr Val His Pro Gly Ala Val Tyr Leu His Gln Gly Asp Gln Trp

130	135	140
Leu Val Asp Glu Tyr Asn Pro Val Glu His His Ala Leu Val His Gln		
145	150	155
Asp Leu Pro Gly Tyr Trp Thr Gln Pro Gln Ser Ala Ser Thr Val Arg		
	165	170
Ile Leu Arg Glu Glu Arg Arg Arg Ala Cys Gly Pro Gly Tyr Val Ala		175
	180	185
Cys Gly Gln Val Glu Leu Thr Glu Gln Val Val Gly Tyr Leu Arg Arg		190
	195	200
Asp Glu Phe Thr Asn Asp Val Trp Tyr Ser Leu Ala Leu Glu Met Pro		205
210	215	220

<210> 1133
 <211> 796
 <212> DNA
 <213> Homo sapiens

<400> 1133
 acgcgtgaag ggggggtccag cgggtgtggc actcgatgac aagacagttt gagagcggct
 60
 tgtctccggg gacctggcgt aggtctctctc tgccttaacc cttggctttt gcacttctctc
 120
 tgtctgtcct ccatacaagc ttcttgcccc tagggaggac gggcttctta acagggggag
 180
 ccggttctctg tcttaacccc actggcatct tacactctgg gagatagctt cccctgaga
 240
 ggcgagttag ccacgtaagg ggaggtgggc gatggcttcc cttctgtctt gggttggggg
 300
 agtcaggtag agtatttttt cttttaaaag atcattgatc acataataag gtttgtcata
 360
 gtccttaatc acagacctgt gaaatttgga gaattcacgg cacctaggat gggagttagc
 420
 ttctgattgt gagctgattt gggagctaac ctcaaggaaa ctctcttgc aagccccctg
 480
 ctgggtgtcg gggccttcgc caggacctc cgggggactc tggacgctct ttgtctgccc
 540
 ttccttttcc ctcacctgc tccccgtga gaaagtggg ctcatgcagc tcagctcagt
 600
 gacagagggt ttattagggg tagctctggg acccatctt tggatgattc ttctctctct
 660
 ttctctaata gaataattgt ttctgtctac acttctttat tttctctct ctacagctgc
 720
 cttctaaaaa tgtgcttttc tgttctgca gaactgaagc ttgcatggcc tttgttgtga
 780
 ctttcccttc acgcgt
 796

<210> 1134
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 1134
 Met Gly Pro Arg Ala Thr Pro Asn Lys Pro Ser Val Thr Glu Leu Ser

```

1           5           10           15
Cys Met Ser Pro Thr Phe Ser Arg Gly Ser Glu Val Arg Glu Lys Glu
                20           25           30
Gly Gln Thr Lys Ser Val Gln Ser Pro Arg Glu Val Pro Gly Glu Gly
                35           40           45
Pro Asp Thr Gln Gln Gly Ala Cys Lys Arg Ser Phe Leu Glu Val Ser
                50           55           60
Ser Gln Ile Ser Ser Gln Ser Glu Ala His Ser His Pro Arg Cys Arg
65           70           75           80
Glu Phe Ser Lys Phe His Arg Ser Val Ile Lys Asp Tyr Asp Lys Pro
                85           90           95
Tyr Tyr Val Ile Asn Asp Ala Leu Lys Glu Lys Ile Leu Tyr Leu Thr
                100           105           110
Pro Pro Thr Gln Asp Arg Arg Glu Ala Ile Ala His Leu Pro Leu Arg
                115           120           125
Gly Ser Leu Ala Ser Gln Gly Glu Ala Ile Ser Gln Ser Val Arg Cys
                130           135           140
Gln Trp Gly
145

```

<210> 1135

<211> 376

<212> DNA

<213> Homo sapiens

<400> 1135

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gatcaggcca cacaggacaa cttcgagaag ggctccatct tcccaccctt caccagcatc
60
agaaagatct ctgcgcacat cgctgcagcc gtggctgcaa aagcctacga gctcgggtctg
120
gcgacccgctc tgccctcccc cagcgacctg gtgaaatatg cagagaactg catgtacact
180
cccgtctacc gcaactaccg gtagtgctgc ggggatcaat tttgcagtaa taaaaaatct
240
actatcaacg cggatgggtac tctgttgttt atagtccctg ctgctaacca cccttgttgc
300
tggtgctgct ggagaggcat tgtacctgtc catgcatata tgatatatat atgttgtaac
360
gttgtgaaag caaact
376

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<210> 1136

<211> 67

<212> PRT

<213> Homo sapiens

<400> 1136

```

Asp Gln Ala Thr Gln Asp Asn Phe Glu Lys Gly Ser Ile Phe Pro Pro
1           5           10           15
Phe Thr Ser Ile Arg Lys Ile Ser Ala His Ile Ala Ala Val Ala
                20           25           30
Ala Lys Ala Tyr Glu Leu Gly Leu Ala Thr Arg Leu Pro Pro Ser
                35           40           45
Asp Leu Val Lys Tyr Ala Glu Asn Cys Met Tyr Thr Pro Val Tyr Arg

```

50 55 60
 Asn Tyr Arg
 65
 <210> 1137
 <211> 357
 <212> DNA
 <213> Homo sapiens
 <400> 1137
 acgcgtcgct ggaacccgaa gatgaagcgc ttcattcttca ccgagcgcaa cggatatctac
 60
 atcattgacc tgcaccagtc gctgacctac attgataagg cgtacgcctt cgtcaaggag
 120
 actgtcgcca agggcgccca gattcttttc gtcggcacga agaagcaggc ccaggagtcc
 180
 atcgttgagc aggccactcg cgttggcatg ccctatgtca accagcgttg gcttggggga
 240
 atgctcacta atttccagac catctcgaag cgcattgccc ggctcaagga gctcgaggcc
 300
 atggactttg acaaggtttc cggctccggt ctcaccaaga aggagctgct tatgctc
 357

<210> 1138
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 1138
 Thr Arg Arg Trp Asn Pro Lys Met Lys Arg Phe Ile Phe Thr Glu Arg
 1 5 10 15
 Asn Gly Ile Tyr Ile Ile Asp Leu His Gln Ser Leu Thr Tyr Ile Asp
 20 25 30
 Lys Ala Tyr Ala Phe Val Lys Glu Thr Val Ala Lys Gly Gly Gln Ile
 35 40 45
 Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ser Ile Val Glu Gln
 50 55 60
 Ala Thr Arg Val Gly Met Pro Tyr Val Asn Gln Arg Trp Leu Gly Gly
 65 70 75 80
 Met Leu Thr Asn Phe Gln Thr Ile Ser Lys Arg Ile Ala Arg Leu Lys
 85 90 95
 Glu Leu Glu Ala Met Asp Phe Asp Lys Val Ser Gly Ser Gly Leu Thr
 100 105 110
 Lys Lys Glu Leu Leu Met Leu
 115

<210> 1139
 <211> 456
 <212> DNA
 <213> Homo sapiens

<400> 1139
 gtgcacaggt cgtctgaggc catgccgcgg acgatcgatc cgagtatggc ggcaccttca
 60

ccaatcccgt aggacccgtc tcgtccagca tcgaccaagg cgctgttgag gcgttcggct
 120
 tcggtaatga actcgatgcy ctcaatatcc acgggggtag cgaaatcgta gatcttgccc
 180
 agactgaggc cttggaggag cgcggccgtc ggggggacgt ggcctgcggc cgggcgttcc
 240
 ttgctctcaa ggacttcgtc gtcgcggtc acaaggaata cgtttgtgtg gtcgcctgca
 300
 atgcatgctc gagcgtggtg accatcgagg tgaaggacgg tttcggcata gaggtcatcg
 360
 tccacatcgg ccacagttag ttcgacgact cctgagtcga ctagatgacg cgccttctct
 420
 gccgcgtctt cgctgacgtc ggccaggacc gctagc
 456

<210> 1140
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1140
 Met Trp Thr Met Thr Ser Met Pro Lys Pro Ser Phe Thr Ser Met Val
 1 5 10 15
 Thr Thr Leu Glu His Ala Leu Gln Ala Thr Thr Gln Thr Tyr Ser Leu
 20 25 30
 Ser Ala Ala Thr Thr Lys Ser Leu Arg Ala Arg Asn Ala Arg Pro Gln
 35 40 45
 Ala Thr Ser Pro Arg Arg Pro Arg Ser Ser Lys Ala Ser Val Trp Pro
 50 55 60
 Arg Ser Thr Ile Ser Leu Pro Pro Trp Ile Leu Ser Ala Ser Ser Ser
 65 70 75 80
 Leu Pro Lys Pro Asn Ala Ser Thr Ala Pro Trp Ser Met Leu Asp Glu
 85 90 95
 Thr Gly Pro Thr Gly Leu Val Lys Val Pro Pro Tyr Ser Asp Arg Ser
 100 105 110
 Ser Ala Ala Trp Pro Gln Thr Thr Cys Ala
 115 120

<210> 1141
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 1141
 ggcgccatgc tcggcgggct ggtgctgggt gtggccgaag cctttggcgc cgatatcttc
 60
 ggcgaccagt acaaggacgt ggtggcggtt ggctgttg ttctggtgct gttgttcgt
 120
 ccgaccggca ttctgggccc tccggagggt gagaaagtat gagcagatat cttaaatcgg
 180
 cgtttttcag cgcctgttg gtgtgggccc tggcctttcc ggtactcggc ctcaagctga
 240
 gcattgtcgg gatcaaccac gaagtgcatt gcaccgggtc cgtgaccttg accatcatcg
 300

ccctgtgctc ggtgccgatg ttctgcgcg tgctgtttac ccagcaagtc ggtg
354

<210> 1142
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1142
Gly Ala Met Leu Gly Gly Leu Val Leu Gly Val Ala Glu Ala Phe Gly
1 5 10 15
Ala Asp Ile Phe Gly Asp Gln Tyr Lys Asp Val Val Ala Phe Gly Leu
20 25 30
Leu Val Leu Val Leu Leu Phe Arg Pro Thr Gly Ile Leu Gly Arg Pro
35 40 45
Glu Val Glu Lys Val
50

<210> 1143
<211> 353
<212> DNA
<213> Homo sapiens

<400> 1143
acgcgttgca catccccag gaccatcaac cgcggcattg ccgcatagac ctggagatcc
60
catgcaacgt gaaatgaagt tcgaatcgat caaggcaaag gccaaggcga tgctcatcgg
120
cgcagccgac gacacagcaa gcgcaggcgc gaccaaccga gggtaggctca acagcgccgc
180
attcgaaatc ctggcccacg tggccgtcaa tgcccaacac tacgcgctct ccgagagacc
240
ggcgctggag gagttcgcca agagcttcca gccgcgcaac aaccaggact acgtggccgc
300
gatcgccaag aaggccgca accacaccat gcatcccggc aggcagtcga ttt
353

<210> 1144
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1144
Met His Gly Val Val Arg Gly Leu Leu Gly Asp Arg Gly His Val Val
1 5 10 15
Leu Val Val Ala Arg Leu Glu Ala Leu Gly Glu Leu Leu Gln Arg Arg
20 25 30
Ser Leu Gly Glu Arg Val Val Leu Gly Ile Asp Gly His Val Gly Gln
35 40 45
Asp Phe Glu Cys Gly Ala Val Glu Pro Pro Ser Val Gly Arg Ala Cys
50 55 60
Ala Cys Cys Val Val Gly Cys Ala Asp Glu His Arg Leu Gly Leu Cys
65 70 75 80
Leu Asp Arg Phe Glu Leu His Phe Thr Leu His Gly Ile Ser Arg Ser

85
Met Arg Gln Cys Arg Gly
100

90

95

<210> 1145
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1145
gtcttcggcg ggctcggcct gttctattgc gtcacgaccc cgggtgtactg gttctcggcc
60
catgaagtgg ccggcacctg ggtactcggg ctgtcggcgg cgatggctct gatgggtgtt
120
ttctacgtcc aggtcatcgc caagaagatc aatcctcgac cctccgacga gaaggacgcc
180
gaggtgatcg acggggctgg tccggtcggt ttcttcccgc cacagagtat ctggccgttc
240
tggtgcgcgc tcgttgctgc catcatgtgc ctcggcccga tcttcggctg gtggatctct
300
ctgctcgggc tgggcattgt tatctgggcc gcctcgggtt gggcttttga gtactaccgc
360

<210> 1146
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1146
Val Phe Gly Gly Leu Gly Leu Phe Tyr Cys Val Met Thr Pro Val Tyr
1 5 10 15
Trp Phe Ser Ala His Glu Val Ala Gly Thr Trp Val Leu Gly Leu Ser
20 25 30
Ala Ala Met Ala Leu Met Val Phe Phe Tyr Val Gln Val Ile Ala Lys
35 40 45
Lys Ile Asn Pro Arg Pro Ser Asp Glu Lys Asp Ala Glu Val Ile Asp
50 55 60
Gly Ala Gly Pro Val Gly Phe Phe Pro Pro Gln Ser Ile Trp Pro Phe
65 70 75 80
Trp Cys Ala Leu Val Val Ala Ile Met Cys Leu Gly Pro Ile Phe Gly
85 90 95
Trp Trp Ile Ser Leu Leu Gly Leu Gly Ile Val Ile Trp Ala Ala Ser
100 105 110
Gly Trp Ala Phe Glu Tyr Tyr Arg
115 120

<210> 1147
<211> 409
<212> DNA
<213> Homo sapiens

<400> 1147
tgtacattgg ctatgcagtc tggcctcctg aagggttatga tagtagccaa aaatatagaa
60

gccccaaagg catccacctt cttcatcaat ccagaattga tcatgctcat gcctgtgggt
 120
 ggatcactat gtgctctcca aattgggagg ggaagtctac tctcctctct cctctctctc
 180
 ccaccttccc ctctctcttc tctcctttct attcccaggg cagtggaaca tgatgaggtt
 240
 cttttccctt catggatata ctctttctgc cctccacata aaggggcatt gatggatctt
 300
 caagaatggg atgcctttcc ctagaaaggc taaatattca tgaggctgaa tgtgaggatc
 360
 cagagtacac tgaaatataa ctggatcatca gtacacatag aatctgatn
 409

<210> 1148
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1148
 Met Gln Ser Gly Leu Leu Lys Val Met Ile Val Ala Lys Asn Ile Glu
 1 5 10 15
 Ala Lys Lys Ala Ser Thr Phe Phe Ile Asn Pro Glu Leu Ile Met Leu
 20 25 30
 Met Pro Val Gly Gly Ser Leu Cys Ala Leu Gln Ile Gly Arg Gly Ser
 35 40 45
 Leu Leu Ser Ser Leu Leu Ser Leu Pro Pro Ser Pro Leu Ser Ser Leu
 50 55 60
 Leu Ser Ile Pro Arg Ala Val Glu His Asp Glu Val Leu Phe Pro Ser
 65 70 75 80
 Trp Ile Ser Ser Phe Cys Pro Pro His Lys Gly Ala Leu Met Asp Leu
 85 90 95
 Gln Glu Trp Asp Ala Phe Pro
 100

<210> 1149
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 1149
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 60
 cgtgaggcgg tatcgagat cattaccttc ggtaccatgg cggcgaaagc ggttattcgt
 120
 gacgtgggccc gtgtactggg tcacccgtat ggcttcgtcg atcgcatctc caagctgggtg
 180
 ccgcccgatc cgggcatgac gctggaaaaa gcctttgccg ccgaaccgca gttgccggaa
 240
 atctacgagg ccgatgagga agtcaaagcg ctgatcgaca tggcgcgcaa gctgggaagg
 300
 gtgacgcgg
 309

<210> 1150

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1150
 Val Asp Phe Cys Met Glu Lys Arg Asp Leu Val Ile Glu His Val Ala
 1 5 10 15
 Glu Met Tyr Gly Arg Glu Ala Val Ser Gln Ile Ile Thr Phe Gly Thr
 20 25 30
 Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val Leu Gly His
 35 40 45
 Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Val Pro Pro Asp Pro
 50 55 60
 Gly Met Thr Leu Glu Lys Ala Phe Ala Ala Glu Pro Gln Leu Pro Glu
 65 70 75 80
 Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp Met Ala Arg
 85 90 95
 Lys Leu Gly Arg Val Thr Arg
 100

<210> 1151
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 1151
 ggcgcgcattt tttgcaaccc aagcgacgtc attatggccg agtcgccggc ttatgtcggg
 60
 gcgctcaata ccttcgcctc gtaccaaact gaggtcattc acgtcgacat ggacgacagc
 120
 ggggttggttc cggaatccct gcgtgagaaa gtgactgcag cgcgtcaaga cggcaagtcg
 180
 gtgaagtcc tttacacggt tccaaactac tcgaaccggt cgggaatctc gcaatccacc
 240
 gagcgtcgcc gggagatcct agcgggtggct gacgagctgg atctgttggt ggttgaggac
 300
 aaccggtacg gggtactcaa cctcgatggg gatccactgc cgacgttgaa gtcgatggat
 360

<210> 1152
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1152
 Ala Arg Ile Phe Cys Asn Pro Ser Asp Val Ile Met Ala Glu Ser Pro
 1 5 10 15
 Ala Tyr Val Gly Ala Leu Asn Thr Phe Ala Ser Tyr Gln Thr Glu Val
 20 25 30
 Ile His Val Asp Met Asp Asp Ser Gly Leu Val Pro Glu Ser Leu Arg
 35 40 45
 Glu Lys Val Thr Ala Ala Arg Gln Asp Gly Lys Ser Val Lys Phe Leu
 50 55 60
 Tyr Thr Val Pro Asn Tyr Ser Asn Pro Ser Gly Ile Ser Gln Ser Thr

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65              70              75              80
Glu Arg Arg Arg Glu Ile Leu Ala Val Ala Asp Glu Leu Asp Leu Leu
              85              90              95
Val Val Glu Asp Asn Pro Tyr Gly Leu Leu Asn Leu Asp Gly Asp Pro
              100              105              110
Leu Pro Thr Leu Lys Ser Met Asp
              115              120

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<210> 1153
 <211> 416
 <212> DNA
 <213> Homo sapiens

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<400> 1153
gcgtggattc gtctggcgg cgctcgtacc gacctgccc agaccgggct cgaccagttg
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cgtgacctca tcaagcggat ggaaaagtac ctccccgaga tcggtcagtt ctgcaatgag
120
aatccgatct ttaaggcccc cactcagggc attggttacg ctgatctgtc tacctgtatg
180
gccctgggag ttactggtcc tgctctgcgc gctaccggcc tgccgtggga cctgcgcaag
240
accagccct attgcgatta cgacacgtat gacttcgacg tcgccacctg ggatacctgt
300
gactgttacg ggcgtttccg catccgcctg gaagagatgg accagtcggt gcgcattctc
360
aagcaatgcc tcaaacgcct cgaggacacc cagggtgacc gtaatatggt cgagga
416

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<210> 1154
 <211> 138
 <212> PRT
 <213> Homo sapiens

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<400> 1154
Ala Trp Ile Arg Pro Gly Gly Val Ala Thr Asp Leu Pro Glu Thr Gly
1              5              10              15
Leu Asp Gln Leu Arg Asp Leu Ile Lys Arg Met Glu Lys Tyr Leu Pro
              20              25              30
Glu Ile Gly Gln Phe Cys Asn Glu Asn Pro Ile Phe Lys Ala Arg Thr
              35              40              45
Gln Gly Ile Gly Tyr Ala Asp Leu Ser Thr Cys Met Ala Leu Gly Val
50              55              60
Thr Gly Pro Ala Leu Arg Ala Thr Gly Leu Pro Trp Asp Leu Arg Lys
65              70              75              80
Thr Gln Pro Tyr Cys Asp Tyr Asp Thr Tyr Asp Phe Asp Val Ala Thr
              85              90              95
Trp Asp Thr Cys Asp Cys Tyr Gly Arg Phe Arg Ile Arg Leu Glu Glu
100              105              110
Met Asp Gln Ser Val Arg Ile Leu Lys Gln Cys Leu Lys Arg Leu Glu
115              120              125
Asp Thr Gln Gly Asp Arg Asn Met Val Glu
130              135

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<210> 1155
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 1155
 cttaagttat tttggtcttt gcctctctcc tcaggttgtag aagattacag aaatctggga
 60
 tggcttatgg gacgcttctc agccctaagt aggaaaacag cagtgaaaat ggcaaccaa
 120
 acatcacgca ggactggggg ttttggggaa acagctcact ttagagcagt gcagtgtaga
 180
 gctttccgtc ttctaccagg gtccaccttt aacactggtt atctgaaaat tttccccctg
 240
 gcttactcgc ttgcagctgc ccactttgca gaaagatggc gctctgatct ctacgctccc
 300
 tgttccttca gggactccat agtatttttt ttcacgcgt
 339

<210> 1156
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1156
 Met Gly Arg Phe Ser Ala Leu Ser Arg Lys Thr Ala Val Lys Met Ala
 1 5 10 15
 Thr Lys Thr Ser Arg Arg Thr Gly Gly Phe Gly Glu Thr Ala His Phe
 20 25 30
 Arg Ala Val Gln Cys Arg Ala Phe Arg Leu Leu Pro Gly Ser Thr Phe
 35 40 45
 Asn Thr Val Tyr Leu Lys Ile Phe Pro Leu Ala Tyr Ser Leu Ala Ala
 50 55 60
 Ala His Phe Ala Glu Arg Trp Arg Ser Asp Leu Tyr Ala Pro Cys Ser
 65 70 75 80
 Phe Arg Asp Ser Ile Val Phe Phe Phe Thr Arg
 85 90

<210> 1157
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1157
 nnacagcctc tctccgaccc ggcggcggtt gcacacgtcc ccgtctgagg agtattcgtg
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 ctggcaaaac tcgtgacccg acacctgagg gcctatcggg tgcaagttgc cgatcatc
 120
 gttatgcagg tttgcgccc aatcgcggcc ctgaccttgc caaccatcaa cgcagacatc
 180
 atcaacaagg gcgtcgtgac agcggatacc ggatatgtca ccaccactc cctcttcatg
 240
 ctggcggtcg ctttagggca ggccatctgc caggtcattg cggtttatct cgccgctcag
 300

gtggcgatgg gaatggggccg tgacgttcgc gacgccatct tcacccgcac ccttgacttc
 360
 tcggccccggg agatcaacaa attcggagca ccatcactca ttacccggac taccaacgac
 420
 gtccag
 426

<210> 1158
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1158
 Val Leu Ala Lys Leu Val Thr Arg His Leu Arg Ala Tyr Arg Leu His
 1 5 10 15
 Val Ala Val Ile Ile Val Met Gln Val Cys Ala Gln Ile Ala Ala Leu
 20 25 30
 Thr Leu Pro Thr Ile Asn Ala Asp Ile Ile Asn Lys Gly Val Val Thr
 35 40 45
 Ala Asp Thr Gly Tyr Val Thr His Ser Leu Phe Met Leu Ala Val
 50 55 60
 Ala Leu Gly Gln Ala Ile Cys Gln Val Ile Ala Val Tyr Leu Ala Ala
 65 70 75 80
 Gln Val Ala Met Gly Met Gly Arg Asp Val Arg Asp Ala Ile Phe Thr
 85 90 95
 Arg Thr Leu Asp Phe Ser Ala Arg Glu Ile Asn Lys Phe Gly Ala Pro
 100 105 110
 Ser Leu Ile Thr Arg Thr Thr Asn Asp Val Gln
 115 120

<210> 1159
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 1159
 tctctccgac cgcgcctggg gcccggtggg gtctcgctgg gacgcgggag aggacggcgc
 60
 ggacgaggca ggagcaggcc gggctctcgc catgggtcac tgcgcctct gccacgggaa
 120
 gttttcctcg agaagcctgc gcagcatctc cgagagggcg cctggagcga gcatggagag
 180
 gccatccgca gaggagcgcg tgctcgtagc ggacttccag cgctgcttg gtgtggctgt
 240
 ccgccaggac ccaccttgt ctccgtttgt ctgcaagagc tgccacgccc agttctacca
 300
 gtgccacagc cttctcaagt cttcctgca gagggtcaac gcctccccgg ctggtcgccc
 360
 gaagccttgt gcaaaggctg gtgccagcc cccaacaggg gcagaggagg gagcgtgtct
 420
 ggtggatctg atca
 434

<210> 1160

<211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1160
 Met Gly His Cys Arg Leu Cys His Gly Lys Phe Ser Ser Arg Ser Leu
 1 5 10 15
 Arg Ser Ile Ser Glu Arg Ala Pro Gly Ala Ser Met Glu Arg Pro Ser
 20 25 30
 Ala Glu Glu Arg Val Leu Val Arg Asp Phe Gln Arg Leu Leu Gly Val
 35 40 45
 Ala Val Arg Gln Asp Pro Thr Leu Ser Pro Phe Val Cys Lys Ser Cys
 50 55 60
 His Ala Gln Phe Tyr Gln Cys His Ser Leu Leu Lys Ser Phe Leu Gln
 65 70 75 80
 Arg Val Asn Ala Ser Pro Ala Gly Arg Arg Lys Pro Cys Ala Lys Val
 85 90 95
 Gly Ala Gln Pro Pro Thr Gly Ala Glu Glu Gly Ala Cys Leu Val Asp
 100 105 110
 Leu Ile

<210> 1161
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 1161
 ctgcacacac accaggccac gcccacgagg acggccagtc agcatgcagc caatacaccc
 60
 acagagggat ggggagcagc cctcagtgcc agctccaaca ggcccactgc aggtcctgtc
 120
 actgcaccca aggagctgcc ttccatttca cctgacattt ccactaaggg cccagcgttt
 180
 atcattccag aagagcagca ggcagaacct tcacctcca agagctgcaa gtgcgctgtg
 240
 gcaggaaaag aagatctggc gtctgaagtc agctcctgct ctccaggaaa agagggacga
 300
 tgacatagga cttgagcaaa atgagagccc cgtgatggga gagaacacct gatca
 355

<210> 1162
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1162
 Met Gln Pro Ile His Pro Gln Arg Asp Gly Glu Gln Pro Ser Val Pro
 1 5 10 15
 Ala Pro Thr Gly Pro Leu Gln Val Leu Ser Leu His Pro Arg Ser Cys
 20 25 30
 Leu Pro Phe His Leu Thr Phe Pro Leu Arg Ala Gln Arg Leu Ser Phe
 35 40 45
 Gln Lys Ser Ser Arg Gln Asn Leu His Leu Pro Arg Ala Ala Ser Ala

50 55 60
 Leu Trp Gln Glu Lys Lys Ile Trp Arg Leu Lys Ser Ala Pro Ala Leu
 65 70 75 80
 Gln Glu Lys Arg Asp Asp Asp Ile Gly Leu Glu Gln Asn Glu Ser Pro
 85 90 95
 Val Met Gly Glu Asn Thr
 100

<210> 1163
 <211> 466
 <212> DNA
 <213> Homo sapiens

<400> 1163
 ngcgcgccag gaagcgggag gtcagctgta caccaggggt aatagaactt ctaccctcag
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 aggagtcaaaa gagaaggcag aactatggca ggaaagctcc ggaagtccca catccctgga
 120
 gtgagcatct ggcagctggt ggaggagatc cctgaaggct gcagcacgcc ggactttgag
 180
 cagaagcccg tcacctcggc tctgccagag gggaaaaatg ctgtctttcg ggctgtggtc
 240
 tgtggggagc ccaggcccga ggtgcgttgg cagaactcca aaggtgacct cagtgattcc
 300
 agcaagtaca agatctcttc cagccctggc agcaaggagc acgtgctgca gatcaacaag
 360
 ctgacaggcg aggacacgga tctgtaccac tgcacagcag taaatgcgta cggagaggcc
 420
 gcttgctcag tgagactcac cgtcatcgaa gttggctttc ggaaga
 466

<210> 1164
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 1164
 Met Ala Gly Lys Leu Arg Lys Ser His Ile Pro Gly Val Ser Ile Trp
 1 5 10 15
 Gln Leu Val Glu Glu Ile Pro Glu Gly Cys Ser Thr Pro Asp Phe Glu
 20 25 30
 Gln Lys Pro Val Thr Ser Ala Leu Pro Glu Gly Lys Asn Ala Val Phe
 35 40 45
 Arg Ala Val Val Cys Gly Glu Pro Arg Pro Glu Val Arg Trp Gln Asn
 50 55 60
 Ser Lys Gly Asp Leu Ser Asp Ser Ser Lys Tyr Lys Ile Ser Ser Ser
 65 70 75 80
 Pro Gly Ser Lys Glu His Val Leu Gln Ile Asn Lys Leu Thr Gly Glu
 85 90 95
 Asp Thr Asp Leu Tyr His Cys Thr Ala Val Asn Ala Tyr Gly Glu Ala
 100 105 110
 Ala Cys Ser Val Arg Leu Thr Val Ile Glu Val Gly Phe Arg Lys
 115 120 125

<210> 1165
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 1165
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 60
 tgcttttagta aagtccttgt tgagccgctg ctgctcaagc tcaacttgac nattatgtgt
 120
 ctgcacattc tgctgatgtc cacgttcgtg gccctgcccg gtcagttggc tgcagcagga
 180
 ttccccgccg ctgaacactg gaaagtgtat ctggtgacga tgctcatctc cttcgtctcc
 240
 gttgtccctt tcattatcta tgcagaagtg aaacgccgca tgaagcgctg attcctgacg
 300
 tgtgttgccg tgctgttgat tgccgaaatc gtactatggg gctccggtcc acacttctgg
 360
 gaactgggtca tcggcgtaga gcttttcttc ctgccttta atctcatgga agcc
 414

<210> 1166
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 1166
 Trp Val Val Pro Asp Thr Xaa Asn His Val Leu Asn Arg Ile Ser Gly
 1 5 10 15
 Met Val Lys Gly Cys Phe Ser Lys Val Leu Val Glu Pro Arg Leu Leu
 20 25 30
 Lys Leu Asn Leu Thr Ile Met Cys Leu His Ile Leu Leu Met Ser Thr
 35 40 45
 Phe Val Ala Leu Pro Gly Gln Leu Ala Ala Ala Gly Phe Pro Ala Ala
 50 55 60
 Glu His Trp Lys Val Tyr Leu Val Thr Met Leu Ile Ser Phe Val Ser
 65 70 75 80
 Val Val Pro Phe Ile Ile Tyr Ala Glu Val Lys Arg Arg Met Lys Arg
 85 90 95
 Val Phe Leu Thr Cys Val Ala Leu Leu Ile Ala Glu Ile Val Leu
 100 105 110
 Trp Gly Ser Gly Pro His Phe Trp Glu Leu Val Ile Gly Val Gln Leu
 115 120 125
 Phe Phe Leu Ala Phe Asn Leu Met Glu Ala
 130 135

<210> 1167
 <211> 464
 <212> DNA
 <213> Homo sapiens

<400> 1167
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ctgttgggac cggctggcta aggcctgggc accggtagcg gcctggtgga taccctcatg
 120
 tagccgggtg acctgcctga ccatcttcgg caaaccagtg cgcagttgtg tggatgaactc
 180
 attgaccctt cgagacagtc gtgaggaacc gtcagcaagt tcgtcgatgc cgtcgtcgat
 240
 gctcttgcca gagttcggat ccttgatcgc catcgcttg acggccaccc ccgaccacgc
 300
 ccgcacgccc agggcgtagc catcggtcat cgcgtcgcgg acgatgggta ccaggtcgtg
 360
 gcattcctgc gcggtgtggc ttgcacgca tcgacgcagg aagtcagcct cgccccggga
 420
 cagggtctcc ttactaagtt ccgcggtttt ctttcccgac gcgt
 464

<210> 1168

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1168

Met	Thr	Asp	Gly	Tyr	Ala	Leu	Gly	Val	Arg	Ala	Gly	Ser	Gly	Val	Ala
1				5					10					15	
Val	Lys	Ala	Met	Ala	Ile	Lys	Asp	Pro	Asn	Ser	Gly	Lys	Ser	Ile	Asp
		20						25					30		
Asp	Gly	Ile	Asp	Glu	Leu	Ala	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Arg	Gly
		35					40					45			
Val	Asn	Glu	Phe	Thr	Thr	Gln	Leu	Arg	Thr	Gly	Leu	Pro	Lys	Met	Val
	50					55					60				
Arg	Gln	Val	Thr	Arg	Leu	His	Glu	Gly	Ile	His	Gln	Ala	Ala	Thr	Gly
65					70					75				80	
Ala	Gln	Ala	Leu	Ala	Ser	Arg	Ser	Gln	Gln	Leu	Lys	Ala	Gly	Gly	Val
			85					90						95	
Lys	Leu	Ser	Ser	Gly	Ala	Ala	Thr	Leu	Ala	His	Gly	Val	Asp		
			100					105					110		

<210> 1169

<211> 486

<212> DNA

<213> Homo sapiens

<400> 1169

nacgcgtgaa gggagcagaa cggacaccag ttactagtgg ctctgggtcgg ggacagcctc
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 ctagagcctt tctggccaat gggaacagga atagcccggg gctttctagc tgctatggac
 120
 tctgcctgga tgggtccgaag ttggtctcta ggaacgagcc ctttggaagt gctggcagag
 180
 agggaaagta ttacaggtt gctgcctcag accaccctg agaatgtgag taagaacttc
 240
 agccagtaca gtatcgaccc tgtcactcgg tatcccaata tcaacgtcaa cttcctccgg
 300
 ccaagccagg tgcgccattt atatgatact ggcgaaacaa aagatattca cctggaaatg
 360

gagagcctgg tgaattcccg aaccaccccc aaattgactc gcaatgagtc tgtagctcgt
 420
 tcaagcaaac tgctgggttg gtgccagagg cagacagatg gctatgcagg ggtaaactg
 480
 acagat
 486

<210> 1170
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1170
 Arg Glu Gln Asn Gly His Gln Leu Leu Val Ala Leu Val Gly Asp Ser
 1 5 10 15
 Leu Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Ile Ala Arg Gly Phe
 20 25 30
 Leu Ala Ala Met Asp Ser Ala Trp Met Val Arg Ser Trp Ser Leu Gly
 35 40 45
 Thr Ser Pro Leu Glu Val Leu Ala Glu Arg Glu Ser Ile Tyr Arg Leu
 50 55 60
 Leu Pro Gln Thr Thr Pro Glu Asn Val Ser Lys Asn Phe Ser Gln Tyr
 65 70 75 80
 Ser Ile Asp Pro Val Thr Arg Tyr Pro Asn Ile Asn Val Asn Phe Leu
 85 90 95
 Arg Pro Ser Gln Val Arg His Leu Tyr Asp Thr Gly Glu Thr Lys Asp
 100 105 110
 Ile His Leu Glu Met Glu Ser Leu Val Asn Ser Arg Thr Thr Pro Lys
 115 120 125
 Leu Thr Arg Asn Glu Ser Val Ala Arg Ser Ser Lys Leu Leu Gly Trp
 130 135 140
 Cys Gln Arg Gln Thr Asp Gly Tyr Ala Gly Val Asn Val Thr Asp
 145 150 155

<210> 1171
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 1171
 acgcgttcaa caaagcacag aaccggagat gcagtgggag ccgagagcag gaagcgcgga
 60
 ggcagcgcca ggtgctggcg ctgcccagagg ccccgtagca agtggggccc atagcagccg
 120
 actcgctaga ccctcccaaa acgcacacca cgcgcgacca ggaccgagag gcccgcacgg
 180
 ccctgctagg ccacaaacac tccactgtct ccagggtaaa agacaaacac agcctcgctt
 240
 gtccctccaa gagtacaacc tctgtctgat gaaaaacaaa cgaccagag agggagcagc
 300
 tgccgggaca ctgcaggctg ggcccgcgc gcccttggag ggcagggtcaa aatccccgaa
 360
 caggcacagt gttcaggctg attgactgtc ccaggccagg gcggcctcaa ctgccagagc
 420

acctcctac
429

<210> 1172
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1172
Met Gln Trp Glu Pro Arg Ala Gly Ser Ala Glu Ala Ala Pro Gly Ala
1 5 10 15
Gly Ala Ala Arg Gly Pro Val Pro Ser Gly Ala His Ser Ser Arg Leu
20 25 30
Ala Arg Pro Ser Gln Asn Ala His His Ala Arg Pro Gly Pro Arg Gly
35 40 45
Pro His Gly Pro Ala Arg Pro Gln Thr Leu His Cys Leu Gln Gly Lys
50 55 60
Arg Gln Thr Gln Pro Arg Leu Ser Leu Gln Glu Tyr Asn Leu Cys Leu
65 70 75 80
Met Lys Asn Lys Arg Pro Arg Glu Glu Ala Ala Ala Gly Thr Leu Gln
85 90 95
Ala Gly Pro Ala Ala Pro Leu Glu Gly Arg Ser Lys Ser Arg Asn Arg
100 105 110
His Ser Val Gln Ala Asp
115

<210> 1173
<211> 435
<212> DNA
<213> Homo sapiens

<400> 1173
cgcgctcaatg acgacggcga gcattctgcc gagcagggtga tgcgagccac ccgcggtgct
60
ggacttgggg ccgaggccaa gcgtcgcatc atcttgggta cctatgcctt gtcggctggg
120
tactatgacg cctactacgg ctcggtcag aaagtccgta ccctcatcca acgcgacttc
180
gagaaagcat ggcagatgtg cgatgtgctc gtgtcaccgg ccacgccaac gactgccttc
240
cggtctgggtg agcgtactgc tgaccgatg gcgatgtacc gtcctgatct atgcacggtc
300
ccggccaata tggccggaag tcccgcagga tctttccga tcggtctatc agagaccgac
360
ggcatgcccc tcggcatgca ggtgatggcg ccaatcatgg cggacgatcg aatctaccga
420
gttggggccg ctcta
435

<210> 1174
<211> 145
<212> PRT
<213> Homo sapiens

<400> 1174

Arg Val Asn Asp Asp Gly Glu His Ser Ala Glu Gln Val Met Arg Ala
 1 5 10 15
 Thr Arg Gly Ala Gly Leu Gly Ala Glu Ala Lys Arg Arg Ile Ile Leu
 20 25 30
 Gly Thr Tyr Ala Leu Ser Ala Gly Tyr Tyr Asp Ala Tyr Tyr Gly Ser
 35 40 45
 Ala Gln Lys Val Arg Thr Leu Ile Gln Arg Asp Phe Glu Lys Ala Trp
 50 55 60
 Gln Met Cys Asp Val Leu Val Ser Pro Ala Thr Pro Thr Thr Ala Phe
 65 70 75 80
 Arg Leu Gly Glu Arg Thr Ala Asp Pro Met Ala Met Tyr Arg Ser Asp
 85 90 95
 Leu Cys Thr Val Pro Ala Asn Met Ala Gly Ser Pro Ala Gly Ser Phe
 100 105 110
 Pro Ile Gly Leu Ser Glu Thr Asp Gly Met Pro Val Gly Met Gln Val
 115 120 125
 Met Ala Pro Ile Met Ala Asp Asp Arg Ile Tyr Arg Val Gly Ala Ala
 130 135 140
 Leu
 145

<210> 1175

<211> 729

<212> DNA

<213> Homo sapiens

<400> 1175

gatcgactg caatccaccc acatctactt gatatgaaaa ttggtcaagg caaatatgag
 60
 caggggttct ttccaaagtt acagtccgat gtcttgga caggaccaac cagtaacaat
 120
 cgctgggtaa gtcggagtgc cactgcacag cgcaggaaa gacgccttcg ccagcattct
 180
 gagcatgttg ggctggacaa cgacttgagg gagaaatata tgcaagaggc acgaagttaa
 240
 ggaaaaaacc tgaggcaacc caaactgtca gacctctctc ctgcagttat tgcacagacc
 300
 aactgtaaat tcgtagaagg cttattaaaa gaatgtagaa ataagacaaa gcgcattgtg
 360
 gtggagaaga tgggacatga agcgggtggaa cttggccatg gagaagcaaa catcaccggc
 420
 ctggaggaga acaccttgat cgccagcctt tgtgacctgc tggagaggat atggagccat
 480
 ggcttgcagg tcaagcaggg gaagtcggtt ttgtggtcac atttaattcc ttttcaggac
 540
 agagaagaga accaagagcc ccttgacaaa tcaccagttg ccctcggacc agaaagaaaa
 600
 aaatctgact caggagttat gttgccaacg ctcagggtct ctcttattca ggacatgagg
 660
 catattcaaa acatgagtga gatcaagact gatgttggac gagctcgggc gtggataaga
 720
 ctgtctcta
 729

<210> 1176
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 1176
 Asp Arg Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln
 1 5 10 15
 Gly Lys Tyr Glu Gln Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu
 20 25 30
 Ala Thr Gly Pro Thr Ser Asn Asn Arg Trp Val Ser Arg Ser Ala Thr
 35 40 45
 Ala Gln Arg Arg Lys Gly Arg Leu Arg Gln His Ser Glu His Val Gly
 50 55 60
 Leu Asp Asn Asp Leu Arg Glu Lys Tyr Met Gln Glu Ala Arg Ser Leu
 65 70 75 80
 Gly Lys Asn Leu Arg Gln Pro Lys Leu Ser Asp Leu Ser Pro Ala Val
 85 90 95
 Ile Ala Gln Thr Asn Cys Lys Phe Val Glu Gly Leu Leu Lys Glu Cys
 100 105 110
 Arg Asn Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly His Glu Ala
 115 120 125
 Val Glu Leu Gly His Gly Glu Ala Asn Ile Thr Gly Leu Glu Glu Asn
 130 135 140
 Thr Leu Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His
 145 150 155 160
 Gly Leu Gln Val Lys Gln Gly Lys Ser Val Leu Trp Ser His Leu Ile
 165 170 175
 Pro Phe Gln Asp Arg Glu Glu Asn Gln Glu Pro Leu Ala Glu Ser Pro
 180 185 190
 Val Ala Leu Gly Pro Glu Arg Lys Lys Ser Asp Ser Gly Val Met Leu
 195 200 205
 Pro Thr Leu Arg Val Ser Leu Ile Gln Asp Met Arg His Ile Gln Asn
 210 215 220
 Met Ser Glu Ile Lys Thr Asp Val Gly Arg Ala Arg Ala Trp Ile Arg
 225 230 235 240
 Leu Ser Leu

<210> 1177
 <211> 581
 <212> DNA
 <213> Homo sapiens

<400> 1177
 acgcgtgatg agttgcgcga gaccagcaac tgcagccgaa tacagttttc ttgtgtaccc
 60
 cgctgcacag ctgcgagagg tgggcattgc cgagtgaggc aacgatgtct aaggcggaaa
 120
 gctcatcctc ggcagacggg aagactttgt cgtcggggat gttgtcaatg agagcgggga
 180
 cgtcgatctc ggtactgcc atggcgtcat gaaggatcgc gcgatacggg ggcacgaccc
 240

cgatgagggc gtcgtcgaat ccagcgatga tcgatacctc tctcggtagc acgtccgtgg
 300
 ccaacagggtg gtcgacttgg gcggggggcta gccatgtaat tgttccgagc acatggaggg
 360
 tggctgccag gaggcggatg gccggttctg gggcatcttt ggagatcttc agccggacat
 420
 cagtgggcag tccggccggg acttggcaga gggcctgggc gggatgggag cgctgggcga
 480
 cgacgaaacg ccccgacgcc gtaacgccgt gggcttggag atcgcaggtc cacttctctg
 540
 ggctttcacc ggcagagatc atggtgtgga ccaccattgt g
 581

<210> 1178
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 1178
 Met Val Val His Thr Met Ile Ser Ala Gly Glu Ser Pro Glu Lys Trp
 1 5 10 15
 Thr Cys Asp Leu Gln Ala His Gly Val Thr Ala Ser Gly Arg Phe Val
 20 25 30
 Val Ala Gln Arg Ser His Pro Ala Gln Ala Leu Cys Gln Val Pro Ala
 35 40 45
 Gly Leu Pro Thr Asp Val Arg Leu Lys Ile Ser Lys Asp Ala Pro Glu
 50 55 60
 Pro Ala Ile Arg Leu Leu Ala Ala Thr Leu His Val Leu Gly Thr Ile
 65 70 75 80
 Thr Trp Leu Ala Pro Ala Gln Val Asp His Leu Leu Ala Thr Asp Val
 85 90 95
 Leu Pro Arg Glu Val Ser Ile Ile Ala Gly Phe Asp Asp Ala Leu Ile
 100 105 110
 Gly Val Val Ala Pro Tyr Arg Ala Ile Leu His Asp Ala Met Gly Ser
 115 120 125
 Thr Glu Ile Asp Val Pro Ala Leu Ile Asp Asn Ile Pro Asp Asp Lys
 130 135 140
 Val Phe Pro Ser Ala Glu Asp Glu Leu Ser Ala Leu Asp Ile Val Ala
 145 150 155 160
 Ser Leu Gly Asn Ala His Leu Ser Gln Leu Cys Asp Gly Val His Lys
 165 170 175
 Lys Thr Val Phe Gly Cys Ser Cys Trp Ser Arg Ala Thr His His Ala
 180 185 190

<210> 1179
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 1179
 gtgcactttc tggcttctaa ctgtggcccc agccctgact ccttgagggtg ctctgtgct
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 gattggggct tctggacatg ctgccacaag atgtctggaa actccagggg gcacctgccg
 120

agaccctgcc ctgggaacgg ccggaagaat cccaaaacat gagattccgg tgcagctgag
 180
 ccccgccaat tcattgtctc ttccagtcct ttctgaaggc tgcatttggc aatgtgaccc
 240
 tcggggtggg gaaggcatca gaggaatata ggctatggga cgccagaggc agcgtcctgg
 300
 ggacaaagcc cacttcttcc catgcccagg gcttctcat ggacccagca tgggtggacgt
 360
 ggccctcaga cgtccatggg tgggtggggga ggcaagtgt gtttggccct gtctctgctc
 420
 agagtctcat aggaagatgc atggtccaca caacagttag tcggcagggg gtccaggctt
 480
 cccctcccaa ccagtgggtg tgagacgctt gggtttataac ccaagatccc ttgtccatt
 540
 ggtgcctcct gaatctccca cctcccgcgg cacctgcatg gcctctacct gacgcgt
 597

<210> 1180

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1180

Met	Gly	Arg	Gln	Arg	Gln	Arg	Pro	Gly	Asp	Lys	Ala	His	Phe	Phe	Pro
1				5					10					15	
Cys	Pro	Gly	Leu	Pro	His	Gly	Pro	Ser	Met	Val	Asp	Val	Ala	Leu	Arg
			20					25					30		
Arg	Pro	Trp	Val	Val	Gly	Glu	Ala	Arg	Ala	Val	Trp	Pro	Cys	Leu	Cys
		35					40					45			
Ser	Glu	Ser	His	Arg	Lys	Met	His	Gly	Pro	His	Asn	Ser	Glu	Ser	Ala
	50					55				60					
Gly	Ser	Pro	Gly	Phe	Pro	Ser	Gln	Pro	Val	Val	Leu	Arg	Arg	Leu	Val
65					70					75				80	
Tyr	Asn	Pro	Arg	Ser	Leu	Val	Pro	Leu	Val	Pro	Pro	Glu	Ser	Pro	Thr
			85					90						95	
Ser	Arg	Gly	Thr	Cys	Met	Ala	Ser	Thr							
			100					105							

<210> 1181

<211> 352

<212> DNA

<213> Homo sapiens

<400> 1181

gtcgactacc tcgatgtttc cccgcgtcag atggtctccg tggctactgc catgattccg
 60
 ttctctgagc acgacgacgc taaccgtgcc ctgatgggtg cgaacatgca gcgtcagget
 120
 gtgccgtgc tgcgttcgga ggctccgttc gtcggtaccg gtatggagca gcgtgctgct
 180
 tacgacgccg gcgatgtcat tgctcgcttcg gccacagggtg tggctcgagac cgtgtcggca
 240
 ggcttcatca ccatcatgga cgatgagggc cagcgccaca cctacctgct gcgcaagttc
 300

gagcgcacca accagggcac ctgctacaac cagaagccac tgttgacgag gg
352

<210> 1182
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1182
Val Asp Tyr Leu Asp Val Ser Pro Arg Gln Met Val Ser Val Ala Thr
1 5 10 15
Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met
20 25 30
Gly Ala Asn Met Gln Arg Gln Ala Val Pro Leu Leu Arg Ser Glu Ala
35 40 45
Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly
50 55 60
Asp Val Ile Val Ala Ser Ala Thr Gly Val Val Glu Thr Val Ser Ala
65 70 75 80
Gly Phe Ile Thr Ile Met Asp Asp Glu Gly Gln Arg His Thr Tyr Leu
85 90 95
Leu Arg Lys Phe Glu Arg Thr Asn Gln Gly Thr Cys Tyr Asn Gln Lys
100 105 110
Pro Leu Leu Thr Arg
115

<210> 1183
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1183
gatccttctg ggcgctggtc caagcgctg gtgaggccgt cctctcctgc agaaccgccg
60
cctcttcgcc cctgcccgt cacctgttct gtctgctca cctcctccag gaagcctgcc
120
tggccttctc catgctgatg ggcgtggccc ttgtccctgc agccatgcat tgacctccgt
180
ggctcctgga ggccaggcca cgtctcatc ccctctgggt gaggagagg cacagcctgg
240
gtgcgtgggg ccgtggcggc tccgaggcgc caccgctgtg tcctctcatg agtgggtgcc
300
gtccagggtct gtctggggt ggctgcgagg aggaggttgg cctcgcgcgg ccatgtgcgt
360
gacagtggag acatcgccag cctcctgctt gcacagctga cggcagcccc tctctctcca
420
gccatgtccc ca
432

<210> 1184
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1184

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Met Ala Gly Glu Arg Gly Ala Ala Val Ser Cys Ala Ser Arg Arg Leu
 1           5           10           15
Ala Met Ser Pro Leu Ser Arg Thr Trp Pro Arg Glu Ala Asn Leu Leu
      20           25           30
Leu Ala Ala Ser Pro Gly Gln Thr Trp Thr Ala Pro Thr His Glu Arg
      35           40           45
Thr Gln Arg Trp Arg Leu Gly Ala Ala Thr Ala Pro Arg Thr Gln Ala
      50           55           60
Val Pro Leu Thr His Pro Glu Gly Met Arg Thr Trp Pro Gly Leu Gln
      65           70           75           80
Glu Pro Arg Arg Ser Met His Gly Cys Arg Asp Lys Gly His Ala His
      85           90           95
Gln His Gly Glu Gly Gln Ala Gly Phe Leu Glu Glu Val Ser Arg Thr
      100           105           110
Glu Gln Val Ser Gly Gln Gly Arg Arg Gly Arg Gly Ser Ala Gly Glu
      115           120           125
Asp Gly Leu Thr Thr Arg Leu Asp Gln Arg Pro Glu Gly
      130           135           140

```

<210> 1185

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1185

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accggtgaat ttggccttaa cagcgatgga actcctggcc catcttatga acctggcatg
60
gaattacgcg gcaaatatgt attgttgggt gaagggtgac ggggctctct atctaaacaa
120
gtcatcaata aataccaatt atccgagggt catgaaccac aaaagttcgg ccttggctta
180
aaagaaatctt gggaaataga cccagaaaaa cacaaagaag gcagagtcag tcataccatg
240
ggctggccat taaatggcaa tgctggcggc ggttctttta tttatcatgc agaaaacaat
300
caagtcttta tcggctttgt ggtgcatctt aattacgcca acccttacct atccccctac
360
caagaatttc aacgctttta acaccatccg attatcgagg agctattaac tggcggtaaa
420
cgc
423

```

<210> 1186

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1186

```

Thr Gly Glu Phe Gly Leu Asn Ser Asp Gly Thr Pro Gly Pro Ser Tyr
 1           5           10           15
Glu Pro Gly Met Glu Leu Arg Gly Lys Tyr Val Leu Leu Gly Glu Gly
      20           25           30
Val Arg Gly Ser Leu Ser Lys Gln Val Ile Asn Lys Tyr Gln Leu Ser

```

```

      35              40              45
Glu Gly His Glu Pro Gln Lys Phe Gly Leu Gly Leu Lys Glu Ile Trp
      50              55              60
Glu Ile Asp Pro Glu Lys His Lys Glu Gly Arg Val Ser His Thr Met
65              70              75              80
Gly Trp Pro Leu Asn Gly Asn Ala Gly Gly Gly Ser Phe Ile Tyr His
      85              90              95
Ala Glu Asn Asn Gln Val Phe Ile Gly Phe Val Val His Leu Asn Tyr
      100             105             110
Ala Asn Pro Tyr Leu Ser Pro Tyr Gln Glu Phe Gln Arg Phe Lys His
      115             120             125
His Pro Ile Ile Ala Glu Leu Leu Thr Gly Gly Lys Arg
      130             135             140

```

<210> 1187

<211> 387

<212> DNA

<213> Homo sapiens

<400> 1187

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acgcgtgctg gtgagtttaa attgaatgct gatggtaatt tggtagacgaa ttcaggggct
60
aagggtccagg gctataatgc aatagatggc atagtcggtg ggaacttaga agatatggta
120
gtaccactg ctcgaatttc tctcaagca acatcaagtg ttgatttaaa agtgaatctt
180
aattccgaag gtgaggatgt gccgccttat attcgagcgg actttgatcc agccaatcca
240
gatacttatg actatactca gacccaaacg gttgcggatg ggagtggtaa taatcattta
300
attagttatt actatgctaa aagtgatgta gcaaatacct atcaggttta tgccacggta
360
gatgggaagt cgactgatga taccggt
387

```

<210> 1188

<211> 129

<212> PRT

<213> Homo sapiens

<400> 1188

```

Thr Arg Ala Gly Glu Phe Lys Leu Asn Ala Asp Gly Asn Leu Val Thr
  1              5              10              15
Asn Ser Gly Ala Lys Val Gln Gly Tyr Asn Ala Ile Asp Gly Ile Val
      20              25              30
Gly Gly Asn Leu Glu Asp Met Val Val Pro Thr Ala Arg Ile Ser Pro
      35              40              45
Gln Ala Thr Ser Ser Val Asp Leu Lys Val Asn Leu Asn Ser Glu Gly
      50              55              60
Glu Asp Val Pro Pro Tyr Ile Arg Ala Asp Phe Asp Pro Ala Asn Pro
65              70              75              80
Asp Thr Tyr Asp Tyr Thr Gln Thr Gln Thr Val Ala Asp Gly Ser Gly
      85              90              95
Asn Asn His Leu Ile Ser Tyr Tyr Tyr Ala Lys Ser Asp Val Ala Asn

```

	100		105		110										
Thr	Tyr	Gln	Val	Tyr	Ala	Thr	Val	Asp	Gly	Lys	Ser	Thr	Asp	Asp	Thr
	115		120		125										
Gly															

<210> 1189
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1189
 tcgatcgccg accgcccggg ccttgccccc ggcgatgatcg gtggcctggt ggccagcacc
 60
 ctgggtgctg gtttcattgg cggcatcggt gcaggttttc tggccgggta cagcgccaag
 120
 gccattgccc gctgggcacg gctgcccagc agcctggatg cgctcaaacc gattctgatc
 180
 atttcgctgc tggccagcct gttcactggg ttggtgatga tctacgtggt cggccagccg
 240
 gtggcgggcca tgctcggagg cctgacacac tttctcgaca gcatgggtac caccaacgcc
 300
 attctcctgg gcntgttgct cggcggctag
 330

<210> 1190
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1190
 Ser Ile Ala Asp Arg Pro Gly Leu Ala Pro Gly Met Ile Gly Gly Leu
 1 5 10 15
 Leu Ala Ser Thr Leu Gly Ala Gly Phe Ile Gly Gly Ile Val Ala Gly
 20 25 30
 Phe Leu Ala Gly Tyr Ser Ala Lys Ala Ile Ala Arg Trp Ala Arg Leu
 35 40 45
 Pro Ser Ser Leu Asp Ala Leu Lys Pro Ile Leu Ile Ile Ser Leu Leu
 50 55 60
 Ala Ser Leu Phe Thr Gly Leu Val Met Ile Tyr Val Val Gly Gln Pro
 65 70 75 80
 Val Ala Ala Met Leu Gly Gly Leu Thr His Phe Leu Asp Ser Met Gly
 85 90 95
 Thr Thr Asn Ala Ile Leu Leu Gly Xaa Leu Leu Gly Gly
 100 105

<210> 1191
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1191
 cggccgacga tgtgcggtga gcaagagatt tggagagcca tgatgacgtc agcagacaaa
 60

gcagggacta acggacagac catgcagaca ccgccggtgg tgtcgccgca ggactgggag
 120
 gcagcccgtc agcaactgct cgtgaaggaa aaggcgcata cccgtgcccg cgacgcactc
 180
 gccgccgaac ggaggcgcat gccgtggatg gaagtgacaa aaacctacgc attcgaggcg
 240
 ccctcggggca aggccagtct gctcgatctg ttccagggcc ggaagcagct gatcctgtac
 300
 cgggccttct tcgagccggg cgtgttcggc tggcccgacc atgcctgccg c
 351

<210> 1192
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1192
 Met Cys Gly Glu Gln Glu Ile Trp Arg Ala Met Met Thr Ser Ala Asp
 1 5 10 15
 Lys Ala Gly Thr Asn Gly Gln Thr Met Gln Thr Pro Pro Val Val Ser
 20 25 30
 Pro Gln Asp Trp Glu Ala Ala Arg Gln Gln Leu Leu Val Lys Glu Lys
 35 40 45
 Ala His Thr Arg Ala Arg Asp Ala Leu Ala Ala Glu Arg Arg Arg Met
 50 55 60
 Pro Trp Met Glu Val Thr Lys Thr Tyr Ala Phe Glu Ala Pro Ser Gly
 65 70 75 80
 Lys Ala Ser Leu Leu Asp Leu Phe Gln Gly Arg Lys Gln Leu Ile Leu
 85 90 95
 Tyr Arg Ala Phe Phe Glu Pro Gly Val Phe Gly Trp Pro Asp His Ala
 100 105 110
 Cys Arg

<210> 1193
 <211> 722
 <212> DNA
 <213> Homo sapiens

<400> 1193
 ggatcccagc ctccagatcc catcttgtag ctcttctttc tctacactna ggttgctccc
 60
 cgacttagga cgcccagttt gtactcagtg tttgctcttt tatggcagag cctctgcact
 120
 cccagcctcc tggccccttc tgtacatgat ttcccttggt gccactccat gcatttttct
 180
 tggctcagga cttagtgggc ctccatggga cttggtacct ctacttggtc ccttctggaa
 240
 tctgtaactt tgtgttcccc accattcttt cctttatgaa ccgatggtgc aacagcatga
 300
 ctacctgaaa ttcttagtca ctcccagctg ctttagtgga gggaaaatgc ccacagcaca
 360
 ggaaatagtc ctgcccttcg agagaggcca ggggatggga gcgtgtccag agaagggcga
 420

tgggttgatg aagggtggcc acagcgcccg ggaggaaggg gccagaacgc tctctgttct
 480
 gttccatgag gaggattatg ttggtgtgtg tagtcccctg gttcagagtt gtccagaaat
 540
 agtctagtgt aaggaacaat tttccaaaga tcaaaagagc tgtctcaaga tagcagtgcg
 600
 ttcccagccc ctacaggtgt atacagcaca aaggaggagg ccccttagtg tggctgtcac
 660
 agaggggaagt ggacgtcctg tggtttgacc ccaccagatg gctttagaga tctgggccccg
 720
 ag
 722

<210> 1194
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1194
 Met Val Gln Gln His Asp Tyr Leu Lys Phe Leu Val Thr Pro Ser Cys
 1 5 10 15
 Phe Ser Gly Gly Lys Met Pro Thr Ala Gln Glu Ile Val Leu Pro Phe
 20 25 30
 Glu Arg Gly Gln Gly Met Gly Ala Cys Pro Glu Lys Gly Asp Gly Leu
 35 40 45
 Met Lys Gly Gly His Ser Ala Arg Glu Glu Gly Ala Arg Thr Leu Ser
 50 55 60
 Val Leu Phe His Glu Glu Asp Tyr Val Gly Val Cys Ser Pro Leu Val
 65 70 75 80
 Gln Ser Cys Pro Glu Ile Ala Gln Cys Lys Glu Gln Phe Ser Lys Asp
 85 90 95
 Gln Lys Ser Cys Leu Lys Ile Ala Val Arg Ser Gln Pro Leu Gln Val
 100 105 110
 Tyr Thr Ala Gln Arg Glu Gly Pro Pro Ser Val Ala Val Thr Glu Gly
 115 120 125
 Ser Gly Arg Pro Val Val
 130

<210> 1195
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 1195
 tctagagcat gatattccgc gggcgcggcc ggggtggactt tggttcgaga gtggaactaa
 60
 gtgagtaatg ggggcgggcg gccagacgc gctcccagcc tcctggcgag agtgctgccc
 120
 gggtttcccg gggcacggga gtgtgtctag gaggggaggg caggatcctt cctcgagtcc
 180
 tgtctgaac aaaagaaaac gaggtgggtg gtgcttgaac ggccctgttt actctgcaga
 240
 tagccgaact ggtaggactc cggcgcgccc tatttatctt gattggctct gcctgaaggc
 300

aagcgttaat cccgtccaac ctgtatcact gcgaagagct cgttcgggag cgctttttgg
 360
 aaatgcagat tcttagcccc caccagatc t
 391

<210> 1196
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1196
 Met Gly Ala Ala Arg Pro Asp Ala Leu Pro Ala Ser Trp Arg Glu Cys
 1 5 10 15
 Cys Pro Val Ser Arg Gly His Gly Ser Val Ser Arg Arg Gly Gly Gln
 20 25 30
 Asp Pro Ser Ser Ser Pro Val Leu Asn Lys Arg Lys Arg Gly Gly Trp
 35 40 45
 Cys Leu Asn Gly Pro Val Tyr Ser Ala Asp Ser Arg Thr Gly Arg Thr
 50 55 60
 Pro Ala Arg Pro Ile Tyr Leu Asp Trp Leu Cys Leu Lys Ala Ser Val
 65 70 75 80
 Asn Pro Val Gln Pro Val Ser Leu Arg Arg Ala Arg Ser Gly Ala Leu
 85 90 95
 Phe Gly Asn Ala Asp Ser
 100

<210> 1197
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 1197
 acgcgtgatg atcatgaaaa tggtagacag cgtctagcag aagtcgcctc tgtgatgggc
 60
 tggcagcaag atgaaatcat cgtaaactga caaggggatg aaccctttct gcctgttgca
 120
 cttattcatg ccacgggttaa agcgtagcc gatgatgctg aatctgaaat ggccacgatt
 180
 gcctgtgcga ttgataacgt agcagagctg tttaacccaa atgtagttaa agtcggttgt
 240
 gatgaaaaac agcgcgcctt gtatttcagt cgtgcgcta tgccatggga ccgtaatggt
 300
 tttatggaaa aaacagacga tcaagcgta ccagcggatt ttctgcgtt gcgtcatatt
 360
 ggtccgatg tttaccgcac gacatn
 386

<210> 1198
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1198
 Thr Arg Asp Asp His Glu Asn Gly Thr Glu Arg Leu Ala Glu Val Ala

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      1           5           10           15
Ser Val Met Gly Trp Gln Gln Asp Glu Ile Ile Val Asn Val Gln Gly
      20           25           30
Asp Glu Pro Phe Leu Pro Val Ala Leu Ile His Ala Thr Val Lys Ala
      35           40           45
Leu Ala Asp Asp Ala Glu Ser Glu Met Ala Thr Ile Ala Cys Ala Ile
      50           55           60
Asp Asn Val Ala Glu Leu Phe Asn Pro Asn Val Val Lys Val Val Cys
      65           70           75           80
Asp Glu Lys Gln Arg Ala Leu Tyr Phe Ser Arg Ala Pro Met Pro Trp
      85           90           95
Asp Arg Asn Gly Phe Met Glu Lys Thr Asp Asp Gln Ala Leu Pro Ala
      100           105           110
Asp Phe Pro Ala Leu Arg His Ile Gly Pro Tyr Val Tyr Arg Thr Thr
      115           120           125

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<210> 1199

<211> 318

<212> DNA

<213> Homo sapiens

<400> 1199

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acgcgttcag cgctcatgtac agccccgggc cgggtcaattt gatgggcctc aatgccgggc
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ttacggggcaa attgcgtcgc tccagcgggtt tctacatcgg cgtgggggtgc gcgatgctgc
120
tgatgggtcgg gctggttggg ctacccggcg aagcgatcat ctcccaggcg gcgctgccgt
180
atatttcttt gattggcggg gtgtacacgc tgtacctcgc ctaccagggtg ttcaccgcac
240
gtaccgaagt ggatgacgcc ccaagcgcg ctgccaagac cttgaccttc tggaatggcc
300
tggtgatcca gttgctcc
318

```

<210> 1200

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1200

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Met Tyr Ser Pro Gly Pro Val Asn Leu Met Gly Leu Asn Ala Gly Leu
      1           5           10           15
Thr Gly Lys Leu Arg Arg Ser Ser Gly Phe Tyr Ile Gly Val Gly Cys
      20           25           30
Ala Met Leu Leu Met Val Gly Leu Val Gly Leu Thr Gly Glu Ala Ile
      35           40           45
Ile Ser Gln Ala Ala Leu Pro Tyr Ile Ser Leu Ile Gly Gly Val Tyr
      50           55           60
Thr Leu Tyr Leu Ala Tyr Gln Val Phe Thr Ala Arg Thr Glu Val Asp
      65           70           75           80
Asp Ala Pro Ser Ala Pro Ala Lys Thr Leu Thr Phe Trp Asn Gly Leu
      85           90           95
Val Ile Gln Leu Leu

```

100

<210> 1201

<211> 360

<212> DNA

<213> Homo sapiens

<400> 1201

gtcgaacgcac aactccagct ggctcgtccc aacagcccca acatccccct ttatcgcgat
60
atgatacctca ccgtgctgcg catggccaag gatgaccgca accgttggaa tgcaaaaatc
120
acgctgcagg cgatccgcga gctggataac gccttccgcg tgctggaaca gttcaagggc
180
cgccgcaagg tcacgggtgtt tggtcggcg cgacgcccgc tcgaaagccc gctgtacgcc
240
ttggcaaggg aagtcggcac gctgctggcg caatccgacc tgatggtgat caccggcggt
300
ggcggcgggca tcatggccgc tgcccacgag ggcgcaaggt ctggaacaca gcctgggggt
360

<210> 1202

<211> 120

<212> PRT

<213> Homo sapiens

<400> 1202

Val	Asp	Ala	Gln	Leu	Gln	Leu	Val	Ala	Pro	Asn	Ser	Pro	Asn	Ile	Pro
1			5					10					15		
Leu	Tyr	Arg	Asp	Met	Ile	Leu	Thr	Val	Leu	Arg	Met	Ala	Lys	Asp	Asp
			20					25					30		
Arg	Asn	Arg	Trp	Asn	Ala	Lys	Ile	Thr	Leu	Gln	Ala	Ile	Arg	Glu	Leu
			35				40					45			
Asp	Asn	Ala	Phe	Arg	Val	Leu	Glu	Gln	Phe	Lys	Gly	Arg	Arg	Lys	Val
			50			55					60				
Thr	Val	Phe	Gly	Ser	Ala	Arg	Thr	Pro	Val	Glu	Ser	Pro	Leu	Tyr	Ala
65					70					75				80	
Leu	Ala	Arg	Glu	Val	Gly	Thr	Leu	Leu	Ala	Gln	Ser	Asp	Leu	Met	Val
			85						90					95	
Ile	Thr	Gly	Gly	Gly	Gly	Gly	Ile	Met	Ala	Ala	Ala	His	Glu	Gly	Ala
			100					105					110		
Arg	Ser	Gly	Thr	Gln	Pro	Gly	Gly								
			115				120								

<210> 1203

<211> 477

<212> DNA

<213> Homo sapiens

<400> 1203

ccggatatgg cagctcgact tcattcgacc agagttcttg gaacatttgg ctatcatgca
60
cctgagtatg caatgactgg acaacttagc tctaagagtg acgtttacag ttttggagtt
120

ggtcttctcg agctcctgac tggaagaaag cctgtggatc ttccattacc aagaggacag
 180
 caaagtcttg tgacatgggc aactccacgg ctttgtgaag ataaagttag gcaatgcggt
 240
 gattcaagac ttggagtaga atatcctcct aaatccggtg caaagtttgc agctgttgct
 300
 gcactgtgtg tgcaatatga agctgacttt cgacccaaca tgagcatcgt ggtgaaggcg
 360
 cttcagcccc tgctgaatgc acgtgcatcc aacaaccctg gatgaatgaa tgaatgactg
 420
 ccgttgcttt tccctgacga gagtatctga atcagacaat catgtagcat tgaattc
 477

```
<210> 1204
<211> 134
<212> PRT
<213> Homo sapiens
```

```
<400> 1204
Pro Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Thr Phe
  1                      5              10                15
Gly Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Ser Ser Lys
          20                  25                    30
Ser Asp Val Tyr Ser Phe Gly Val Gly Leu Leu Glu Leu Leu Thr Gly
        35              40                45
Arg Lys Pro Val Asp Leu Pro Leu Pro Arg Gly Gln Gln Ser Leu Val
      50            55              60
Thr Trp Ala Thr Pro Arg Leu Cys Glu Asp Lys Val Arg Gln Cys Val
65           70             75               80
Asp Ser Arg Leu Gly Val Glu Tyr Pro Pro Lys Ser Val Ala Lys Phe
          85              90                95
Ala Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ala Asp Phe Arg Pro
         100            105              110
Asn Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Asn Ala Arg
       115           120             125
Ala Ser Asn Asn Pro Gly
    130
```

```
<210> 1205
<211> 407
<212> DNA
<213> Homo sapiens
```

```
<400> 1205
acgcgttgcc attgaagact ggcaattaca cgatttacac atcattgatg ctgcagttga
60
tgtgcacagg gaaacactag ctaccgtgca gcaggaaatg atggggagaaa tcagccatgg
120
taacaagaac caagccatcc tggacacaga cggccgggggt tgtgcgaacg gaacgttagt
180
ctatcaatgt gttgcggaac gattcaaggg atgctggccc ccccatcac ttgcccattc
240
aagatgtgga gggaatctgt ctgctgcagaa cctggatctc gtggttgtac gacgttgtcc
300
```

cctttctcgct cggacgccgc tcatgctccg ccacgtcgct gagcgagtga caaggatatcc
 360
 tgggaccatg cgtatggttt caactgaagc gctggcgaat cgtaaan
 407

<210> 1206
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1206
 Met Met Gly Glu Ile Ser His Gly Asn Lys Asn Gln Ala Ile Leu Asp
 1 5 10 15
 Thr Asp Gly Arg Gly Cys Ala Asn Gly Thr Leu Val Tyr Gln Cys Val
 20 25 30
 Ala Glu Arg Phe Lys Gly Cys Trp Pro Pro Pro Ser Leu Ala Gln Ser
 35 40 45
 Arg Cys Gly Gly Asn Leu Ser Ala Gln Asn Leu Asp Leu Val Val Val
 50 55 60
 Arg Arg Cys Pro Leu Leu Ala Arg Thr Pro Leu Met Leu Arg His Val
 65 70 75 80
 Ala Glu Arg Val Thr Arg Tyr Pro Gly Thr Met Arg Met Val Ser Thr
 85 90 95
 Glu Ala Leu Ala Asn Arg Lys
 100

<210> 1207
 <211> 292
 <212> DNA
 <213> Homo sapiens

<400> 1207
 gctagcatgt cacttttttc ttcagtagat ggactggag agacattgca ggatgaagag
 60
 gcttgcccttc attcctatgt gctttcccg tcttgcttct ccagccatgt gtgggacaac
 120
 caggggtgct caccacctag tgagtttcag ggacactcca catgtcccag caagtcttat
 180
 cagcatctta gctggcttct caacaagact cagtggcacc cctgtggatg tctcccatca
 240
 agtttcatta gtgccccagg gggagactcc cagaaagttt cagcagcacc ac
 292

<210> 1208
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 1208
 Met Ser Leu Phe Ser Ser Val Asp Gly Thr Gly Glu Thr Leu Gln Asp
 1 5 10 15
 Glu Glu Ala Cys Leu His Ser Tyr Val Leu Ser Arg Pro Cys Phe Ser
 20 25 30
 Ser His Val Trp Asp Asn Gln Gly Cys Ser Pro Pro Ser Glu Phe Gln

```

      35              40              45
Gly His Ser Thr Cys Pro Ser Lys Ser Tyr Gln His Leu Ser Trp Leu
  50              55              60
Leu Asn Lys Thr Gln Trp His Pro Cys Gly Cys Leu Pro Ser Ser Phe
  65              70              75              80
Ile Ser Ala Pro Gly Gly Asp Ser Gln Lys Val Ser Ala Ala Pro
      85              90              95

```

<210> 1209
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 1209
 ttggttccta taatggcggg agcttacatt tttgctggta tcattatttt gttaatgcat
 60
 gccagtgaag ttattccggc aatatcaact attgtcgagt atgcctttac gccagcttct
 120
 gcgcagggtg gttttgctgg tgcaacggta tggatggcga ttcgttttgg tgttgcccg
 180
 ggtgtatttt caaatgaggc aggtttaggt tcggcgccga tcgctcatgc cagtgcacaa
 240
 actaatgaac cggttcgcca agggttggtg gcgatgtag gtactttcct tgatacactt
 300
 attatttgta caggtttagt gattgttatt tctggtgctt ggacagaagg attgtcgggt
 360
 gctgcgtaaa catctgctgc atttaatctg gcgttacctg gttggggggg atacttagtc
 420
 gctatcagct g
 431

<210> 1210
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 1210
 Leu Val Pro Ile Met Ala Val Ala Tyr Ile Phe Ala Gly Ile Ile Ile
 1 5 10 15
 Leu Leu Met His Ala Ser Glu Val Ile Pro Ala Ile Ser Thr Ile Val
 20 25 30
 Glu Tyr Ala Phe Thr Pro Ala Ser Ala Gln Gly Gly Phe Ala Gly Ala
 35 40 45
 Thr Val Trp Met Ala Ile Arg Phe Gly Val Ala Arg Gly Val Phe Ser
 50 55 60
 Asn Glu Ala Gly Leu Gly Ser Ala Pro Ile Ala His Ala Ser Ala Gln
 65 70 75 80
 Thr Asn Glu Pro Val Arg Gln Gly Leu Val Ala Met Leu Gly Thr Phe
 85 90 95
 Leu Asp Thr Leu Ile Ile Cys Thr Gly Leu Val Ile Val Ile Ser Gly
 100 105 110
 Ala Trp Thr Glu Gly Leu Ser Gly Ala Ala Leu Thr Ser Ala Ala Phe
 115 120 125
 Asn Leu Ala Leu Pro Gly Trp Gly Gly Tyr Leu Val Ala Ile Ser

130

135

140

<210> 1211

<211> 480

<212> DNA

<213> Homo sapiens

<400> 1211

gaggagggac gagaggctgg tgagatggag tccagcacc tgcaggagag ccccagggcc
 60
 agagccgaag ctgtgcttct ccatgagatg gatgaagatg atctggccaa tgcctgatc
 120
 tggcctgaga ttcaacagga gctgaaaatc attgaatctg aggaggagct ctcatcggtg
 180
 ccacctcctg ctctgaagac cagcccaatt cagcctattc tcgagtcgag tctggggccc
 240
 tttattccct cagagcctcc tgggagcttg ccttggtggt ccttcctgc tccagtctcc
 300
 acccctctgg aggtgtggac tagggatcca gccaatcaga gcacacaggg ggcttcaca
 360
 gcagccagca gagagaagcc ggaacctgag cagggcctgc acccagacct cgccagcctg
 420
 gctcctctgg aaatagttcc ttttgagaag gcattctccag aggctggagt gtgctcgca
 480

<210> 1212

<211> 160

<212> PRT

<213> Homo sapiens

<400> 1212

Glu	Glu	Gly	Arg	Glu	Ala	Gly	Glu	Met	Glu	Ser	Ser	Thr	Leu	Gln	Glu
1				5				10						15	
Ser	Pro	Arg	Ala	Arg	Ala	Glu	Ala	Val	Leu	Leu	His	Glu	Met	Asp	Glu
		20						25					30		
Asp	Asp	Leu	Ala	Asn	Ala	Leu	Ile	Trp	Pro	Glu	Ile	Gln	Gln	Glu	Leu
		35					40					45			
Lys	Ile	Ile	Glu	Ser	Glu	Glu	Glu	Leu	Ser	Ser	Leu	Pro	Pro	Pro	Ala
	50					55					60				
Leu	Lys	Thr	Ser	Pro	Ile	Gln	Pro	Ile	Leu	Glu	Ser	Ser	Leu	Gly	Pro
65					70					75				80	
Phe	Ile	Pro	Ser	Glu	Pro	Pro	Gly	Ser	Leu	Pro	Cys	Gly	Ser	Phe	Pro
			85					90						95	
Ala	Pro	Val	Ser	Thr	Pro	Leu	Glu	Val	Trp	Thr	Arg	Asp	Pro	Ala	Asn
			100					105					110		
Gln	Ser	Thr	Gln	Gly	Ala	Ser	Thr	Ala	Ala	Ser	Arg	Glu	Lys	Pro	Glu
		115					120					125			
Pro	Glu	Gln	Gly	Leu	His	Pro	Asp	Leu	Ala	Ser	Leu	Ala	Pro	Leu	Glu
	130					135					140				
Ile	Val	Pro	Phe	Glu	Lys	Ala	Ser	Pro	Glu	Ala	Gly	Val	Cys	Ser	Arg
145					150					155				160	

<210> 1213

<211> 1141

<212> DNA

<213> Homo sapiens

<400> 1213

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nntcatgatg gcggcctggt gtgtgggtat gtccacgatg ggcgcgtcac gcgtgtcgcc
60
cgtgatgctc aggggcgggt taccgggata gaggggcat cagggcggtg gagttacggc
120
tacaacgagg ctgggtcact catcagcgcg acggggcccc gcacacaaca taactggact
180
cacgacgcct atggccgggt caccagccac gccacatccg gaaccgacac caccttcgcc
240
tgggaccagg aaggccacct ggcgagacg tgtacgcgtg cacacgggca tgccactgcc
300
accagtatc gctatgacgc agcgggacgg cgcgtcagtg cgaccagctc agacggccag
360
gaggagcgtt actcctggga tggacggggt tggtgtctg acatcaccac cgacgccacg
420
accgtatcga ctacgctga tgcattgggg cgcgccagtc gtatcaccac taaggggcag
480
caggtacgag tggactggga cctcgtgacc ggagccccca cctcgattga tggtcgtcct
540
gtgcttcccc tggccggagg acgcatcctc ggcgccacac ccacggcgga taccaacctc
600
tggcgtgagg tcatgcccac cgaccctgac aacccttacc agcccggcac ggccactatt
660
gagggtgtcc ccgagacgat caggatggcc gggaacacgc tagtggttga tggtcaccct
720
tggtgggggc gcgcctctac gacccaacta ccaccacctt cttgtctcct gaccggtaa
780
ccccgcccgc cggcgcgcta tgggccaaca acccctacga ctacgccaac aacaaccccc
840
tcaccctcac cgatcctctc gggacccacc ccgtcaccga cgaccaactg gcactcctca
900
cccaccccat cggcacactc gcacactacg tcgccaactc cgtcagcaca ctcgatcgc
960
acatcaccga tccgatcagc cactggtggg ccaccacaaa agaccggatc ctctccggg
1020
acttctgat cggtgccggc ctcgatcgc gcggtatcgc gtagcgcca cgggcgtagg
1080
aggaccctc ctagccggcg ccatttcggg gggactcgc tcaggcggtt tttccgtag
1140
c
1141

```

<210> 1214

<211> 259

<212> PRT

<213> Homo sapiens

<400> 1214

```

Xaa His Asp Gly Gly Leu Val Cys Gly Tyr Val His Asp Gly Arg Val
  1             5             10             15
Thr Arg Val Ala Arg Asp Ala Gln Gly Arg Val Thr Gly Ile Glu Gly

```

```
<210> 1215
<211> 317
<212> DNA
<213> Homo sapiens
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```
<210> 1216
<211> 102
<212> PRT
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<213> Homo sapiens

<400> 1216

```

Met Tyr Cys Gly Glu Pro Thr Leu Phe Ser Thr Met Asn Ala Ser Thr
 1           5           10           15
Arg Pro Arg Asp Ser Asp Gly Ser Ser Pro Pro Lys Val Val Pro Arg
      20           25           30
Tyr Phe Phe His Ala Pro Thr Pro Ala Thr Ala Arg Thr Pro Pro Pro
      35           40           45
Arg Ser Gly Val Leu Pro Val Met Ala Gly Leu Thr Pro Gly Ala Val
      50           55           60
Pro Ile Lys Gly Lys Gln Val Gly Ile Pro Pro Asp Ala Gly Cys Arg
      65           70           75           80
His Ala His Val Val His Pro Gln Val Asp Arg Ala His Arg Arg Leu
      85           90           95
Asp Leu Gln Arg Thr Arg
      100

```

<210> 1217

<211> 548

<212> DNA

<213> Homo sapiens

<400> 1217

```

naccgcgtggg ttgacgcgct attaaacgat aagagcaaaa aaacatttcc tcatttatta
60
cgttgtcggg tgaatgatgt ttctggtgat agtcagtgga tagagatgcg aggcagtgtg
120
acagggttggg acagccgtca tcgagctcag atggtgagag ggacattcga gcgtattaac
180
catcttattg acgctgaaaa tgaattaatt gcggcccgtg aagatgctca gcgacgagag
240
cttattttat cggctttgct aaataatatt ccagaccctg tttggtctaa agatgaaagc
300
ggtcggttatt tggactgtaa ccatgcgttt tgtctgttta atggtttaga gcagagtgtat
360
gttcagggggc aaaaagacag tgaattaaac ttagataata atggtcaata ttatcaagat
420
atgggcggtg aggtattagc gcgaggggag atttttcatg aacattgttg gggtagcctt
480
gcagatggaa gtgacaaccg cttgtttgaa gtatatcgag tccctatcaa agagcctacc
540
gtgaattc
548

```

<210> 1218

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1218

```

Xaa Ala Trp Val Asp Ala Leu Leu Asn Asp Lys Ser Lys Lys Thr Phe
 1           5           10           15
Pro His Leu Leu Arg Cys Arg Val Asn Asp Val Ser Gly Asp Ser Gln

```

20 25 30
 Trp Ile Glu Met Arg Gly Ser Val Thr Gly Trp Asp Ser Arg His Arg
 35 40 45
 Ala Gln Met Val Arg Gly Thr Phe Glu Arg Ile Asn His Leu Ile Asp
 50 55 60
 Ala Glu Asn Glu Leu Ile Ala Ala Arg Glu Asp Ala Gln Arg Arg Glu
 65 70 75 80
 Leu Ile Leu Ser Ala Leu Leu Asn Asn Ile Pro Asp Pro Val Trp Ser
 85 90 95
 Lys Asp Glu Ser Gly Arg Tyr Leu Asp Cys Asn His Ala Phe Cys Leu
 100 105 110
 Phe Asn Gly Leu Glu Gln Ser Asp Val Gln Gly Gln Lys Asp Ser Glu
 115 120 125
 Leu Asn Leu Asp Asn Asn Gly Gln Tyr Tyr Gln Asp Met Gly Gly Glu
 130 135 140
 Val Leu Ala Arg Gly Glu Ile Phe His Glu His Cys Trp Gly Thr Pro
 145 150 155 160
 Ala Asp Gly Ser Asp Asn Arg Leu Phe Glu Val Tyr Arg Val Pro Ile
 165 170 175
 Lys Glu Pro Thr Val Asn
 180

<210> 1219
 <211> 308
 <212> DNA
 <213> Homo sapiens

<400> 1219
 acgcgtgaag ggaggaatac agatggagaa atgggtccac caaaaaatga tgagggtacc
 60
 tccagagaaa attaccaaga ccattctgtt agtattttcc agctccacag gcctttggaa
 120
 gttcccagac caccctccct cttttcaaac taaaacaggg atggctctta accaccaccc
 180
 aaaggcaagg ggggtcttaa aacccaaacc aagtggggca ggggccagcc tcttcaggag
 240
 ggcccaaccc tgcagcctct gcccatcttg gaaagaccgt gagttggaat tatgggtcgg
 300
 tgggggggc
 308

<210> 1220
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 1220
 Met Glu Lys Trp Val His Gln Lys Met Met Arg Val Pro Pro Glu Lys
 1 5 10 15
 Ile Thr Lys Thr Ile Leu Leu Val Phe Ser Ser Ser Thr Gly Leu Trp
 20 25 30
 Lys Phe Pro Asp His Pro Pro Ser Phe Gln Thr Lys Thr Gly Met Ala
 35 40 45
 Leu Asn His His Pro Lys Ala Arg Gly Val Leu Lys Pro Lys Pro Ser

50 55 60
 Gly Ala Gly Ala Ser Leu Phe Arg Arg Ala Gln Pro Cys Ser Leu Cys
 65 70 75 80
 Pro Phe Gly Lys Asp Arg Glu Leu Glu Leu Trp Val Gly Gly Gly
 85 90 95

<210> 1221
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 1221
 gcgcgccagg ggcaggtagc ctgtggcagg tgaggctgcg tgtgggggtgt gctcccagag
 60
 gcccgtccag gaaagctgca cctcagagaa gcagtttctt tccttacctg ggaagtttct
 120
 tctgtaacac gttaagcccc acaggtaagg cctgatcccc cctggacggc tccccctctcc
 180
 agtggtccca gtctggaggt antcttttct aagccatcct ctcagaatgt gatgggtacc
 240
 aggatgcaca cccgggtggcc ctgtggtgtg aggctcagc aaacacggtc agaagatgaa
 300
 cacacagaga cccgcccgtc ggaaggagag gagggagcgg atacggaggc ccacgtgcc
 360
 gaagggtccc ttgcagtgtg gtggttatgt gcctgcaatc ccagagtgtc ctcgaaggac
 420
 ctcagatcta acgagctcag ccggcagctg cacgtgggac cagccctctg agcttcactt
 480
 gttttctctt gtgccatcag aaaccaatac gaagataaaa tgggaaaaaa aaaaatccca
 540
 ttcacggcac agcctgccga gaaacgcgt
 569

<210> 1222
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1222
 Met Asn Thr Gln Arg Pro Ala Arg Arg Lys Glu Arg Arg Glu Arg Ile
 1 5 10 15
 Arg Arg Pro Thr Cys Gln Lys Gly Pro Leu Gln Trp Cys Gly Tyr Val
 20 25 30
 Pro Ala Ile Pro Glu Cys Pro Arg Arg Thr Ser Asp Leu Thr Ser Ser
 35 40 45
 Ala Gly Ser Cys Thr Trp Asp Gln Pro Ser Glu Leu His Leu Phe Ser
 50 55 60
 Ser Val Pro Ser Glu Thr Asn Thr Lys Ile Lys Trp Glu Lys Lys Lys
 65 70 75 80
 Ser His Ser Arg His Ser Leu Pro Arg Asn Ala
 85 90

<210> 1223
 <211> 450

<212> DNA

<213> Homo sapiens

<400> 1223

```

aagcttgctc aggctagtgc cgacgctgct gctctcaaac tcgtcgatgc ccaccggttg
60
ttgtgcgctc accgagaggg gccatacggg gtagacgagt ggtctcagcg catggttact
120
gtactttcag atgtgttgcc tgggtgtggc caaggccggt gggttctcgg cgaaactgca
180
atagtaacgc ataacctgc acaattggga gtcaataacg gtgattgcgg ggatcatcgtt
240
gaaacaaggc ccgtccccac gatagctcta ccgggaccgg gtggagtccc cagacgggtg
300
ccctgttccc tcatcccatc gctgcaaccc ttacaggcga tgacgattca caaagcgag
360
ggcagccaat tcacggacgt aacggtggtc ctgccaccac ccgactcgcc cctcctctct
420
cgtgagttgc tctataccgc catcacgcgt
450

```

<210> 1224

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1224

```

Lys Leu Ala Gln Ala Ser Ala Asp Ala Ala Leu Lys Leu Val Asp
1      5      10      15
Ala His Arg Leu Leu Cys Ala His Arg Glu Gly Pro Tyr Gly Val Asp
20     25     30
Glu Trp Ser Gln Arg Met Val Thr Val Leu Ser Asp Val Leu Pro Gly
35     40     45
Val Gly Gln Gly Arg Trp Val Leu Gly Glu Thr Ala Ile Val Thr His
50     55     60
Asn Leu Ala Gln Leu Gly Val Asn Asn Gly Asp Cys Gly Val Ile Val
65     70     75     80
Glu Thr Arg Pro Val Pro Thr Ile Ala Leu Pro Gly Pro Gly Gly Val
85     90     95
Pro Arg Arg Leu Pro Cys Ser Leu Ile Pro Ser Leu Gln Pro Leu Gln
100    105    110
Ala Met Thr Ile His Lys Ala Gln Gly Ser Gln Phe Thr Asp Val Thr
115    120    125
Val Val Leu Pro Pro Pro Asp Ser Pro Leu Leu Ser Arg Glu Leu Leu
130    135    140
Tyr Thr Ala Ile Thr Arg
145    150

```

<210> 1225

<211> 436

<212> DNA

<213> Homo sapiens

<400> 1225

ncccatcccc caccgggat ggtgaacact gggatggcca cttgggagct caaagtgttg
 60
 tcagtgggag gacaagggtcc tcaattcctg gcacattggc ccagagaagt catgaaaacc
 120
 caaagcccc cgaaagtaag aagtagaaaa aaacccgacc ccgaccagat gaagggacct
 180
 gggaagtgtt tggaagag actgctgaag tgtctccttg caggcatcac cgtgagctgg
 240
 ggctttgcac acagcatctt catggctttc cacaatgatc ccagaactga tccagagaaa
 300
 cccagggatc aggggttgac ccgacctgt catcatccca ttctacaaat gaggacactg
 360
 aggcttggtg aaaagggagg ggtggatgga accaggtggc ctggctctaa gaccagagg
 420
 ctggagtgtg ctcatg
 436

<210> 1226

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1226

Met	Val	Asn	Thr	Gly	Met	Ala	Thr	Trp	Glu	Leu	Lys	Val	Leu	Ser	Val
1				5				10					15		
Gly	Gly	Gln	Gly	Pro	Gln	Phe	Leu	Ala	His	Trp	Pro	Arg	Glu	Val	Met
		20				25						30			
Lys	Thr	Gln	Ser	Pro	Pro	Lys	Val	Arg	Ser	Arg	Lys	Lys	Pro	Asp	Pro
		35				40						45			
Asp	Gln	Met	Lys	Gly	Pro	Gly	Lys	Phe	Leu	Glu	Lys	Arg	Leu	Leu	Lys
	50					55				60					
Cys	Leu	Leu	Ala	Gly	Ile	Thr	Val	Ser	Trp	Gly	Phe	Ala	His	Ser	Ile
65					70					75				80	
Phe	Met	Ala	Phe	His	Asn	Asp	Pro	Arg	Thr	Asp	Pro	Glu	Lys	Pro	Arg
				85					90					95	
Asp	Gln	Gly	Leu	Thr	Arg	Pro	Cys	His	His	Pro	Ile	Leu	Gln	Met	Arg
			100					105					110		
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Gly	Gly	Val	Asp	Gly	Thr	Arg	Trp	Pro
		115				120						125			
Gly	Ser	Lys	Thr	Gln	Arg	Leu	Glu	Cys	Ala	His					
		130				135									

<210> 1227

<211> 756

<212> DNA

<213> Homo sapiens

<400> 1227

gttgagttcc acgtgaaaca aaatgcactt tacaatagaa tgacgattcg tatcaaagat
 60
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 120
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<210> 1228

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1228

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			20				25						30		
Ile	Phe	Asp	Arg	Phe	Tyr	Arg	Val	Asp	Lys	Ala	Arg	Thr	Arg	Lys	Met
		35					40					45			
Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Lys	Glu	Ile	Val	Glu	Ala
		50				55					60				
His	Asn	Gly	Arg	Ile	Trp	Ala	Asn	Ser	Val	Glu	Gly	Gln	Gly	Thr	Ser
65				70						75				80	
Ile	Phe	Ile	Thr	Leu	Pro	Cys	Glu	Ile	Ile	Glu	Asp	Gly	Asp	Trp	Asp
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Glu

<210> 1229

<211> 377

<212> DNA

<213> Homo sapiens

<400> 1229

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 180

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<210> 1230
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 <212> PRT
 <213> Homo sapiens

<400> 1230
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 35 40 45
 Trp Asp Tyr Phe Ser Gln Leu Phe Ala Gln Val Thr Asn Pro Pro Leu
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 Asp Ala Ile Arg Glu Glu Leu Val Thr Ser Leu Thr Gly Thr Ile Gly
 65 70 75 80
 Pro Glu Ala Asn Leu Leu Glu Pro Gly Pro Glu Ser Cys Arg Gln Val
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 His Ile Asp Ala Asp Gly Glu His Pro
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<210> 1231
 <211> 351
 <212> DNA
 <213> Homo sapiens

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<210> 1232
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<213> Homo sapiens

<400> 1232

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Val Leu Ala Leu Leu Glu His Gly Glu Asp Val Val Val Leu Asp Asn
      20           25           30
Leu Ser Asn Ser Ser Asp Glu Ser Leu Arg Arg Val Glu Lys Leu Ala
      35           40           45
Gly Arg Ser Ala Gln Phe Tyr Gln Gly Asp Ile Leu Asp Ala Glu Cys
      50           55           60
Leu His Arg Ile Phe Glu Ala His Asp Ile Ser Ala Val Ile His Phe
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<210> 1233

<211> 4982

<212> DNA

<213> Homo sapiens

<400> 1233

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960

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<210> 1234

<211> 708

<212> PRT

<213> Homo sapiens

<400> 1234

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			20					25					30		
Ser	Gly	Thr	Ile	Ile	Thr	Glu	Asp	Pro	Phe	Lys	Ser	Gly	Ser	Ser	Asp
		35					40					45			
Val	Gly	Arg	Asp	Trp	Asp	Pro	Ser	Ser	Thr	Glu	Gly	Gly	Ser	Ser	Pro
	50					55					60				
Leu	Ile	Cys	Pro	Asp	Ser	Ser	Ala	Arg	Pro	Arg	Val	Lys	Ser	Ser	Tyr
65					70					75				80	
Ser	Met	Glu	Asn	Ala	Asn	Lys	Trp	Ser	Cys	His	Met	Cys	Thr	Tyr	Leu
			85					90						95	
Asn	Trp	Pro	Arg	Ala	Ile	Arg	Cys	Thr	Gln	Cys	Leu	Ser	Gln	Arg	Arg
		100						105					110		
Thr	Arg	Ser	Pro	Thr	Glu	Ser	Pro	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Arg
		115					120					125			
Pro	Val	Ala	Phe	Ser	Val	Asp	Pro	Cys	Glu	Glu	Tyr	Asn	Asp	Arg	Asn
	130					135					140				
Lys	Leu	Asn	Thr	Arg	Thr	Gln	His	Trp	Thr	Cys	Ser	Val	Cys	Thr	Tyr

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 165 170 175
 Pro Asn Asn Ile Glu Ala Ile Glu Leu Ala Glu Thr Glu Glu Ala Ser
 180 185 190
 Ser Ile Ile Asn Glu Gln Asp Arg Ala Arg Trp Arg Gly Ser Cys Ser
 195 200 205
 Ser Gly Asn Ser Gln Arg Arg Ser Pro Pro Ala Thr Lys Arg Asp Ser
 210 215 220
 Glu Val Lys Met Asp Phe Gln Arg Ile Glu Leu Ala Gly Ala Val Gly
 225 230 235 240
 Ser Lys Glu Glu Leu Glu Val Asp Phe Lys Lys Leu Lys Gln Ile Lys
 245 250 255
 Asn Arg Met Lys Lys Thr Asp Trp Leu Phe Leu Asn Ala Cys Val Gly
 260 265 270
 Val Val Glu Gly Asp Leu Ala Ala Ile Glu Ala Tyr Lys Ser Ser Gly
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 Gly Asp Ile Ala Arg Gln Leu Thr Ala Asp Glu Val Arg Leu Leu Asn
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 Arg Pro Ser Ala Phe Asp Val Gly Tyr Thr Leu Val His Leu Ala Ile
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 Gln Gln Ala Ala Lys Cys Ile Pro Ala Met Val Cys Pro Glu Leu Thr
 340 345 350
 Glu Gln Ile Arg Arg Glu Ile Ala Ala Ser Leu His Gln Arg Lys Gly
 355 360 365
 Asp Phe Ala Cys Tyr Phe Leu Thr Asp Leu Val Thr Phe Thr Leu Pro
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 Ala Asp Ile Glu Asp Leu Pro Pro Thr Val Gln Glu Lys Leu Phe Asp
 385 390 395 400
 Glu Val Leu Asp Arg Asp Val Gln Lys Glu Leu Glu Glu Glu Ser Pro
 405 410 415
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 Tyr Ala Leu Trp Asn Arg Thr Ala Gly Asp Cys Leu Leu Asp Ser Val
 435 440 445
 Leu Gln Ala Thr Trp Gly Ile Tyr Asp Lys Asp Ser Val Leu Arg Lys
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 Ala Leu His Asp Ser Leu His Asp Cys Ser His Trp Phe Tyr Thr Arg
 465 470 475 480
 Trp Lys Asp Trp Glu Ser Trp Tyr Ser Gln Ser Phe Gly Leu His Phe
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 Ser Leu Arg Glu Glu Gln Trp Gln Glu Asp Trp Ala Phe Ile Leu Ser
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 Leu Ala Ser Gln Pro Gly Ala Ser Leu Glu Gln Thr His Ile Phe Val
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 545 550 555 560
 Val Tyr Leu Pro Leu Trp Glu Gln Ser Phe Cys Trp Lys Ser Pro
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580 585 590
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 595 600 605
 Asp Asp Asp Val Thr Ile Thr Phe Leu Pro Leu Val Asp Ser Glu Arg
 610 615 620
 Lys Leu Leu His Val His Phe Leu Ser Ala Gln Glu Leu Gly Asn Glu
 625 630 635 640
 Glu Gln Gln Glu Lys Leu Leu Arg Glu Trp Leu Asp Cys Cys Val Thr
 645 650 655
 Glu Gly Gly Val Leu Val Ala Met Gln Lys Ser Ser Arg Arg Arg Asn
 660 665 670
 His Pro Leu Val Thr Gln Met Val Glu Lys Trp Leu Asp Arg Tyr Arg
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<210> 1235
 <211> 383
 <212> DNA
 <213> Homo sapiens

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<210> 1236
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 <212> PRT
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 Phe Leu Gly Gly Gly Glu Met Ile Glu Val Val Arg Met Glu Gly Ser
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<210> 1238

<211> 458

<212> PRT

<213> Homo sapiens

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		20						25					30		
Phe	Pro	Glu	Leu	Gln	Leu	Pro	Val	Ser	Pro	Ser	Val	Cys	Leu	Asp	Gln
	35						40					45			
Gly	Met	Gln	Leu	Lys	Pro	Ser	Thr	Ser	Ser	His	Leu	Leu	Lys	Thr	Val
	50					55					60				
Lys	Pro	Arg	Val	Trp	Lys	Pro	Gly	Asp	Trp	Ser	Arg	Glu	Gln	Leu	Asn
65					70					75				80	
Glu	Thr	Thr	Val	Leu	Ala	Pro	His	Glu	Thr	Ile	Phe	Arg	Ala	Lys	Asp
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Leu	Ser	Val	Ile	Leu	Lys	Ala	Tyr	Val	Leu	Val	Thr	Ser	Leu	Thr	Pro
		100						105					110		
Leu	Arg	Ala	Phe	Ile	His	Ser	Thr	Gly	Thr	Val	Trp	Asn	Pro	Pro	Lys
		115					120					125			
Lys	Lys	Arg	Phe	Thr	Val	Lys	Leu	Gln	Thr	Phe	Phe	Glu	Thr	Phe	Leu
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Pro	Asn	Glu	Ser	Ser	Leu	Ser	Ile	Phe	Ser	Glu	Ile	Phe	Gln	Arg	Leu
			245						250				255		
Tyr	Arg	Ser	Asp	Val	Phe	Lys	Gly	Glu	Asn	Tyr	Gln	Lys	Glu	Leu	Asn

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Glu Leu Gly Ser Leu Gly Gln Phe Gln Leu Leu Phe Pro Ser Thr Thr
                290                295                300
Pro Gly Ile Gln Ser Leu Met His Glu Phe Tyr Asp Val Ala Asn Pro
305                310                315                320
Val Gly Asn Pro Gly Ser Val Leu Thr Gln Tyr Trp Ser Leu Leu Asn
                325                330                335
Val Phe Glu Gln Phe Gln Phe Met Asn Lys Lys Thr Gln Pro His Pro
                340                345                350
Leu Glu Trp Asn Ser Phe Thr Glu Asp Lys Asn Ile Glu Lys Pro Gln
                355                360                365
Val Pro Phe Asp Ala Ile Glu Asn Lys Lys Ala Ala Val Pro Gln Ile
                370                375                380
Lys Asn Glu Asn Lys Glu Ile His Cys Ser Asp Asp Glu Asn Thr Pro
385                390                395                400
Cys His Ile Lys Gln Ile Phe Thr His Pro His Leu Glu Leu Asn Pro
                405                410                415
Asp Phe His Pro Lys Ile Lys Asp Tyr Tyr Cys Glu Val Pro Phe Asp
                420                425                430
Val Val Thr Val Thr Ile Gly Val Glu Thr Pro Lys Cys Leu Cys Lys
                435                440                445
Val His Leu Tyr Glu Gln Ala Gly Pro Ser
                450                455

```

<210> 1239

<211> 447

<212> DNA

<213> Homo sapiens

<400> 1239

```

atacctactg aacgtgaacg aacagaaagg ctaattaa ccaaattaag ggagatcatg
60
atgcagaagg atttgagaa tattacatcc aaagagataa gaacagagtt ggaaatgcaa
120
atggtgtgca acttgcgga attcaaggaa tttatagaca atgaaatgat agtgatcctt
180
ggtcaaatgg atagccctac acagatat ttt gagcatgtgt tcctgggctc agaatggaat
240
gcctccaact tagaggactt acagaaccga ggggtacggt atatcttgaa tgtcactcga
300
gagatagata actttttccc aggagtcttt gagtatcata acattcgggt atatgatgaa
360
gaggcaacgg atctcctggc gtactggaat gacacttaca aattcatctc taaagcaaag
420
aaacatggat ctaaatgcct tgtgcac
447

```

<210> 1240

<211> 149

<212> PRT

<213> Homo sapiens

<400> 1240

Ile Pro Thr Glu Arg Glu Arg Thr Glu Arg Leu Ile Lys Thr Lys Leu
 1 5 10 15
 Arg Glu Ile Met Met Gln Lys Asp Leu Glu Asn Ile Thr Ser Lys Glu
 20 25 30
 Ile Arg Thr Glu Leu Glu Met Gln Met Val Cys Asn Leu Arg Glu Phe
 35 40 45
 Lys Glu Phe Ile Asp Asn Glu Met Ile Val Ile Leu Gly Gln Met Asp
 50 55 60
 Ser Pro Thr Gln Ile Phe Glu His Val Phe Leu Gly Ser Glu Trp Asn
 65 70 75 80
 Ala Ser Asn Leu Glu Asp Leu Gln Asn Arg Gly Val Arg Tyr Ile Leu
 85 90 95
 Asn Val Thr Arg Glu Ile Asp Asn Phe Phe Pro Gly Val Phe Glu Tyr
 100 105 110
 His Asn Ile Arg Val Tyr Asp Glu Glu Ala Thr Asp Leu Leu Ala Tyr
 115 120 125
 Trp Asn Asp Thr Tyr Lys Phe Ile Ser Lys Ala Lys Lys His Gly Ser
 130 135 140
 Lys Cys Leu Val His
 145

<210> 1241

<211> 489

<212> DNA

<213> Homo sapiens

<400> 1241

agcgtgtgc agcgtatcca gcaccgtcct cagaataata gctgtgaaaa ggaggaaggg
 60
 aactaggcag acagaccgac agataggggg aaaccgggat gtttaatgtg tccgaacaag
 120
 taggaagatc aatgaggcgc gagtgtgtgt gtgtacgtgt gcgcgtgtgt gtgtgagaga
 180
 gagagaaaaga aagaagaaag gtcccgattg caacgtgtca gatcttgcaa ccttcccccc
 240
 acccaacaca acaaccctca gacacaaaaa caccattgct gactgatacc ccaggtcttc
 300
 aggggttaaag gaaccgtgtg ttggcagcgc aattgtgcag acgctgtaag gccaaaacga
 360
 ggatttgtgt tgtgaggctg gtggtgcgtt cttttctttc ttttctcgcc tgttttcccg
 420
 gagtgcctgg gttgcgagaa aggcgcacgc caggctgtgc agccgaatcg cttcgcaatt
 480
 attcatgct
 489

<210> 1242

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1242

Met Asn Asn Cys Glu Ala Ile Arg Leu His Ser Leu Arg Cys Ala Phe

```

      1           5           10           15
Leu Ala Thr Gln Ala Leu Arg Glu Asn Arg Arg Glu Glu Lys Glu Lys
      20           25           30
Asn Ala Pro Pro Thr Ser Gln His Lys Ser Ser Phe Trp Pro Tyr Ser
      35           40           45
Val Cys Thr Ile Ala Leu Pro Thr His Gly Ser Phe Asn Pro Glu Asp
      50           55           60
Leu Gly Tyr Gln Ser Ala Met Val Phe Leu Cys Leu Arg Val Val Val
      65           70           75           80
Leu Gly Gly Gly Lys Val Ala Arg Ser Asp Thr Leu Gln Ser Gly Pro
      85           90           95
Phe Phe Phe Leu Ser Leu Ser Leu Thr His Thr Arg Ala His Val His
      100          105          110
Thr His Thr Arg Ala Ser Leu Ile Phe Leu Leu Val Arg Thr His
      115          120          125

```

<210> 1243

<211> 390

<212> DNA

<213> Homo sapiens

<400> 1243

```

ntagactccg tcgatcccct catggagaat ccagtgtgcc aggtcccttc ggcgtactgg
60
gagatgatat acctaccggg aatgttcact gtctacttcg atggccagtt ctgggtcgga
120
gtcctagaga ggcgcgacga ggggttggtg cgtgccgtaa aagtcacgtt tggcgccgaa
180
cgtctgaca cggaattgta cgggtgggtt agccgtcatg gcaacgcact tatagagcga
240
ttggagtcta ccgctgctgt ccctaccacc cgcagtcgcc gagccaagcg actgaacccc
300
aagagggcgt tacgagatgc agcgcgagct gcccaagcac accgtgccag cacgnccgca
360
caggccgcga ttaaggccga tcaggaagct
390

```

<210> 1244

<211> 130

<212> PRT

<213> Homo sapiens

<400> 1244

```

Xaa Asp Ser Val Asp Pro Leu Met Glu Asn Pro Val Cys Gln Val Pro
      1           5           10           15
Ser Ala Tyr Trp Glu Met Ile Tyr Leu Pro Gly Met Phe Thr Val Tyr
      20           25           30
Phe Asp Gly Gln Phe Trp Val Gly Val Leu Glu Arg Arg Asp Glu Gly
      35           40           45
Leu Val Arg Ala Val Lys Val Thr Phe Gly Ala Glu Pro Ser Asp Thr
      50           55           60
Glu Leu Tyr Gly Trp Val Ser Arg His Gly Asn Ala Leu Ile Glu Arg
      65           70           75           80
Leu Glu Ser Thr Ala Ala Val Pro Thr Thr Arg Ser Pro Arg Ala Lys

```

```

      85              90              95
Arg Leu Asn Pro Lys Arg Ala Leu Arg Asp Ala Ala Arg Ala Ala Gln
      100              105              110
Ala His Arg Ala Ser Thr Xaa Ala Gln Ala Ala Ile Lys Ala Asp Gln
      115              120              125
Glu Ala
      130

```

<210> 1245
 <211> 339
 <212> DNA
 <213> Homo sapiens

```

<400> 1245
gccaaagcagc aaaaaccaca gatcattgct atgggaaatg tgtcattttc ttgttcacaa
60
ccacaatcta tgcccgtagc ttttctgagc tccaggagtt ttttagcact gccagacttc
120
tctggagagg aggaggtttc tgccactttt caatttcgaa cttggaataa ggcagggcctt
180
ctgctgttca gtgaacttca gctgatttca gggggtatcc tcctctttct gagtgatgga
240
aaacttaagt cgaatctcta ccagccaaga aaattaccca gtgacatcac agcaggtgtc
300
gaattaaatg atgggacagt gcattctgtc tctttatct
339

```

<210> 1246
 <211> 113
 <212> PRT
 <213> Homo sapiens

```

<400> 1246
Ala Lys Gln Gln Lys Pro Gln Ile Ile Ala Met Gly Asn Val Ser Phe
1      5      10      15
Ser Cys Ser Gln Pro Gln Ser Met Pro Val Thr Phe Leu Ser Ser Arg
      20      25      30
Ser Phe Leu Ala Leu Pro Asp Phe Ser Gly Glu Glu Glu Val Ser Ala
      35      40      45
Thr Phe Gln Phe Arg Thr Trp Asn Lys Ala Gly Leu Leu Leu Phe Ser
      50      55      60
Glu Leu Gln Leu Ile Ser Gly Gly Ile Leu Leu Phe Leu Ser Asp Gly
65      70      75      80
Lys Leu Lys Ser Asn Leu Tyr Gln Pro Arg Lys Leu Pro Ser Asp Ile
      85      90      95
Thr Ala Gly Val Glu Leu Asn Asp Gly Gln Trp His Ser Val Ser Leu
      100      105      110
Ser

```

<210> 1247
 <211> 366
 <212> DNA
 <213> Homo sapiens

<400> 1247

ttgacctcca acccgggcac gcgcattctg cccagatcc cgatggatgg gcatgacctc
60
aaccgggtgt ggcgggacgt cggcctgac gtgcacccgc cgatgctcta catgggctac
120
gtcggtttct cctgggcctt tgcgtttgcc atcgccgcct tgctcggcgg gcgcctcgat
180
gcggcctggg cgcgtggtc gcggccatgg accattgtgg cctgggcgtt cctcggtatc
240
ggatcacccc tcggttcgtg gtgggcctac tacgaactcg gctggngcgg ctggtggttc
300
tgggaccccc gggaaaaccc cttcttcatt ccctggctgg ggggcacccc gctgattcac
360
tcgctg
366

<210> 1248

<211> 122

<212> PRT

<213> Homo sapiens

<400> 1248

Leu	Thr	Ser	Asn	Pro	Gly	Thr	Arg	Ile	Leu	Pro	Gln	Ile	Pro	Met	Asp
1			5					10					15		
Gly	His	Asp	Leu	Asn	Pro	Val	Trp	Arg	Asp	Val	Gly	Leu	Ile	Val	His
		20					25					30			
Pro	Pro	Met	Leu	Tyr	Met	Gly	Tyr	Val	Gly	Phe	Ser	Val	Ala	Phe	Ala
		35				40					45				
Phe	Ala	Ile	Ala	Ala	Leu	Leu	Gly	Gly	Arg	Leu	Asp	Ala	Ala	Trp	Ala
	50					55				60					
Arg	Trp	Ser	Arg	Pro	Trp	Thr	Ile	Val	Ala	Trp	Ala	Phe	Leu	Gly	Ile
65				70					75				80		
Gly	Ile	Thr	Leu	Gly	Ser	Trp	Trp	Ala	Tyr	Tyr	Glu	Leu	Gly	Trp	Xaa
			85					90					95		
Gly	Trp	Trp	Phe	Trp	Asp	Pro	Gly	Glu	Asn	Pro	Phe	Phe	Met	Pro	Trp
			100					105					110		
Leu	Gly	Gly	Thr	Pro	Leu	Ile	His	Ser	Leu						
		115				120									

<210> 1249

<211> 374

<212> DNA

<213> Homo sapiens

<400> 1249

acgcgtgtcc tcaacaccct ggcgcccacg ctgattgccg tggaaccggt gccggcaatg
60
ggcgcgcagt tgagcaagct gctgccggat gtgcacctgg tcaatggcac tgccgaggcc
120
attccactgg aaagcgccgt ggcggtatgc gtggtgtgcg cacaagcctt ccattggttt
180
tccagcgagg cggccctggc ggaaatccat cgggtactca aaccggatgg gcgcctgggg
240

ctggtgtgga atgtgcgga cgagtcggtg gattgggtcg ccgccattac tcaaatacatc
 300
 acgccttatg aaggcgacac gccgcgcttt cataccggcc gttggcgga agccttcact
 360
 ggcgagtatt ttg
 374

<210> 1250
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 1250
 Thr Arg Val Leu Asn Thr Leu Ala Pro Thr Leu Ile Ala Val Glu Pro
 1 5 10 15
 Val Pro Ala Met Gly Ala Gln Leu Ser Lys Leu Leu Pro Asp Val His
 20 25 30
 Leu Val Asn Gly Thr Ala Glu Ala Ile Pro Leu Glu Ser Ala Val Ala
 35 40 45
 Asp Ala Val Val Cys Ala Gln Ala Phe His Trp Phe Ser Ser Glu Ala
 50 55 60
 Ala Leu Ala Glu Ile His Arg Val Leu Lys Pro Asp Gly Arg Leu Gly
 65 70 75 80
 Leu Val Trp Asn Val Arg Asp Glu Ser Val Asp Trp Val Ala Ala Ile
 85 90 95
 Thr Gln Ile Ile Thr Pro Tyr Glu Gly Asp Thr Pro Arg Phe His Thr
 100 105 110
 Gly Arg Trp Arg Glu Ala Phe Thr Gly Glu Tyr Phe
 115 120

<210> 1251
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 1251
 accggtctct tcctcggaag ggcagggccg aggggcttgc ggggcagcca tggaggcgac
 60
 gcggaggcgg cagcacgtgg gagcgacggg cgggccaggc gcgcagttgg gcgcctcctt
 120
 ccctgcaggc caggcatggc tctgtgagcg ctgatgaggc tgcccgcacg gctcccttcc
 180
 acctcgacct ctggttctac ttcacactgc agaactgggt tctggacttt gggcgtecca
 240
 ttgccatgct ggtattccct ctcgagtggg ttccactcaa caagcccagt gttggggact
 300
 acttccacat ggcctacaac gtcacacgc cctttctctt gctcaagctc atcgagcggg
 360
 cccccgcac cctgctacgc tccatcacgt acgtgagcat catcatcttc atcatgggtg
 420
 ccagcatcca cctggtgggt gactctgtca accaccgcct gctcttcagt gggtaccagc
 480
 accacctgtc tgcccgtag aaccccatca tcaagaatct caagccggag acgctgatcg
 540

aetcccttga gctgctctac tattatgatg agtacctggg tcaactgcatg tggtagatcc
 600
 ccttcttcct cactctcttc atgtacttca gcggtgctn ttactgcctc taaagctgag
 660
 agcttgattc cagggcctgc cctgctcctg gtggcaccca gtggcctgta ctactggtac
 720
 ctggtcaccg agggccagat ct
 742

<210> 1252

<211> 80

<212> PRT

<213> Homo sapiens

<400> 1252

Met	Arg	Leu	Pro	Ala	Arg	Leu	Pro	Ser	Thr	Ser	Thr	Ser	Gly	Ser	Thr
1				5					10					15	
Ser	His	Cys	Arg	Thr	Gly	Phe	Trp	Thr	Leu	Gly	Val	Pro	Leu	Pro	Cys
			20					25					30		
Trp	Tyr	Ser	Leu	Ser	Ser	Gly	Phe	His	Ser	Thr	Ser	Pro	Val	Leu	Gly
		35				40						45			
Thr	Thr	Ser	Thr	Trp	Pro	Thr	Thr	Ser	Ser	Arg	Pro	Phe	Ser	Cys	Ser
	50					55				60					
Ser	Ser	Ser	Ser	Gly	Pro	Pro	Ala	Pro	Cys	Tyr	Ala	Pro	Ser	Arg	Thr
65					70					75					80

<210> 1253

<211> 675

<212> DNA

<213> Homo sapiens

<400> 1253

gggccccctc ccaggcgctt tctgggagct tttagaactg cgctctgaag tttccagaga
 60
 gcgaggagct tttgcggcag gcagagacaa tggaagaaaa tgaaagccag aaatgtgagc
 120
 cgtgccttcc ttactcagca gacagaagac agatgcagga acaaggcaaa ggcaatctgc
 180
 atgtaacatc accagaagat gcagaatgcc gcagaaccaa ggaacgcctt tctaattggaa
 240
 acagtcgtgg ttcagtttcc aagtcttccc gcaatatccc aaggagacac accctagggg
 300
 ggccccgaag ttccaaggaa atactgggaa tgcaaaccatc tgagatggat cggaagagag
 360
 gaaaaagcgt tcctagaaca tctgaagcag aagtaccccc accacgcctc tgcaatcatg
 420
 ggtaaccaag agaggctgag agaccagaca aggatcccca aactgtctca cagtctctca
 480
 ccacccagtg tgggtgaccc ggtcgagcat ttatcagaga cgtccgctga ttctttggaa
 540
 gccatgtctg agggggatgc tccaaccct tttccagag gcagccggac tcgtgagagc
 600
 cttctgtgg tgaggtcaac caaccagacg aaagaaagat ctctgggggt tctctatctc
 660

cagtatggag atgaa
675

<210> 1254
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1254
Met Gly His Gln Glu Arg Leu Arg Asp Gln Thr Arg Ile Pro Lys Leu
1 5 10 15
Ser His Ser Pro Gln Pro Pro Ser Val Gly Asp Pro Val Glu His Leu
20 25 30
Ser Glu Thr Ser Ala Asp Ser Leu Glu Ala Met Ser Glu Gly Asp Ala
35 40 45
Pro Thr Pro Phe Ser Arg Gly Ser Arg Thr Arg Ala Ser Leu Pro Val
50 55 60
Val Arg Ser Thr Asn Gln Thr Lys Glu Arg Ser Leu Gly Val Leu Tyr
65 70 75 80
Leu Gln Tyr Gly Asp Glu
85

<210> 1255
<211> 401
<212> DNA
<213> Homo sapiens

<400> 1255
ncgccgatta ccaaggctat ggatgtgtgg gccttgggcg taacgctata ctgtctgctg
60
ttcggtcgag tgccatttga tgcagagacg gactacttgc tgctggaaag taccctgcat
120
gacgattatg ccgtcccgac gcacatgggt agcgaccgcg tgttggtagg cccgcgacca
180
gcacgttggc cctcgtcgca agagacgccc aacgtgccgc tgtccggcga ggcgcatgca
240
gtacgccatc tgctcgatgc ccttctcgac aaggatccag cgacgcgcct cactctcgat
300
cgtgttataa cacacccatg gctcgtggca gagtcattgt aatagtagca attgtatata
360
ccctcatcac caagatggcc aaagcggtag aaggcccgcg g
401

<210> 1256
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1256
Xaa Pro Ile Thr Lys Ala Met Asp Val Trp Ala Leu Gly Val Thr Leu
1 5 10 15
Tyr Cys Leu Leu Phe Gly Arg Val Pro Phe Asp Ala Glu Thr Glu Tyr
20 25 30
Leu Leu Leu Glu Ser Ile Leu His Asp Asp Tyr Ala Val Pro Thr His

```

          35          40          45
Met Gly Ser Asp Arg Val Leu Val Gly Pro Arg Pro Ala Arg Trp Pro
   50          55          60
Ser Ser Gln Glu Thr Pro Asn Val Pro Leu Ser Gly Glu Ala His Ala
65          70          75          80
Val Arg His Leu Leu Asp Ala Leu Leu Asp Lys Asp Pro Ala Thr Arg
          85          90          95
Leu Thr Leu Asp Arg Val Ile Thr His Pro Trp Leu Val Ala Glu Ser
   100          105          110
Trp

```

<210> 1257
 <211> 294
 <212> DNA
 <213> Homo sapiens

```

<400> 1257
cgcgtacagc tgattgaagg tgatgtcgcc aacgccgacc tggtaggcgca agccgccatc
60
ggcgccacgg cggtggtgca tttggcagcg gtggcttcgg tgcaagcctc ggtggatgac
120
ccggtcagca cgcgccagag caattttgtc ggcaccttga atgtctgcga agccatgcgc
180
aaggccggtg tgaagcgtgt ggattttgct tccagcgttg cggtgtatgg caacaatggc
240
gagggcgctt cgattgacga agagaccatc aaggccccgc tgacgcctta cgcg
294

```

<210> 1258
 <211> 98
 <212> PRT
 <213> Homo sapiens

```

<400> 1258
Arg Val Gln Leu Ile Glu Gly Asp Val Ala Asn Ala Asp Leu Val Ala
1          5          10          15
Gln Ala Ala Ile Gly Ala Thr Ala Val Val His Leu Ala Ala Val Ala
          20          25          30
Ser Val Gln Ala Ser Val Asp Asp Pro Val Ser Thr Arg Gln Ser Asn
          35          40          45
Phe Val Gly Thr Leu Asn Val Cys Glu Ala Met Arg Lys Ala Gly Val
          50          55          60
Lys Arg Val Val Phe Ala Ser Ser Val Ala Val Tyr Gly Asn Asn Gly
65          70          75          80
Glu Gly Ala Ser Ile Asp Glu Glu Thr Ile Lys Ala Pro Leu Thr Pro
          85          90          95
Tyr Ala

```

<210> 1259
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 1259

nnacactcta gcctctgact caaggaagct gccacgggtc ttgcccttcg gtttgggggg
 60
 atccccgtctc ccttcgtctg gagcagacat agtgagaacg tgagaagctg caggcgtggc
 120
 ctcaccgtgg tgtgttccaa gatgtccagg gccaaaggatg ccgtgtcctc cgggggtggcc
 180
 agcgtgggtgg acgtggctaa gggagtgggtc cagggaggcc tggacaccac tcggtctgca
 240
 cttacgggca ccaaggaggc ggtgtccagc ggggtcacag gggccatgga catggctaag
 300
 ggggccgtcc aaggggggtct ggacacctcg aaggctgtcc tcaccggcac caaggacacg
 360
 gtgtccactg ggctcacggg ggcagtgaat gtggccaaag ggcccgtaca ggccggc
 417

<210> 1260

<211> 133

<212> PRT

<213> Homo sapiens

<400> 1260

Leu	Lys	Glu	Ala	Gln	Gly	Leu	Ala	Leu	Arg	Phe	Gly	Gly	Ile	Pro
1			5					10					15	
Ser	Pro	Phe	Val	Trp	Ser	Arg	His	Ser	Glu	Asn	Val	Arg	Ser	Cys
			20					25					30	Arg
Arg	Gly	Leu	Thr	Val	Val	Cys	Ser	Lys	Met	Ser	Arg	Ala	Lys	Asp
		35					40				45			Ala
Val	Ser	Ser	Gly	Val	Ala	Ser	Val	Val	Asp	Val	Ala	Lys	Gly	Val
	50					55				60				Val
Gln	Gly	Gly	Leu	Asp	Thr	Thr	Arg	Ser	Ala	Leu	Thr	Gly	Thr	Lys
65					70					75				80
Ala	Val	Ser	Ser	Gly	Val	Thr	Gly	Ala	Met	Asp	Met	Ala	Lys	Gly
			85					90					95	Ala
Val	Gln	Gly	Gly	Leu	Asp	Thr	Ser	Lys	Ala	Val	Leu	Thr	Gly	Thr
		100						105					110	Lys
Asp	Thr	Val	Ser	Thr	Gly	Leu	Thr	Gly	Ala	Val	Asn	Val	Ala	Lys
		115					120					125		Gly
Pro	Val	Gln	Ala	Gly										
														130

<210> 1261

<211> 330

<212> DNA

<213> Homo sapiens

<400> 1261

ngtgcacgtg ccgttcggca tcaggagatg aacatggatt tgaacgctga agtcgatcag
 60
 ctgggtccgcc aatcccagac ctggatcccc ttgatcatgg agtacggcag ccgcctgctg
 120tgaccctggc ggtcggctgg tggatcgaca acaaggctcag cgcccgcctg 180
 ggcaaaactgg taggcctgcg caacgccgac ctggcactgc aaggctttat cagcaccttg
 240

tcgaacatcg ggctgaaagt gctgctgttc gtcagtgtgg cgtcgatgat cggcattgag
 300
 accacctcgt tcgtcgcgga catcgggtgct
 330

<210> 1262
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1262
 Xaa Ala Arg Ala Val Arg His Gln Glu Met Asn Met Asp Leu Asn Ala
 1 5 10 15
 Glu Val Asp Gln Leu Val Arg Gln Ser Gln Thr Trp Ile Pro Leu Ile
 20 25 30
 Met Glu Tyr Gly Ser Arg Leu Leu Ala Leu Leu Thr Leu Ala Val
 35 40 45
 Gly Trp Trp Ile Asp Asn Lys Val Ser Ala Arg Leu Gly Lys Leu Val
 50 55 60
 Gly Leu Arg Asn Ala Asp Leu Ala Leu Gln Gly Phe Ile Ser Thr Leu
 65 70 75 80
 Ser Asn Ile Gly Leu Lys Val Leu Leu Phe Val Ser Val Ala Ser Met
 85 90 95
 Ile Gly Ile Glu Thr Thr Ser Phe Val Ala Asp Ile Gly Ala
 100 105 110

<210> 1263
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1263
 acgcgtggac gatggacttc gtcggtctgc ggtacgacga agggctcaac attgccggtg
 60
 gcatcgatga tgagtttgct cgcctgggca acacctagca gcaatggcat cgatagtccc
 120
 tgcccagcct gctccatttc gacgacgatg gtcgccgggt tcagtttctt ctcgctccac
 180
 gtcaacagac cgtcaccgtg gttgacgac tcgccggtgg aggcgctcctt gacgacgac
 240
 tggccacgcg ccagggaata catctcccca tccacccaaa agaacgcccc caagctgggc
 300
 atcttggcca gcccgatgat cgagagggtt tcaacaagcg actcgggac c
 351

<210> 1264
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 1264
 Met Pro Ser Leu Gly Ala Phe Phe Trp Val Asp Gly Glu Met Tyr Ser
 1 5 10 15
 Leu Ala Arg Gly Gln Ile Val Val Lys Asp Ala Ser Thr Gly Glu Ile

```

      20      25      30
Val Asn His Gly Asp Gly Leu Leu Thr Trp Ser Glu Lys Lys Leu Asn
      35      40      45
Pro Ala Thr Ile Val Val Glu Met Glu Gln Ala Gly Gln Gly Leu Ser
      50      55      60
Met Pro Leu Leu Leu Gly Val Ala Gln Ala Ser Lys Leu Ile Ile Asp
      65      70      75      80
Ala Thr Gly Asn Val Glu Pro Phe Val Val Pro Gln Thr Asp Glu Val
      85      90      95
His Arg Pro Arg
      100

```

<210> 1265
 <211> 318
 <212> DNA
 <213> Homo sapiens

```

<400> 1265
accggtgtat gcaactgaaa tgctgtccga tatgcctgcg ctccagctcg tgaatcgaaa
60
gttggataac gctcgcttgg tggaatcgct gctacggaag cttatcaagg ataccggatgc
120
tgctgcaccg ccaaaattat ggacgcccc cgacccact cgctctgacg ataccattgc
180
acagccgaaa gtgcaaccag cccaagcagt gggagatgac tcgatcatgt cggtcgatga
240
gctgatgca accgtccatg acatgccact caccacgaca ctcgacaacg tgggtcgctc
300
agatccatcg cgacgcgt
318

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<210> 1266
 <211> 99
 <212> PRT
 <213> Homo sapiens

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<400> 1266
Met Leu Ser Asp Met Pro Ala Leu Gln Leu Val Asn Arg Lys Leu Asp
1      5      10      15
Asn Ala Arg Leu Val Glu Ser Ser Leu Arg Lys Leu Ile Lys Asp Thr
      20      25      30
Asp Ala Ala Ala Pro Pro Lys Leu Trp Thr Pro Pro Asp Pro Thr Arg
      35      40      45
Ser Asp Asp Thr Ile Ala Gln Pro Lys Val Gln Pro Ala Gln Ala Val
      50      55      60
Gly Asp Asp Ser Ile Met Ser Val Asp Glu Pro Asp Ala Thr Val His
      65      70      75      80
Asp Met Pro Leu Thr Thr Leu Asp Asn Val Gly Arg Ser Asp Pro
      85      90      95
Ser Arg Arg

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<210> 1267
 <211> 343

<212> DNA

<213> Homo sapiens

<400> 1267

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 120
 aacctgtgtt tttgttcccc ttgtgaacac tcgtgggaaa tgccccacaa cctgtgtttt
 180
 tattccccctt gtgaacactc gtgggaaatg tcccatggcc cgtgtttccg tgcacctgcg
 240
 gatactcatc aaacaccagg ctgtcattgg ggacaggggtg agctctggct gttggtgcag
 300
 catggttagga agagcaccaa gtccctggact ctgttgattt ata
 343

<210> 1268

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1268

Met	Pro	His	Ser	Leu	Cys	Phe	Tyr	Ser	Pro	Cys	Glu	His	Leu	Trp	Glu
1				5					10					15	
Leu	Ser	His	Gly	Pro	Cys	Phe	Cys	Ala	Pro	Ala	Asp	Thr	Arg	Gly	Lys
			20					25					30		
Cys	Pro	Thr	Thr	Cys	Val	Phe	Val	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
		35					40					45			
Cys	Pro	Thr	Thr	Cys	Val	Phe	Ile	Pro	Leu	Val	Asn	Thr	Arg	Gly	Lys
		50				55					60				
Cys	Pro	Met	Ala	Arg	Val	Ser	Val	His	Leu	Arg	Ile	Leu	Ile	Lys	His
65					70					75				80	
Gln	Ala	Val	Ile	Gly	Asp	Arg	Val	Ser	Ser	Gly	Cys	Trp	Cys	Ser	Met
			85					90						95	
Val	Gly	Arg	Ala	Pro	Ser	Pro	Gly	Leu	Cys						
			100					105							

<210> 1269

<211> 391

<212> DNA

<213> Homo sapiens

<400> 1269

tcgcgatccg gagcgatcgg tgctgcagat ggctggcgac gccctgcggg gcgcattgcg
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 ggacgccgac ctggagccgg ccgccctaga cgggctgac gtccaggtgg ggtccccccg
 120
 cggcgccgac tacgacaccg tgtccgaaac ctttggctct tcgccacaat tctgcagcca
 180
 gacctggggc gcacggccgg ttcaccgcaa cgggtgaccc ggcagcggcc atggcggtgt
 240
 ccagcggcct cgcgcggcgg gtggcttgcc tcatgggcat gaagaattcg gacctcgggc
 300

ggttgggtga ggcggacaat ccctttcatc atgagcaatt ccggggagaat ggcgggcccgc
 360
 acggggaaga gggttggatc ggcattggcct c
 391

<210> 1270
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 1270
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 1 5 10 15
 Leu His Ala His Glu Ala Ser His Pro Pro Arg Glu Ala Ala Gly His
 20 25 30
 Arg His Gly Arg Cys Gln Asp His Arg Cys Gly Glu Pro Ala Val Arg
 35 40 45
 Pro Arg Ser Gly Cys Arg Ile Val Ala Lys Asp Gln Arg Phe Arg Thr
 50 55 60
 Arg Cys Arg Ser Pro Arg Arg Gly Gly Thr Pro Pro Gly Arg Ser Ala
 65 70 75 80
 Arg Leu Gly Arg Pro Ala Pro Gly Arg Arg Pro Ala Met Arg Pro Ala
 85 90 95
 Gly Arg Arg Gln Pro Ser Ala Ala Pro Ile Ala Pro Asp Arg
 100 105 110

<210> 1271
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 1271
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 60
 accagaaagc gtcattcgagg tggatgaacga gaacgggcca tggatgtggtg ggacggataa
 120
 ccccggttg cgtcaccata tggcccaacta aagagttcac cagggttgat ttaccagccc
 180
 cggctgaccc tctaccacc gccagaagcg gcgcatcaat agtctctaag cgcggcaaaa
 240
 tatagtcggt aagctgggta gcatgcgctc gtgcccagccc ggcctgagta atagcctccg
 300
 gcaaatccaa ggggaactgg gcctgacgca ggttgtgccg cagatcggtc aacgacagca
 360
 gtattctgctc agtggtcatg gtgatccttc ctggtcactc gtcaggcctg tggcggcgcc
 420
 cactgcaact cgttggtgac cggctgggtg cgacgtcgct tgaggaatgc gggcagtctc
 480
 ggcttcgaca atttggcacc tggggcgacg gtgatagccg cggggcgag cacgttcata
 540
 cgggttgatga gctcgatctg aagcggacca ggatcatcgt ccaaccacg cacaatggcg
 600
 tcacgaagat aagcaagatc tgtccaacg cgcaggaact ctaacgtgtg ccaccaccgg
 660

t
661

<210> 1272
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1272
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Leu Arg Gln Ala Gln Phe Pro Leu Asp Leu Pro Glu Ala Ile Thr Gln
20 25 30
Ala Gly Leu Ala Arg Arg Ile Ala Asn Gln Leu Asn Asp Tyr Ile Leu
35 40 45
Pro Arg Leu Glu Thr Ile Asp Ala Pro Leu Leu Ala Val Val Gly Gly
50 55 60
Ser Thr Gly Ala Gly Lys Ser Thr Leu Val Asn Ser Leu Val Gly His
65 70 75 80
Met Val Thr Gln Pro Gly Val Ile Arg Pro Thr Thr Thr Ser Pro Val
85 90 95
Leu Val His His Pro Asp Asp Ala Phe Trp Phe Asp Gly Asp Arg Val
100 105 110
Leu Pro Thr Leu Val Arg Ser Gln Val Ala Ser Asn Asp Ala
115 120 125

<210> 1273
<211> 489
<212> DNA
<213> Homo sapiens

<400> 1273
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60
gacaaggctg aactggatt ggtccggcat ggctgcgatc gtgccgtcgt cgaagccggt
120
ctcgacacgc ctgatgccgg tcgctgcagc gagcttgccg gaacagtcga ggatgggtgag
180
gttatctgcg ctcgacacat cagagtcgt cgctctcgag cgctgcttgg aggagctcaa
240
gttaccgcta gtcagctggc ccacatcggt ggggatcagg tgaccatcca tggccaatct
300
gaacaagtga ggttggtcga cgcagcgcgg cagctcgacg tcgttgaccg ggctgccgga
360
gatgagctgg caggctacct aagtcgacat gcacagctgt ggtcggagtt tcgtgctgca
420
tccagcgtc ttcagcgct caacgaggat cgcgctgggg ccgagatgga acgcgaggtg
480
cttacgcgt
489

<210> 1274
<211> 163
<212> PRT